

Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly Gly Met Gln Ile Phe
65 70 75 80
Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu Val Glu Ser Ser
85 90 95
Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile
100 105 110
Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys Gln Leu Glu Asp
115 120 125
Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu Ser Thr Leu His
130 135 140
Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu Arg Lys Asp Phe
145 150 155 160
Asp Arg Lys Asp His His Ser
165

(2) INFORMATION FOR SEQ ID NO:1321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr Leu Glu
1 5 10 15
Val Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Asp Gly Arg Thr Leu Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Phe Ala Ser Ala Trp Arg Tyr Ala Asp Leu
65 70 75 80
Arg Lys Asp Phe Asp Arg Lys Asp His His Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

ctctcttcgt gtctgcgcac tcttcttctt cttcttcaat ggcttttcgcg tttgagaaac 60
cataaaagga aacttttcag agttttctct tgtctcctgt tcgtctccgt gccgtgtatg 120
tcactaaatt taggtttatc aatggagatg aaatgcacat ttcaatcaac tcgtgctcca 180
ttccaatgcg cttgggtggt cccaaattca atctattgga ctctcaaaga accaatcggt 240
ttgaaaatac ctaattcact tgcttctttg aggtctatca gacacttgga gttgaaatct 300
gtaggttcat tgtacaatgt gtttgagatt cataggaaag aagtcaattc aagtcttttg 360
gaagtgaag ctatgaacaa agatactgaa gctgatagtg atagtgatag gaagattaaa 420
gaagaggaaa ggagaaggaa gattggatta gctaataagag gaaagggtgcc atggaacaaa 480
gggaggaaac acagtgaaga cactcgaaga cgaatcaagc agagaacaat cgaagctttg 540
acaaatccca aggttcggaa gaagatgtcc gatcatcaac aaccacacag taatgaaacc 600
aaggagaaga taagagcttc agtgaaacaa gtttgggcag aacggtcaag atcgaagcga 660

ttaaaggaga	agttcatgtc	ttcgtgggtca	gaaaacattg	cagaagctgc	aaggaaagga	720
ggaagtggcg	aggcagaact	tgactgggac	agctatgaaa	gaataaaaca	agatttttca	780
tctgagcagc	ttcagtttagc	tgaagagaaa	gcaagagcta	aggaacaaac	caagatgata	840
gcaaaagaag	ctgcaaaagc	caggaccgag	aagatgagga	gagccgcaga	aaaaaagaaa	900
gaacgtgagg	agaaagaccg	acgagaagga	aagattcgaa	agccaaagca	ggaaagggag	960
aatccaacca	ttgcttcacg	ttctaaacta	aagaagagac	taacaaagat	tcacaagaag	1020
aaaacaagtc	ttggtaaaat	cgcaattgga	acggataggg	ttgtttcagt	tgacagctaaa	1080
ctggagaaac	tggatttgga	tttgataagg	aaagagcgaa	caagaggaga	tatctcactt	1140
gctgatcaga	tccaagctgc	taagaaccaa	cgaggaagtg	atgttttatc	gagatttggg	1200
ctttttgcca	tgaaatcaat	ggattttgat	taactctttt	ctactcctag	tttatagagc	1260
tttctctttt	tttttcttgt	gccactaaat	aaataaacia	gattgacttg	aggatataat	1320

aaataaatag attgacgc

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1500058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

Leu	Ser	Ser	Cys	Leu	Arg	Thr	Leu	Leu	Leu	Leu	Gln	Trp	Leu	Ser
1				5				10					15	
Arg	Leu	Arg	Asn	His	Lys	Arg	Lys	Leu	Phe	Arg	Val	Phe	Ser	Cys
			20					25					30	Leu
Leu	Phe	Val	Ser	Val	Pro	Cys	Met	Ser	Leu	Asn	Leu	Gly	Leu	Ser
		35					40					45		Met
Glu	Met	Lys	Cys	Thr	Phe	Gln	Ser	Thr	Arg	Ala	Pro	Phe	Gln	Cys
	50					55					60			Ala
Trp	Trp	Phe	Pro	Asn	Ser	Ile	Tyr	Trp	Thr	Leu	Lys	Glu	Pro	Ile
				70						75				80
Leu	Lys	Ile	Pro	Asn	Ser	Leu	Ala	Ser	Leu	Arg	Ser	Ile	Arg	His
				85				90					95	Leu
Glu	Leu	Lys	Ser	Val	Gly	Ser	Leu	Tyr	Asn	Val	Phe	Glu	Ile	His
			100					105					110	Arg
Lys	Glu	Val	Asn	Ser	Ser	Leu	Leu	Glu	Val	Lys	Ala	Met	Asn	Lys
		115					120					125		Asp
Thr	Glu	Ala	Asp	Ser	Asp	Ser	Asp	Arg	Lys	Ile	Lys	Glu	Glu	Glu
	130						135					140		Arg
Arg	Arg	Lys	Ile	Gly	Leu	Ala	Asn	Arg	Gly	Lys	Val	Pro	Trp	Asn
				150						155				160
Gly	Arg	Lys	His	Ser	Glu	Asp	Thr	Arg	Arg	Ile	Lys	Gln	Arg	Thr
				165				170					175	
Ile	Glu	Ala	Leu	Thr	Asn	Pro	Lys	Val	Arg	Lys	Lys	Met	Ser	Asp
		180					185						190	His
Gln	Gln	Pro	His	Ser	Asn	Glu	Thr	Lys	Glu	Lys	Ile	Arg	Ala	Ser
		195					200					205		Val
Lys	Gln	Val	Trp	Ala	Glu	Arg	Ser	Arg	Ser	Lys	Arg	Leu	Lys	Glu
		210					215				220			Lys
Phe	Met	Ser	Ser	Trp	Ser	Glu	Asn	Ile	Ala	Glu	Ala	Ala	Arg	Lys
				230						235				240
Gly	Ser	Gly	Glu	Ala	Glu	Leu	Asp	Trp	Asp	Ser	Tyr	Glu	Arg	Ile
				245					250					255
Gln	Asp	Phe	Ser	Ser	Glu	Gln	Leu	Gln	Leu	Ala	Glu	Glu	Lys	Ala
			260					265					270	Arg
Ala	Lys	Glu	Gln	Thr	Lys	Met	Ile	Ala	Lys	Glu	Ala	Ala	Lys	Ala
		275					280					285		Arg
Thr	Glu	Lys	Met	Arg	Arg	Ala	Ala	Glu	Lys	Lys	Lys	Glu	Arg	Glu

Met	Ser	Leu	Asn	Leu	Gly	Leu	Ser	Met	Glu	Met	Lys	Cys	Thr	Phe	Gln
1				5					10					15	
Ser	Thr	Arg	Ala	Pro	Phe	Gln	Cys	Ala	Trp	Trp	Phe	Pro	Asn	Ser	Ile
			20					25					30		
Tyr	Trp	Thr	Leu	Lys	Glu	Pro	Ile	Val	Leu	Lys	Ile	Pro	Asn	Ser	Leu
			35				40					45			
Ala	Ser	Leu	Arg	Ser	Ile	Arg	His	Leu	Glu	Leu	Lys	Ser	Val	Gly	Ser
	50					55					60				
Leu	Tyr	Asn	Val	Phe	Glu	Ile	His	Arg	Lys	Glu	Val	Asn	Ser	Ser	Leu
65					70					75					80
Leu	Glu	Val	Lys	Ala	Met	Asn	Lys	Asp	Thr	Glu	Ala	Asp	Ser	Asp	Ser
				85					90					95	
Asp	Arg	Lys	Ile	Lys	Glu	Glu	Glu	Arg	Arg	Arg	Lys	Ile	Gly	Leu	Ala
			100					105					110		
Asn	Arg	Gly	Lys	Val	Pro	Trp	Asn	Lys	Gly	Arg	Lys	His	Ser	Glu	Asp
			115				120					125			
Thr	Arg	Arg	Arg	Ile	Lys	Gln	Arg	Thr	Ile	Glu	Ala	Leu	Thr	Asn	Pro
						135					140				
Lys	Val	Arg	Lys	Lys	Met	Ser	Asp	His	Gln	Gln	Pro	His	Ser	Asn	Glu
145					150					155					160
Thr	Lys	Glu	Lys	Ile	Arg	Ala	Ser	Val	Lys	Gln	Val	Trp	Ala	Glu	Arg
				165					170					175	
Ser	Arg	Ser	Lys	Arg	Leu	Lys	Glu	Lys	Phe	Met	Ser	Ser	Trp	Ser	Glu
			180					185					190		
Asn	Ile	Ala	Glu	Ala	Ala	Arg	Lys	Gly	Gly	Ser	Gly	Glu	Ala	Glu	Leu
			195				200					205			
Asp	Trp	Asp	Ser	Tyr	Glu	Arg	Ile	Lys	Gln	Asp	Phe	Ser	Ser	Glu	Gln
	210					215					220				
Leu	Gln	Leu	Ala	Glu	Glu	Lys	Ala	Arg	Ala	Lys	Glu	Gln	Thr	Lys	Met
225					230					235					240
Ile	Ala	Lys	Glu	Ala	Ala	Lys	Ala	Arg	Thr	Glu	Lys	Met	Arg	Arg	Ala
				245					250					255	
Ala	Glu	Lys	Lys	Lys	Glu	Arg	Glu	Glu	Lys	Asp	Arg	Arg	Glu	Gly	Lys
			260					265					270		

Ile Arg Lys Pro Lys Gln Glu Arg Glu Asn Pro Thr Ile Ala Ser Arg
275 280 285
Ser Lys Leu Lys Lys Arg Leu Thr Lys Ile His Lys Lys Lys Thr Ser
290 295 300
Leu Gly Lys Ile Ala Ile Gly Thr Asp Arg Val Val Ser Val Ala Ala
305 310 315 320
Lys Leu Glu Lys Leu Asp Leu Asp Leu Ile Arg Lys Glu Arg Thr Arg
325 330 335
Gly Asp Ile Ser Leu Ala Asp Gln Ile Gln Ala Ala Lys Asn Gln Arg
340 345 350
Gly Ser Asp Val Leu Ser Arg Phe Gly Leu Phe Ala Met Lys Ser Met
355 360 365
Asp Phe Asp
370

(2) INFORMATION FOR SEQ ID NO:1325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

Met Glu Met Lys Cys Thr Phe Gln Ser Thr Arg Ala Pro Phe Gln Cys
1 5 10 15
Ala Trp Trp Phe Pro Asn Ser Ile Tyr Trp Thr Leu Lys Glu Pro Ile
20 25 30
Val Leu Lys Ile Pro Asn Ser Leu Ala Ser Leu Arg Ser Ile Arg His
35 40 45
Leu Glu Leu Lys Ser Val Gly Ser Leu Tyr Asn Val Phe Glu Ile His
50 55 60
Arg Lys Glu Val Asn Ser Ser Leu Leu Glu Val Lys Ala Met Asn Lys
65 70 75 80
Asp Thr Glu Ala Asp Ser Asp Ser Asp Arg Lys Ile Lys Glu Glu Glu
85 90 95
Arg Arg Arg Lys Ile Gly Leu Ala Asn Arg Gly Lys Val Pro Trp Asn
100 105 110
Lys Gly Arg Lys His Ser Glu Asp Thr Arg Arg Arg Ile Lys Gln Arg
115 120 125
Thr Ile Glu Ala Leu Thr Asn Pro Lys Val Arg Lys Lys Met Ser Asp
130 135 140
His Gln Gln Pro His Ser Asn Glu Thr Lys Glu Lys Ile Arg Ala Ser
145 150 155 160
Val Lys Gln Val Trp Ala Glu Arg Ser Arg Ser Lys Arg Leu Lys Glu
165 170 175
Lys Phe Met Ser Ser Trp Ser Glu Asn Ile Ala Glu Ala Ala Arg Lys
180 185 190
Gly Gly Ser Gly Glu Ala Glu Leu Asp Trp Asp Ser Tyr Glu Arg Ile
195 200 205
Lys Gln Asp Phe Ser Ser Glu Gln Leu Gln Leu Ala Glu Glu Lys Ala
210 215 220
Arg Ala Lys Glu Gln Thr Lys Met Ile Ala Lys Glu Ala Ala Lys Ala
225 230 235 240
Arg Thr Glu Lys Met Arg Arg Ala Ala Glu Lys Lys Lys Glu Arg Glu
245 250 255
Glu Lys Asp Arg Arg Glu Gly Lys Ile Arg Lys Pro Lys Gln Glu Arg
260 265 270
Glu Asn Pro Thr Ile Ala Ser Arg Ser Lys Leu Lys Lys Arg Leu Thr

275 280 285
Lys Ile His Lys Lys Lys Thr Ser Leu Gly Lys Ile Ala Ile Gly Thr
290 295 300
Asp Arg Val Val Ser Val Ala Ala Lys Leu Glu Lys Leu Asp Leu Asp
305 310 315 320
Leu Ile Arg Lys Glu Arg Thr Arg Gly Asp Ile Ser Leu Ala Asp Gln
325 330 335
Ile Gln Ala Ala Lys Asn Gln Arg Gly Ser Asp Val Leu Ser Arg Phe
340 345 350
Gly Leu Phe Ala Met Lys Ser Met Asp Phe Asp
355 360

(2) INFORMATION FOR SEQ ID NO:1326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

```
ccaattctaa accaaacaac agattctcat aatcatctct tcttttttcc tctttacgaa      60
aagaagaaag atcaaaccctt ccaagtaatc attttctttc tctctctcac acacacacat      120
tcaactagttt tagcttcaca aaatgtgatc taacttcatt tacctatatg cagggtttaca      180
caaaaagaaa aaagaacgat ggctcttgct accttcttgt ttattgctac ccttggagca      240
atgacgtcac atgtcaatgg ttacgccgga ggaggttggg tcaacgcaca cgccacattc      300
tacggtggtg gtgatgcttc cggcacaatg ggaggtgctt gtggatacgg aaacctatat      360
agccaaggct atggaaccaa cacggcggcg ctaagcacgg ctctattcaa taatggtcta      420
agttgtggtg cttgcttcga gataagatgt caaaacgatg gaaaatggtg tcttcctggc      480
tcaattgtcg tcacagccac aaacttttgc cctcctaaca acgccttacc gaacaacgca      540
ggaggtttgg tgtaaccctc ctcagcagca ttttgatctc tctcagcccg tatttcaacg      600
catcgctcaa tacagagccg gcattgtccc cgctcgcttac cgaagagtgc cgtgcgtgag      660
aagaggagga atacgtttac gataaacgga cactcttact tcaacctagt tctgattact      720
aacgtcggag gagccggaga tgttctacta gcgatggtta aagggttcaag aactggatgg      780
caagcgatgt caagaaactg gggacagaac tggcagagta actcttacct taacggacaa      840
tctctgtcat tcaaagtcac aacaagcgat ggccaaacca ttgtctctaa caacgtcgct      900
aacgcaggct ggtcttttgg ccagaccttc accggtgcgc agctacgtta ggaagagtga      960
ttcggtgaaa attcatctca ttgatcgtgt ggtattgacg tggtgtagta gaagcagtta     1020
gagagagggg catgatagta atttggctct tcttttcaat tgaggtttac ctaaaaagaa     1080
gtggtgcttc gagtgcctga ttttgacga ggccttgatg atgtcatctt ttgggaacct     1140
tttcttatct ttcttcattt ttattggtaa ggttttatgt tatactgatg cagaggtggg     1200
attgagttga agtaccaccc gctagtagta gtagtctctc atgtcatttg tatcccttct     1260
cgaagcgaga gggagagttt tagattttta ttaatctcgt taaagtcatt tgtatgttgt     1320
aaatttttca atttctacaa gtaagaaata ttggagattt gtttggt
```

(2) INFORMATION FOR SEQ ID NO:1327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

Met Ala Leu Val Thr Phe Leu Phe Ile Ala Thr Leu Gly Ala Met Thr
1 5 10 15
Ser His Val Asn Gly Tyr Ala Gly Gly Gly Trp Val Asn Ala His Ala

20 25 30
Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly Ala Cys
35 40 45
Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala
50 55 60
Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe
65 70 75 80
Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly Ser Ile
85 90 95
Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn
100 105 110
Asn Ala Gly Gly Leu Val
115

(2) INFORMATION FOR SEQ ID NO:1328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

Met Thr Ser His Val Asn Gly Tyr Ala Gly Gly Gly Trp Val Asn Ala
1 5 10 15
His Ala Thr Phe Tyr Gly Gly Gly Asp Ala Ser Gly Thr Met Gly Gly
20 25 30
Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr
35 40 45
Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala
50 55 60
Cys Phe Glu Ile Arg Cys Gln Asn Asp Gly Lys Trp Cys Leu Pro Gly
65 70 75 80
Ser Ile Val Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Asn Ala Leu
85 90 95
Pro Asn Asn Ala Gly Gly Leu Val
100

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

Met Phe Thr Gln Arg Trp Leu Lys Val Gln Glu Leu Asp Gly Lys Arg
1 5 10 15
Cys Gln Glu Thr Gly Asp Arg Thr Gly Arg Val Thr Leu Thr Leu Thr
20 25 30
Asp Asn Leu Cys His Ser Lys Ser Gln Gln Ala Met Ala Lys Pro Leu
35 40 45
Ser Leu Thr Thr Ser Leu Thr Gln Ala Gly Leu Leu Ala Arg Pro Ser
50 55 60
Pro Val Arg Ser Tyr Val Arg Lys Ser Asp Ser Val Lys Ile His Leu
65 70 75 80

Ile Asp Arg Val Val Leu Thr Cys Cys Ser Arg Ser Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

```
aagattttatt ataaactcct ttttttttta aattcaagag atatcaaaca actacttcat      60
tttttttttt ttgtagcagc cgagtacttt tttttgacgg tgtccgtggt cgtgcttggt      120
ctgaaattga cgaaaaatat tccgacaaga caacaacaac aattagagag attcagacaa      180
gggatttgaa attcggagga tgtttgggat ccaaagcaga cgtgatttaa cgatggagct      240
acaatctcag attccgattc tccgtccaag catccacgca agacgagcca acatcgtcgt      300
taaattccag gacttgtacg gtttcacggt ggaaggaaat gtcgacgacg ttaatgtggt      360
gaacgagggt agagagaaaag tcaggaatca aggacgagtt tgggtgggctc ttgaagctag      420
caaaggagct aattggtatc ttcagccgga gattctcttg atcggtgacg gtatcgcttt      480
gaaaacttct ctcaagctct ccactttgac taatgcgatt acggtgaaga gattgattcg      540
gaaagggatc cctcctgtgc ttagacctaa ggtttggttt tctctttctg gtgctgctaa      600
gaagaaatcc accgtcccag agagttatta tagtgatttg accaaagccg tcgaagggat      660
ggtcacgccg gctacgaggc agattgatca tgatctgcca cgtactttcc caggccatcc      720
atggttgagc actccggaag gtcattgctg tctacgacgt gtgcttggtt ggtattcctt      780
tcgtgattca gatgttggct attgtcaggg tctaaactac gttgcagcgt tactattact      840
tgtcatgaag acagaagaag acgcattctg gatgctagcg gtccttttgg aaaacgtatt      900
agtcctgtat tgttacacaa ccaacttatc tggatgtcat gttgagcagc gggttttcaa      960
agatttgctt gcccaaaaat gttctcgaat agctactcat cttgaagata tgggctttga     1020
tgtttccctt gtagccactg aatggtttct atgcctcttc tctaaaagcc ttccttcaga     1080
gacaactcta aggggtgtgg atgtactttt ctatgaagga gcgaagggtc tattccatgc     1140
agcttttagc atattcaaga tgaaagagaa cgagctgctt atgaccacc aggtcggcga     1200
tgttatcaac dtattacaga aaacttcaca ccagcttttt gaccgggatg aattattaac     1260
ggtggcattt gagaaaatcg gatcaatgac taccaacacg atatcaaagc agaggaagaa     1320
gcaggaacca gcagtgatgg cagaacttga ccagagactt cggagactta actctcttaa     1380
agaaagtggg aagagcacat aaataaaaaa gaactgttgg gagaagatga gccaaaaagt     1440
gcaaacgagg gagtccaaca atggtttatt tatccctctt gatgtttttt tttttttttc     1500
ctttttttct aagtatatat aaataggatt ttttaagttt attttgagag caaaacatta     1560
accaagatcc atttctgaga tgggaaatgt caagtttctt cacattccaa gaggtgtcac     1620
ttgccttttg cattttttac ccctcttcat atatcaattg tgatcttcat gttttt
```

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..400
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

```
Met Phe Gly Ile Gln Ser Arg Arg Asp Leu Thr Met Glu Leu Gln Ser
1           5           10           15
Gln Ile Pro Ile Leu Arg Pro Ser Ile His Ala Arg Arg Ala Asn Ile
20           25           30
Val Val Lys Phe Gln Asp Leu Tyr Gly Phe Thr Val Glu Gly Asn Val
35           40           45
Asp Asp Val Asn Val Leu Asn Glu Val Arg Glu Lys Val Arg Asn Gln
```

50	55	60
Gly Arg Val Trp Trp	Ala Leu Glu Ala Ser Lys	Gly Ala Asn Trp Tyr
65	70	75
Leu Gln Pro Glu Ile	Leu Leu Ile Gly Asp Gly	Ile Ala Leu Lys Thr
85	90	95
Ser Leu Lys Leu Ser	Thr Leu Thr Asn Ala Ile	Thr Leu Lys Arg Leu
100	105	110
Ile Arg Lys Gly Ile	Pro Pro Val Leu Arg	Pro Lys Val Trp Phe Ser
115	120	125
Leu Ser Gly Ala Ala	Lys Lys Lys Ser Thr	Val Pro Glu Ser Tyr Tyr
130	135	140
Ser Asp Leu Thr Lys	Ala Val Glu Gly Met	Val Thr Pro Ala Thr Arg
145	150	155
Gln Ile Asp His Asp	Leu Pro Arg Thr Phe	Pro Gly His Pro Trp Leu
165	170	175
Asp Thr Pro Glu Gly	His Ala Ala Leu Arg	Arg Val Leu Val Gly Tyr
180	185	190
Ser Phe Arg Asp Ser	Asp Val Gly Tyr Cys	Gln Gly Leu Asn Tyr Val
195	200	205
Ala Ala Leu Leu Leu	Leu Val Met Lys Thr	Glu Glu Asp Ala Phe Trp
210	215	220
Met Leu Ala Val Leu	Leu Glu Asn Val Leu	Val Arg Asp Cys Tyr Thr
225	230	235
Thr Asn Leu Ser Gly	Cys His Val Glu Gln	Arg Val Phe Lys Asp Leu
245	250	255
Leu Ala Gln Lys Cys	Ser Arg Ile Ala Thr	His Leu Glu Asp Met Gly
260	265	270
Phe Asp Val Ser Leu	Val Ala Thr Glu Trp	Phe Leu Cys Leu Phe Ser
275	280	285
Lys Ser Leu Pro Ser	Glu Thr Leu Arg Val	Trp Asp Val Leu Phe
290	295	300
Tyr Glu Gly Ala Lys	Val Leu Phe His Ala	Ala Leu Ala Ile Phe Lys
305	310	315
Met Lys Glu Asn Glu	Leu Leu Met Thr His	Gln Val Gly Asp Val Ile
325	330	335
Asn Xaa Leu Gln Lys	Thr Ser His Gln Leu	Phe Asp Pro Asp Glu Leu
340	345	350
Leu Thr Val Ala Phe	Glu Lys Ile Gly Ser	Met Thr Thr Asn Thr Ile
355	360	365
Ser Lys Gln Arg Lys	Lys Gln Glu Pro Ala	Val Met Ala Glu Leu Asp
370	375	380
Gln Arg Leu Arg Arg	Leu Asn Ser Leu Lys	Glu Ser Gly Lys Ser Thr
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1500071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

Met	Glu	Leu	Gln	Ser	Gln	Ile	Pro	Ile	Leu	Arg	Pro	Ser	Ile	His	Ala
1			5				10						15		
Arg	Arg	Ala	Asn	Ile	Val	Val	Lys	Phe	Gln	Asp	Leu	Tyr	Gly	Phe	Thr
		20					25						30		

```

Val Glu Gly Asn Val Asp Asp Val Asn Val Leu Asn Glu Val Arg Glu
      35              40              45
Lys Val Arg Asn Gln Gly Arg Val Trp Trp Ala Leu Glu Ala Ser Lys
      50              55              60
Gly Ala Asn Trp Tyr Leu Gln Pro Glu Ile Leu Leu Ile Gly Asp Gly
65      70              75              80
Ile Ala Leu Lys Thr Ser Leu Lys Leu Ser Thr Leu Thr Asn Ala Ile
      85              90              95
Thr Leu Lys Arg Leu Ile Arg Lys Gly Ile Pro Pro Val Leu Arg Pro
      100             105             110
Lys Val Trp Phe Ser Leu Ser Gly Ala Ala Lys Lys Lys Ser Thr Val
      115             120             125
Pro Glu Ser Tyr Tyr Ser Asp Leu Thr Lys Ala Val Glu Gly Met Val
      130             135             140
Thr Pro Ala Thr Arg Gln Ile Asp His Asp Leu Pro Arg Thr Phe Pro
145      150             155             160
Gly His Pro Trp Leu Asp Thr Pro Glu Gly His Ala Ala Leu Arg Arg
      165             170             175
Val Leu Val Gly Tyr Ser Phe Arg Asp Ser Asp Val Gly Tyr Cys Gln
      180             185             190
Gly Leu Asn Tyr Val Ala Ala Leu Leu Leu Val Met Lys Thr Glu
      195             200             205
Glu Asp Ala Phe Trp Met Leu Ala Val Leu Leu Glu Asn Val Leu Val
      210             215             220
Arg Asp Cys Tyr Thr Thr Asn Leu Ser Gly Cys His Val Glu Gln Arg
225      230             235             240
Val Phe Lys Asp Leu Leu Ala Gln Lys Cys Ser Arg Ile Ala Thr His
      245             250             255
Leu Glu Asp Met Gly Phe Asp Val Ser Leu Val Ala Thr Glu Trp Phe
      260             265             270
Leu Cys Leu Phe Ser Lys Ser Leu Pro Ser Glu Thr Thr Leu Arg Val
      275             280             285
Trp Asp Val Leu Phe Tyr Glu Gly Ala Lys Val Leu Phe His Ala Ala
290      295             300
Leu Ala Ile Phe Lys Met Lys Glu Asn Glu Leu Leu Met Thr His Gln
305      310             315             320
Val Gly Asp Val Ile Asn Xaa Leu Gln Lys Thr Ser His Gln Leu Phe
      325             330             335
Asp Pro Asp Glu Leu Leu Thr Val Ala Phe Glu Lys Ile Gly Ser Met
      340             345             350
Thr Thr Asn Thr Ile Ser Lys Gln Arg Lys Lys Gln Glu Pro Ala Val
      355             360             365
Met Ala Glu Leu Asp Gln Arg Leu Arg Arg Leu Asn Ser Leu Lys Glu
370      375             380
Ser Gly Lys Ser Thr
385

```

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

```

Met Val Thr Pro Ala Thr Arg Gln Ile Asp His Asp Leu Pro Arg Thr
1           5           10           15
Phe Pro Gly His Pro Trp Leu Asp Thr Pro Glu Gly His Ala Ala Leu

```

20				25				30							
Arg	Arg	Val	Leu	Val	Gly	Tyr	Ser	Phe	Arg	Asp	Ser	Asp	Val	Gly	Tyr
		35					40					45			
Cys	Gln	Gly	Leu	Asn	Tyr	Val	Ala	Ala	Leu	Leu	Leu	Leu	Val	Met	Lys
	50					55					60				
Thr	Glu	Glu	Asp	Ala	Phe	Trp	Met	Leu	Ala	Val	Leu	Leu	Glu	Asn	Val
65					70					75				80	
Leu	Val	Arg	Asp	Cys	Tyr	Thr	Thr	Asn	Leu	Ser	Gly	Cys	His	Val	Glu
				85				90					95		
Gln	Arg	Val	Phe	Lys	Asp	Leu	Leu	Ala	Gln	Lys	Cys	Ser	Arg	Ile	Ala
			100					105					110		
Thr	His	Leu	Glu	Asp	Met	Gly	Phe	Asp	Val	Ser	Leu	Val	Ala	Thr	Glu
		115						120				125			
Trp	Phe	Leu	Cys	Leu	Phe	Ser	Lys	Ser	Leu	Pro	Ser	Glu	Thr	Thr	Leu
	130					135					140				
Arg	Val	Trp	Asp	Val	Leu	Phe	Tyr	Glu	Gly	Ala	Lys	Val	Leu	Phe	His
145					150					155				160	
Ala	Ala	Leu	Ala	Ile	Phe	Lys	Met	Lys	Glu	Asn	Glu	Leu	Leu	Met	Thr
				165				170						175	
His	Gln	Val	Gly	Asp	Val	Ile	Asn	Xaa	Leu	Gln	Lys	Thr	Ser	His	Gln
		180					185					190			
Leu	Phe	Asp	Pro	Asp	Glu	Leu	Leu	Thr	Val	Ala	Phe	Glu	Lys	Ile	Gly
		195					200					205			
Ser	Met	Thr	Thr	Asn	Thr	Ile	Ser	Lys	Gln	Arg	Lys	Lys	Gln	Glu	Pro
	210					215					220				
Ala	Val	Met	Ala	Glu	Leu	Asp	Gln	Arg	Leu	Arg	Arg	Leu	Asn	Ser	Leu
225					230				235					240	
Lys	Glu	Ser	Gly	Lys	Ser	Thr									
					245										

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1674
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

agatgtaatt	tgtataattt	tagtaactct	tcagtttttt	tttgttttta	aaatatattt	60
tctctctctc	tgtcttctcg	caatctatcg	ccggccgatt	caataatttc	gctttactct	120
gccaaaaaag	tttgttcttt	tgttttctgg	gattatccaa	agagaagaaa	cagaggaaat	180
cagtctcttt	tttagtttca	gaccctaaat	cctagggttt	gaagttttgt	ttctttagta	240
attttgtcag	gttttgtgtc	tggtgttggg	atttttcgga	gcttggtttc	ttgaaccagc	300
tccattttct	aaaaattcct	tcitttaaatt	cccattgttg	taagtcttaa	agaaaaaaga	360
agatgacttg	ttgtttctct	tgtttgaatc	ctcgaaccaa	ggacataaga	gtcgacattg	420
ataacgctcg	atgcaactct	cgttaccaaa	ccgattcatc	agttcatgga	agtatacaaa	480
caggaacaga	gtcgatttct	ggatatcttg	taaatggtaa	agtgaatagt	ccgataacct	540
gtgggtggagc	tcggagcttc	acgttcaagg	agttagctgc	agctacaaga	aacttccggg	600
aagttaattt	gctcggagaa	ggagggtttg	gcagagttta	taagggacgt	ttagattcag	660
gacaagtagt	ggctattaag	caattgaatc	cagatgggct	tcaagggaa	cagaggttta	720
tagtagaagt	tcttatgctt	agcttattgc	atcatcccaa	tctcgttaca	ttgatcggtt	780
actgtacttc	tggtgatcaa	agacttcttg	tctatgaata	catgccaatg	ggaagcttag	840
aagatcacct	ttttgatctt	gagtcataat	aagaaccatt	aagctggaat	actcgaatga	900
aaatcgcggt	tggtgcagct	cgaggaatag	agtatcttca	ctgcacagct	aacctcgccag	960
tgatttaccg	tgatttgaaa	tccgcaaaca	tattgttaga	taaagagttc	agtccaaaac	1020
tctcggattt	cggattggcg	aaactcggtc	cagttgggtg	tcgaactcat	gtatcgactc	1080
gtgtcatggg	aacttacggt	tactgtgctc	ctgaatacgc	aatgagcggg	aaattaactg	1140
ttaaactcga	tatctactgc	ttcgggtgtg	tggtgcttga	gctgattact	gggagaaaaa	1200

```
ctattgattt aggtcaaaag caaggcgagc agaatcttgt tacttgggtca cgtccataacc 1260
tcaaggatca gaagaagttt ggacatttag tggatccgtc tctacgagga aaatacccaa 1320
gacgggtgtt aaactatgcg attgctgatta ttgcaatgtg tcttaatgaa gaagctcatt 1380
atcgaccgtt cataggtgac atagttgttg cactagagta cttagccgca cagagcagat 1440
ctcatgaagc tcgaaacgtc tcatcaccgt caccagagat ttcaagaacg ccgcgacgag 1500
acttgtaaaa actcaaaaac agctttttaag aatttcagtt tgggtgttgtg taaaaatggt 1560
ttttttgttt cttttctcaga aaacaatata tgtttggttaa atgtttcgtt attagtctct 1620
tttacttgat gtatatggca attatggaaa caattaaagt tcttttatat gtgt
```

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1500074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

```
Met Thr Cys Cys Phe Ser Cys Leu Asn Pro Arg Thr Lys Asp Ile Arg
1          5          10          15
Val Asp Ile Asp Asn Ala Arg Cys Asn Ser Arg Tyr Gln Thr Asp Ser
20          25          30
Ser Val His Gly Ser Asp Thr Thr Gly Thr Glu Ser Ile Ser Gly Ile
35          40          45
Leu Val Asn Gly Lys Val Asn Ser Pro Ile Pro Gly Gly Gly Ala Arg
50          55          60
Ser Phe Thr Phe Lys Glu Leu Ala Ala Ala Thr Arg Asn Phe Arg Glu
65          70          75          80
Val Asn Leu Leu Gly Glu Gly Gly Phe Gly Arg Val Tyr Lys Gly Arg
85          90          95
Leu Asp Ser Gly Gln Val Val Ala Ile Lys Gln Leu Asn Pro Asp Gly
100         105         110
Leu Gln Gly Asn Arg Glu Phe Ile Val Glu Val Leu Met Leu Ser Leu
115         120         125
Leu His His Pro Asn Leu Val Thr Leu Ile Gly Tyr Cys Thr Ser Gly
130         135         140
Asp Gln Arg Leu Leu Val Tyr Glu Tyr Met Pro Met Gly Ser Leu Glu
145         150         155         160
Asp His Leu Phe Asp Leu Glu Ser Asn Gln Glu Pro Leu Ser Trp Asn
165         170         175
Thr Arg Met Lys Ile Ala Val Gly Ala Ala Arg Gly Ile Glu Tyr Leu
180         185         190
His Cys Thr Ala Asn Pro Pro Val Ile Tyr Arg Asp Leu Lys Ser Ala
195         200         205
Asn Ile Leu Leu Asp Lys Glu Phe Ser Pro Lys Leu Ser Asp Phe Gly
210         215         220
Leu Ala Lys Leu Gly Pro Val Gly Asp Arg Thr His Val Ser Thr Arg
225         230         235         240
Val Met Gly Thr Tyr Gly Tyr Cys Ala Pro Glu Tyr Ala Met Ser Gly
245         250         255
Lys Leu Thr Val Lys Ser Asp Ile Tyr Cys Phe Gly Val Val Leu Leu
260         265         270
Glu Leu Ile Thr Gly Arg Lys Ala Ile Asp Leu Gly Gln Lys Gln Gly
275         280         285
Glu Gln Asn Leu Val Thr Trp Ser Arg Pro Tyr Leu Lys Asp Gln Lys
290         295         300
Lys Phe Gly His Leu Val Asp Pro Ser Leu Arg Gly Lys Tyr Pro Arg
305         310         315         320
Arg Cys Leu Asn Tyr Ala Ile Ala Ile Ile Ala Met Cys Leu Asn Glu
```

	325		330		335										
Glu	Ala	His	Tyr	Arg	Pro	Phe	Ile	Gly	Asp	Ile	Val	Val	Ala	Leu	Glu
	340							345					350		
Tyr	Leu	Ala	Ala	Gln	Ser	Arg	Ser	His	Glu	Ala	Arg	Asn	Val	Ser	Ser
	355						360					365			
Pro	Ser	Pro	Glu	Ile	Ser	Arg	Thr	Pro	Arg	Arg	Asp	Leu			
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

Met	Leu	Ser	Leu	Leu	His	His	Pro	Asn	Leu	Val	Thr	Leu	Ile	Gly	Tyr
1			5					10						15	
Cys	Thr	Ser	Gly	Asp	Gln	Arg	Leu	Leu	Val	Tyr	Glu	Tyr	Met	Pro	Met
			20				25						30		
Gly	Ser	Leu	Glu	Asp	His	Leu	Phe	Asp	Leu	Glu	Ser	Asn	Gln	Glu	Pro
			35				40					45			
Leu	Ser	Trp	Asn	Thr	Arg	Met	Lys	Ile	Ala	Val	Gly	Ala	Ala	Arg	Gly
			50				55				60				
Ile	Glu	Tyr	Leu	His	Cys	Thr	Ala	Asn	Pro	Pro	Val	Ile	Tyr	Arg	Asp
65					70				75					80	
Leu	Lys	Ser	Ala	Asn	Ile	Leu	Leu	Asp	Lys	Glu	Phe	Ser	Pro	Lys	Leu
				85					90					95	
Ser	Asp	Phe	Gly	Leu	Ala	Lys	Leu	Gly	Pro	Val	Gly	Asp	Arg	Thr	His
			100					105					110		
Val	Ser	Thr	Arg	Val	Met	Gly	Thr	Tyr	Gly	Tyr	Cys	Ala	Pro	Glu	Tyr
			115				120					125			
Ala	Met	Ser	Gly	Lys	Leu	Thr	Val	Lys	Ser	Asp	Ile	Tyr	Cys	Phe	Gly
			130				135				140				
Val	Val	Leu	Leu	Glu	Leu	Ile	Thr	Gly	Arg	Lys	Ala	Ile	Asp	Leu	Gly
145					150					155				160	
Gln	Lys	Gln	Gly	Glu	Gln	Asn	Leu	Val	Thr	Trp	Ser	Arg	Pro	Tyr	Leu
				165					170					175	
Lys	Asp	Gln	Lys	Lys	Phe	Gly	His	Leu	Val	Asp	Pro	Ser	Leu	Arg	Gly
			180					185					190		
Lys	Tyr	Pro	Arg	Arg	Cys	Leu	Asn	Tyr	Ala	Ile	Ala	Ile	Ile	Ala	Met
			195				200					205			
Cys	Leu	Asn	Glu	Glu	Ala	His	Tyr	Arg	Pro	Phe	Ile	Gly	Asp	Ile	Val
			210				215				220				
Val	Ala	Leu	Glu	Tyr	Leu	Ala	Ala	Gln	Ser	Arg	Ser	His	Glu	Ala	Arg
225					230					235				240	
Asn	Val	Ser	Ser	Pro	Ser	Pro	Glu	Ile	Ser	Arg	Thr	Pro	Arg	Arg	Asp
				245					250					255	

Leu

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..228
(D) OTHER INFORMATION: / Ceres Seq. ID 1500076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

```
Met Pro Met Gly Ser Leu Glu Asp His Leu Phe Asp Leu Glu Ser Asn
1          5          10          15
Gln Glu Pro Leu Ser Trp Asn Thr Arg Met Lys Ile Ala Val Gly Ala
20          25          30
Ala Arg Gly Ile Glu Tyr Leu His Cys Thr Ala Asn Pro Pro Val Ile
35          40          45
Tyr Arg Asp Leu Lys Ser Ala Asn Ile Leu Leu Asp Lys Glu Phe Ser
50          55          60
Pro Lys Leu Ser Asp Phe Gly Leu Ala Lys Leu Gly Pro Val Gly Asp
65          70          75          80
Arg Thr His Val Ser Thr Arg Val Met Gly Thr Tyr Gly Tyr Cys Ala
85          90          95
Pro Glu Tyr Ala Met Ser Gly Lys Leu Thr Val Lys Ser Asp Ile Tyr
100         105         110
Cys Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Arg Lys Ala Ile
115         120         125
Asp Leu Gly Gln Lys Gln Gly Glu Gln Asn Leu Val Thr Trp Ser Arg
130         135         140
Pro Tyr Leu Lys Asp Gln Lys Lys Phe Gly His Leu Val Asp Pro Ser
145         150         155         160
Leu Arg Gly Lys Tyr Pro Arg Arg Cys Leu Asn Tyr Ala Ile Ala Ile
165         170         175
Ile Ala Met Cys Leu Asn Glu Glu Ala His Tyr Arg Pro Phe Ile Gly
180         185         190
Asp Ile Val Val Ala Leu Glu Tyr Leu Ala Ala Gln Ser Arg Ser His
195         200         205
Glu Ala Arg Asn Val Ser Ser Pro Ser Pro Glu Ile Ser Arg Thr Pro
210         215         220
Arg Arg Asp Leu
225
```

(2) INFORMATION FOR SEQ ID NO:1338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1690 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1690
(D) OTHER INFORMATION: / Ceres Seq. ID 1500077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

```
atcaataaac acaaaaaacaa aagaagaaga gaataaacaa aagaagaaaa aaaactaata      60
aaacaaaatc aataaaaaga gaataaaaaa tgggtgggttc tcacaaagca agcggagtgc      120
ttcttgtgct actagtgggt atggccacca caatagcaaa cgggacaccg gttgtcgata      180
aagcaaaaaa tgcagctaca gcagttgaag atacagcaaa aaatgcagct acagcagttg      240
gcggtgcagc tgcattcagtt ggtgctaaag tatcaggtgc caaaccaggc gcagcagttg      300
atgttaaagc atcaggagcc aaaggagacg gcaaaactga tgatagtgcg gcatttgcgg      360
ctgcatggaa agaagcttgt gcagcaggga gcacaattac agtgccaaaa ggtgagtata      420
tggtagagag cctagagttc aaagggtccat gcaaagggtcc agtcactttg gaattgaatg      480
gcaatttcaa ggctccggct acggtcaaga ccactaagcc acatgccgga tggattgatt      540
tcgaaaatat agctgatttc actttgaatg gaaacaaagc tatttttgac ggtcaagggt      600
ccctcgcttg gaaggccaat gattgtgccaa aaactggcaa atgcaactct ctccctatca      660
acatccgatt cactgggtcta acaaaactcaa agattaatag tattacatca acaaacagca      720
aacttttcca catgaacatc cttaactgca agaacattac tctttcggat attggtattg      780
atgcacctcc ggagagtctc aacaccgatg gtatccacat cggaagggtcc aatggagtca      840
acttaattgg ggcaaagatc aaaaccggag atgactgcgt ttccattgga gatggtaccg      900
```

```
aaaatctcat tgttgagaac gtagaatgtg gaccaggaca cggaatttcc attggaagtc 960
ttggaagata ccctaattgag caaccagtaa aaggagtcac cgtgaggaaa tgcctcatca 1020
agaacactga caatggtgtt cgcatacaaga catggccagg atctccccc ggcatcgctt 1080
ccaacattct tttcgaagat atcacaatgg acaatgttag ccttcccgtt ctcatacgacc 1140
aagagtactg tccttatggc cactgcaaaag ctgggggtacc atcgcaagtg aagttgtcag 1200
acgtgactat caagggcatt aagggtacat cagcaacaaa ggtggctgtg aagctaattgt 1260
gcagcaaagg agtgccttgc accaatattg ctctctctga catcaacttg gtccacaacg 1320
gcaaagaggg accagctgtc tcggcatgtt ctaacatcaa gcctattctc agcggaaagt 1380
tggttccagc ggcttgact gaagttgcta aaccgggtcc ataaattaaa gtcgcttgctc 1440
caccataaat ccatccaatc tggcgaagac gctttgatta ggggtgcgatg aaaaaatttt 1500
gcaatatttt tttgacatat aaattatatg gatattttat agataagacg gagtccattc 1560
aggattggag tttataacct gaagagtgcac tcgtgaattg ggtagtaatt gttgtgtgga 1620
ttcgcattta tgcgagaatg ttttaataat tattcgaaaa gtaataatat cattgaaatt 1680
ttgaagtttt
```

(2) INFORMATION FOR SEQ ID NO:1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

```
Met Val Gly Ser His Lys Ala Ser Gly Val Leu Leu Val Leu Leu Val
1          5          10          15
Val Met Ala Thr Thr Ile Ala Asn Gly Thr Pro Val Val Asp Lys Ala
20          25          30
Lys Asn Ala Ala Thr Ala Val Glu Asp Thr Ala Lys Asn Ala Ala Thr
35          40          45
Ala Val Gly Gly Ala Ala Ala Ser Val Gly Ala Lys Val Ser Gly Ala
50          55          60
Lys Pro Gly Ala Ala Val Asp Val Lys Ala Ser Gly Ala Lys Gly Asp
65          70          75          80
Gly Lys Thr Asp Asp Ser Ala Ala Phe Ala Ala Ala Trp Lys Glu Ala
85          90          95
Cys Ala Ala Gly Ser Thr Ile Thr Val Pro Lys Gly Glu Tyr Met Val
100          105          110
Glu Ser Leu Glu Phe Lys Gly Pro Cys Lys Gly Pro Val Thr Leu Glu
115          120          125
Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr Lys Pro
130          135          140
His Ala Gly Trp Ile Asp Phe Glu Asn Ile Ala Asp Phe Thr Leu Asn
145          150          155          160
Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp Lys Ala
165          170          175
Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile Asn Ile
180          185          190
Arg Phe Thr Gly Leu Thr Asn Ser Lys Ile Asn Ser Ile Thr Ser Thr
195          200          205
Asn Ser Lys Leu Phe His Met Asn Ile Leu Asn Cys Lys Asn Ile Thr
210          215          220
Leu Ser Asp Ile Gly Ile Asp Ala Pro Pro Glu Ser Leu Asn Thr Asp
225          230          235          240
Gly Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly Ala Lys
245          250          255
Ile Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr Glu Asn
260          265          270
Leu Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile Ser Ile
```

275	280	285
Gly Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly Val Thr		
290	295	300
Val Arg Lys Cys Leu Ile Lys Asn Thr Asp Asn Gly Val Arg Ile Lys		
305	310	315
Thr Trp Pro Gly Ser Pro Pro Gly Ile Ala Ser Asn Ile Leu Phe Glu		
	325	330
Asp Ile Thr Met Asp Asn Val Ser Leu Pro Val Leu Ile Asp Gln Glu		
	340	345
Tyr Cys Pro Tyr Gly His Cys Lys Ala Gly Val Pro Ser Gln Val Lys		
	355	360
Leu Ser Asp Val Thr Ile Lys Gly Ile Lys Gly Thr Ser Ala Thr Lys		
	370	375
Val Ala Val Lys Leu Met Cys Ser Lys Gly Val Pro Cys Thr Asn Ile		
385	390	395
Ala Leu Ser Asp Ile Asn Leu Val His Asn Gly Lys Glu Gly Pro Ala		
	405	410
Val Ser Ala Cys Ser Asn Ile Lys Pro Ile Leu Ser Gly Lys Leu Val		
	420	425
Pro Ala Ala Cys Thr Glu Val Ala Lys Pro Gly Pro		
	435	440

(2) INFORMATION FOR SEQ ID NO:1340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

Met	Ala	Thr	Thr	Ile	Ala	Asn	Gly	Thr	Pro	Val	Val	Asp	Lys	Ala	Lys
1				5				10						15	
Asn	Ala	Ala	Thr	Ala	Val	Glu	Asp	Thr	Ala	Lys	Asn	Ala	Ala	Thr	Ala
			20					25						30	
Val	Gly	Gly	Ala	Ala	Ala	Ser	Val	Gly	Ala	Lys	Val	Ser	Gly	Ala	Lys
		35					40					45			
Pro	Gly	Ala	Ala	Val	Asp	Val	Lys	Ala	Ser	Gly	Ala	Lys	Gly	Asp	Gly
		50				55					60				
Lys	Thr	Asp	Asp	Ser	Ala	Ala	Phe	Ala	Ala	Ala	Trp	Lys	Glu	Ala	Cys
65				70				75						80	
Ala	Ala	Gly	Ser	Thr	Ile	Thr	Val	Pro	Lys	Gly	Glu	Tyr	Met	Val	Glu
			85					90						95	
Ser	Leu	Glu	Phe	Lys	Gly	Pro	Cys	Lys	Gly	Pro	Val	Thr	Leu	Glu	Leu
		100						105					110		
Asn	Gly	Asn	Phe	Lys	Ala	Pro	Ala	Thr	Val	Lys	Thr	Thr	Lys	Pro	His
		115					120					125			
Ala	Gly	Trp	Ile	Asp	Phe	Glu	Asn	Ile	Ala	Asp	Phe	Thr	Leu	Asn	Gly
		130				135					140				
Asn	Lys	Ala	Ile	Phe	Asp	Gly	Gln	Gly	Ser	Leu	Ala	Trp	Lys	Ala	Asn
145				150						155				160	
Asp	Cys	Ala	Lys	Thr	Gly	Lys	Cys	Asn	Ser	Leu	Pro	Ile	Asn	Ile	Arg
			165					170						175	
Phe	Thr	Gly	Leu	Thr	Asn	Ser	Lys	Ile	Asn	Ser	Ile	Thr	Ser	Thr	Asn
		180					185					190			
Ser	Lys	Leu	Phe	His	Met	Asn	Ile	Leu	Asn	Cys	Lys	Asn	Ile	Thr	Leu
		195				200					205				
Ser	Asp	Ile	Gly	Ile	Asp	Ala	Pro	Pro	Glu	Ser	Leu	Asn	Thr	Asp	Gly
		210				215					220				

```

Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly Ala Lys Ile
225                230                235                240
Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr Glu Asn Leu
                245                250                255
Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile Ser Ile Gly
                260                265                270
Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly Val Thr Val
                275                280                285
Arg Lys Cys Leu Ile Lys Asn Thr Asp Asn Gly Val Arg Ile Lys Thr
                290                295                300
Trp Pro Gly Ser Pro Pro Gly Ile Ala Ser Asn Ile Leu Phe Glu Asp
305                310                315                320
Ile Thr Met Asp Asn Val Ser Leu Pro Val Leu Ile Asp Gln Glu Tyr
                325                330                335
Cys Pro Tyr Gly His Cys Lys Ala Gly Val Pro Ser Gln Val Lys Leu
                340                345                350
Ser Asp Val Thr Ile Lys Gly Ile Lys Gly Thr Ser Ala Thr Lys Val
                355                360                365
Ala Val Lys Leu Met Cys Ser Lys Gly Val Pro Cys Thr Asn Ile Ala
                370                375                380
Leu Ser Asp Ile Asn Leu Val His Asn Gly Lys Glu Gly Pro Ala Val
385                390                395                400
Ser Ala Cys Ser Asn Ile Lys Pro Ile Leu Ser Gly Lys Leu Val Pro
                405                410                415
Ala Ala Cys Thr Glu Val Ala Lys Pro Gly Pro
                420                425

```

(2) INFORMATION FOR SEQ ID NO:1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334

(D) OTHER INFORMATION: / Ceres Seq. ID 1500080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

```

Met Val Glu Ser Leu Glu Phe Lys Gly Pro Cys Lys Gly Pro Val Thr
1                5                10                15
Leu Glu Leu Asn Gly Asn Phe Lys Ala Pro Ala Thr Val Lys Thr Thr
                20                25                30
Lys Pro His Ala Gly Trp Ile Asp Phe Glu Asn Ile Ala Asp Phe Thr
                35                40                45
Leu Asn Gly Asn Lys Ala Ile Phe Asp Gly Gln Gly Ser Leu Ala Trp
                50                55                60
Lys Ala Asn Asp Cys Ala Lys Thr Gly Lys Cys Asn Ser Leu Pro Ile
65                70                75                80
Asn Ile Arg Phe Thr Gly Leu Thr Asn Ser Lys Ile Asn Ser Ile Thr
                85                90                95
Ser Thr Asn Ser Lys Leu Phe His Met Asn Ile Leu Asn Cys Lys Asn
                100                105                110
Ile Thr Leu Ser Asp Ile Gly Ile Asp Ala Pro Pro Glu Ser Leu Asn
                115                120                125
Thr Asp Gly Ile His Ile Gly Arg Ser Asn Gly Val Asn Leu Ile Gly
                130                135                140
Ala Lys Ile Lys Thr Gly Asp Asp Cys Val Ser Ile Gly Asp Gly Thr
145                150                155                160
Glu Asn Leu Ile Val Glu Asn Val Glu Cys Gly Pro Gly His Gly Ile
                165                170                175
Ser Ile Gly Ser Leu Gly Arg Tyr Pro Asn Glu Gln Pro Val Lys Gly

```

```

180      185      190
Val Thr Val Arg Lys Cys Leu Ile Lys Asn Thr Asp Asn Gly Val Arg
195      200      205
Ile Lys Thr Trp Pro Gly Ser Pro Pro Gly Ile Ala Ser Asn Ile Leu
210      215      220
Phe Glu Asp Ile Thr Met Asp Asn Val Ser Leu Pro Val Leu Ile Asp
225      230      235      240
Gln Glu Tyr Cys Pro Tyr Gly His Cys Lys Ala Gly Val Pro Ser Gln
245      250      255
Val Lys Leu Ser Asp Val Thr Ile Lys Gly Ile Lys Gly Thr Ser Ala
260      265      270
Thr Lys Val Ala Val Lys Leu Met Cys Ser Lys Gly Val Pro Cys Thr
275      280      285
Asn Ile Ala Leu Ser Asp Ile Asn Leu Val His Asn Gly Lys Glu Gly
290      295      300
Pro Ala Val Ser Ala Cys Ser Asn Ile Lys Pro Ile Leu Ser Gly Lys
305      310      315      320
Leu Val Pro Ala Ala Cys Thr Glu Val Ala Lys Pro Gly Pro
325      330
```

(2) INFORMATION FOR SEQ ID NO:1342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1396
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

```

aatgtattaa gacttgacaa cttgtctttc tcacaccaa cccctctcct ctgtttcata      60
acatctttctc tttttttttt tcctaagccc ctaatgacaa accataatgc cttaatatctt      120
gatgctaaag gcagcatcgg agttgcggtt agagttccaa accaatctct gttttctccc      180
ggaggtggcc gatacatcag cattccccgg aagaaactcg tgcagaagct agaggccgac      240
ccgagtcaaa cccgtatcca cacttgatc gaagccatga gggcttcttc cccaacccgt      300
acccgaccgg ggaacatatc tcccctcacg gagtccgatg aggaggatga atactcttct      360
tggtatggctc aacaccgcgt agctttaacc atgtttgaag agatagctga agcttcaaaa      420
gggaaacaaa tcgtgatgtt tctcgactat gacggtacat tatcccccat tgttgaaaac      480
cctgatcgag cttacatgtc tgaagagatg agagaggcag tgaaaggcgt ggctagatat      540
ttcccgaccg cgattgtcac tggaagatgc cgtgataagg ttcgtagatt tgtgaaactt      600
cccgactttt actatgcagg tagccatgga atggacatca aaggaccttc caaaagaaac      660
aaacataata agaacaataa aggagttctt ttccaagcgg cgaatgagtt tttgcctatg      720
attgacaagg tctctaagtg tctagtagag aaaatgagag acatagaagg agcaaactc      780
gagaacaaca agttttgtgt ctccgtacat taccgttgtg ttgatcaaaa ggactgggga      840
ttggtagcgg aacacgtgac atcgatatgt agtgagtatc cgaaactgag tttgacacaa      900
ggaagaaaag tcttagagat tcgaccaacc atcaaattgg ataaaggcaa agctctcgag      960
ttcttgctcg aatccttagg attcgctaac tctaacgatg ttttgcccat ctatatagga      1020
gatgatcgta cggacgagga tgctttcaag gttttgagaa acaaaggaca aggctttggt      1080
atacttgtgt ccaaaattcc aaaggaaacg agtgctacat attctctaca agaaccttcc      1140
gaggtaggag agtttttgca gcgactcgtg gaatggaaac aaatgtcact aagaggaaga      1200
tagccaattt cctgacataa atttattttc aattaataaa tgaattagtt ttcactatgc      1260
aacaaaaatt gttgtatata tgatcaatgt ttttttaatt attttactct tcatgaacaa      1320
atgtaagttt ataggaactt tcttaacca gaaaaaaagt aagtttgcta tataatattt      1380
tcatcattct cttttt
```

(2) INFORMATION FOR SEQ ID NO:1343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1500082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

Asn	Val	Leu	Arg	Leu	Asp	Asn	Leu	Ser	Phe	Ser	His	Gln	Thr	Pro	Leu
1				5					10					15	
Leu	Cys	Phe	Ile	Thr	Ser	Ser	Leu	Phe	Phe	Phe	Pro	Lys	Pro	Leu	Met
			20					25				30			
Thr	Asn	His	Asn	Ala	Leu	Ile	Ser	Asp	Ala	Lys	Gly	Ser	Ile	Gly	Val
		35					40					45			
Ala	Val	Arg	Val	Pro	Asn	Gln	Ser	Leu	Phe	Ser	Pro	Gly	Gly	Gly	Arg
	50					55					60				
Tyr	Ile	Ser	Ile	Pro	Arg	Lys	Lys	Leu	Val	Gln	Lys	Leu	Glu	Ala	Asp
65					70					75				80	
Pro	Ser	Gln	Thr	Arg	Ile	His	Thr	Trp	Ile	Glu	Ala	Met	Arg	Ala	Ser
				85					90					95	
Ser	Pro	Thr	Arg	Thr	Arg	Pro	Gly	Asn	Ile	Ser	Pro	Leu	Thr	Glu	Ser
			100					105					110		
Asp	Glu	Glu	Asp	Glu	Tyr	Ser	Ser	Trp	Met	Ala	Gln	His	Pro	Ser	Ala
		115					120					125			
Leu	Thr	Met	Phe	Glu	Glu	Ile	Ala	Glu	Ala	Ser	Lys	Gly	Lys	Gln	Ile
	130					135					140				
Val	Met	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Ser	Pro	Ile	Val	Glu	Asn
145					150					155				160	
Pro	Asp	Arg	Ala	Tyr	Met	Ser	Glu	Glu	Met	Arg	Glu	Ala	Val	Lys	Gly
				165					170					175	
Val	Ala	Arg	Tyr	Phe	Pro	Thr	Ala	Ile	Val	Thr	Gly	Arg	Cys	Arg	Asp
			180					185					190		
Lys	Val	Arg	Arg	Phe	Val	Lys	Leu	Pro	Gly	Leu	Tyr	Tyr	Ala	Gly	Ser
		195					200					205			
His	Gly	Met	Asp	Ile	Lys	Gly	Pro	Ser	Lys	Arg	Asn	Lys	His	Asn	Lys
	210					215					220				
Asn	Asn	Lys	Gly	Val	Leu	Phe	Gln	Ala	Ala	Asn	Glu	Phe	Leu	Pro	Met
225					230					235				240	
Ile	Asp	Lys	Val	Ser	Lys	Cys	Leu	Val	Glu	Lys	Met	Arg	Asp	Ile	Glu
				245					250					255	
Gly	Ala	Asn	Val	Glu	Asn	Asn	Lys	Phe	Cys	Val	Ser	Val	His	Tyr	Arg
			260					265					270		
Cys	Val	Asp	Gln	Lys	Asp	Trp	Gly	Leu	Val	Ala	Glu	His	Val	Thr	Ser
		275					280					285			
Ile	Leu	Ser	Glu	Tyr	Pro	Lys	Leu	Ser	Leu	Thr	Gln	Gly	Arg	Lys	Val
	290					295					300				
Leu	Glu	Ile	Arg	Pro	Thr	Ile	Lys	Trp	Asp	Lys	Gly	Lys	Ala	Leu	Glu
305					310					315				320	
Phe	Leu	Leu	Glu	Ser	Leu	Gly	Phe	Ala	Asn	Ser	Asn	Asp	Val	Leu	Pro
				325					330					335	
Ile	Tyr	Ile	Gly	Asp	Asp	Arg	Thr	Asp	Glu	Asp	Ala	Phe	Lys	Val	Leu
		340						345					350		
Arg	Asn	Lys	Gly	Gln	Gly	Phe	Gly	Ile	Leu	Val	Ser	Lys	Ile	Pro	Lys
		355					360					365			
Glu	Thr	Ser	Ala	Thr	Tyr	Ser	Leu	Gln	Glu	Pro	Ser	Glu	Val	Gly	Glu
	370					375					380				
Phe	Leu	Gln	Arg	Leu	Val	Glu	Trp	Lys	Gln	Met	Ser	Leu	Arg	Gly	Arg
385					390					395					400

(2) INFORMATION FOR SEQ ID NO:1344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..369
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

Met	Thr	Asn	His	Asn	Ala	Leu	Ile	Ser	Asp	Ala	Lys	Gly	Ser	Ile	Gly
1			5					10					15		
Val	Ala	Val	Arg	Val	Pro	Asn	Gln	Ser	Leu	Phe	Ser	Pro	Gly	Gly	Gly
		20						25				30			
Arg	Tyr	Ile	Ser	Ile	Pro	Arg	Lys	Lys	Leu	Val	Gln	Lys	Leu	Glu	Ala
	35						40					45			
Asp	Pro	Ser	Gln	Thr	Arg	Ile	His	Thr	Trp	Ile	Glu	Ala	Met	Arg	Ala
	50					55					60				
Ser	Ser	Pro	Thr	Arg	Thr	Arg	Pro	Gly	Asn	Ile	Ser	Pro	Leu	Thr	Glu
65					70				75					80	
Ser	Asp	Glu	Glu	Asp	Glu	Tyr	Ser	Ser	Trp	Met	Ala	Gln	His	Pro	Ser
			85						90				95		
Ala	Leu	Thr	Met	Phe	Glu	Glu	Ile	Ala	Glu	Ala	Ser	Lys	Gly	Lys	Gln
		100						105					110		
Ile	Val	Met	Phe	Leu	Asp	Tyr	Asp	Gly	Thr	Leu	Ser	Pro	Ile	Val	Glu
	115						120					125			
Asn	Pro	Asp	Arg	Ala	Tyr	Met	Ser	Glu	Glu	Met	Arg	Glu	Ala	Val	Lys
	130						135				140				
Gly	Val	Ala	Arg	Tyr	Phe	Pro	Thr	Ala	Ile	Val	Thr	Gly	Arg	Cys	Arg
145					150				155					160	
Asp	Lys	Val	Arg	Arg	Phe	Val	Lys	Leu	Pro	Gly	Leu	Tyr	Tyr	Ala	Gly
			165						170				175		
Ser	His	Gly	Met	Asp	Ile	Lys	Gly	Pro	Ser	Lys	Arg	Asn	Lys	His	Asn
		180					185					190			
Lys	Asn	Asn	Lys	Gly	Val	Leu	Phe	Gln	Ala	Ala	Asn	Glu	Phe	Leu	Pro
	195						200					205			
Met	Ile	Asp	Lys	Val	Ser	Lys	Cys	Leu	Val	Glu	Lys	Met	Arg	Asp	Ile
	210					215					220				
Glu	Gly	Ala	Asn	Val	Glu	Asn	Asn	Lys	Phe	Cys	Val	Ser	Val	His	Tyr
225					230				235					240	
Arg	Cys	Val	Asp	Gln	Lys	Asp	Trp	Gly	Leu	Val	Ala	Glu	His	Val	Thr
			245						250					255	
Ser	Ile	Leu	Ser	Glu	Tyr	Pro	Lys	Leu	Ser	Leu	Thr	Gln	Gly	Arg	Lys
		260						265				270			
Val	Leu	Glu	Ile	Arg	Pro	Thr	Ile	Lys	Trp	Asp	Lys	Gly	Lys	Ala	Leu
	275						280					285			
Glu	Phe	Leu	Leu	Glu	Ser	Leu	Gly	Phe	Ala	Asn	Ser	Asn	Asp	Val	Leu
	290					295					300				
Pro	Ile	Tyr	Ile	Gly	Asp	Arg	Thr	Asp	Glu	Asp	Ala	Phe	Lys	Val	
305					310				315					320	
Leu	Arg	Asn	Lys	Gly	Gln	Gly	Phe	Gly	Ile	Leu	Val	Ser	Lys	Ile	Pro
			325						330					335	
Lys	Glu	Thr	Ser	Ala	Thr	Tyr	Ser	Leu	Gln	Glu	Pro	Ser	Glu	Val	Gly
		340						345				350			
Glu	Phe	Leu	Gln	Arg	Leu	Val	Glu	Trp	Lys	Gln	Met	Ser	Leu	Arg	Gly
		355					360					365			

Arg

(2) INFORMATION FOR SEQ ID NO:1345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 308 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..308
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500084
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:
Met Arg Ala Ser Ser Pro Thr Arg Thr Arg Pro Gly Asn Ile Ser Pro
1 5 10 15
Leu Thr Glu Ser Asp Glu Glu Asp Glu Tyr Ser Ser Trp Met Ala Gln
 20 25 30
His Pro Ser Ala Leu Thr Met Phe Glu Glu Ile Ala Glu Ala Ser Lys
 35 40 45
Gly Lys Gln Ile Val Met Phe Leu Asp Tyr Asp Gly Thr Leu Ser Pro
 50 55 60
Ile Val Glu Asn Pro Asp Arg Ala Tyr Met Ser Glu Glu Met Arg Glu
65 70 75 80
Ala Val Lys Gly Val Ala Arg Tyr Phe Pro Thr Ala Ile Val Thr Gly
 85 90 95
Arg Cys Arg Asp Lys Val Arg Arg Phe Val Lys Leu Pro Gly Leu Tyr
 100 105 110
Tyr Ala Gly Ser His Gly Met Asp Ile Lys Gly Pro Ser Lys Arg Asn
 115 120 125
Lys His Asn Lys Asn Asn Lys Gly Val Leu Phe Gln Ala Ala Asn Glu
130 135 140
Phe Leu Pro Met Ile Asp Lys Val Ser Lys Cys Leu Val Glu Lys Met
145 150 155 160
Arg Asp Ile Glu Gly Ala Asn Val Glu Asn Asn Lys Phe Cys Val Ser
 165 170 175
Val His Tyr Arg Cys Val Asp Gln Lys Asp Trp Gly Leu Val Ala Glu
 180 185 190
His Val Thr Ser Ile Leu Ser Glu Tyr Pro Lys Leu Ser Leu Thr Gln
195 200 205
Gly Arg Lys Val Leu Glu Ile Arg Pro Thr Ile Lys Trp Asp Lys Gly
210 215 220
Lys Ala Leu Glu Phe Leu Leu Glu Ser Leu Gly Phe Ala Asn Ser Asn
225 230 235 240
Asp Val Leu Pro Ile Tyr Ile Gly Asp Asp Arg Thr Asp Glu Asp Ala
 245 250 255
Phe Lys Val Leu Arg Asn Lys Gly Gln Gly Phe Gly Ile Leu Val Ser
260 265 270
Lys Ile Pro Lys Glu Thr Ser Ala Thr Tyr Ser Leu Gln Glu Pro Ser
275 280 285
Glu Val Gly Glu Phe Leu Gln Arg Leu Val Glu Trp Lys Gln Met Ser
290 295 300
Leu Arg Gly Arg
305

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1510 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1510
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500085
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:
ttttaatttt ttcattcttct tgggttttgggt tgggtcactc ttcaggtcag gtgtgtataaaa

aagaaagaaa gaaaagagag attgttgtgt tgtaaccctt ttgactaaaa tctaataaac 120
ttttttaaca caacaaaact ccttcagatc tgaaagggtt cttcttctct cttagtctct 180
ctgtcctttt attctccgtc gtcgtttcat gatctgactc tctggtcttc tcttcttctt 240
cttcttcttc tattttttct tacttgcgtc ctggtgtgtc tgaacatgcc acgccctttc 300
ttccataagt tgattttctc atccactatc caagaaaaac gtctgagggt cccagataag 360
tttgtgagta aattcaagga tgagctttcg gttgctgttg cactcacagt acctgatggt 420
catgtttggc gtgtaggact aaggaaaagt gacaacaaaa tttggtttca agatggttgg 480
caagagtttg ttgaccgtta ctccattcgc attgattatc ttttgatttt tagatatgaa 540
ggaaactctg ccttcagcgt ctacattttc aatttatccc actctgagat caattaccat 600
tccaccggtc tcatggattc cgctcacaac cacttcaaac gcgcccgttt gtttgaagac 660
cttgaagatg aagatgccga ggtcatcttt ccttcttctg tgtaccatc accacttctt 720
gagtctacag taccagccaa caaagggtat gctagttcag ccatccaaac cttgttctact 780
ggaccagtta aagctgaaga gccaacgcca accccaaaaa tacctaaaaa gagaggagg 840
aagaagaaaa atgctgatcc tgaggaaata aactcatcag ctccgcgaga tgatgatcca 900
gagaaccggt caaagttcta cgagagtgct tctgcgagaa agagaaccgt gactgcagaa 960
gaaagagaga gagccatcaa tgcagccaaa acgttcgaac caacaaacc tttcttcaga 1020
gtggttctgc gaccatccta tctatacaga ggttgcacat tgtatcttcc ttctgggttt 1080
gctgagaagt acctaatgg gatctccggg ttcatacaag tccagcttgc ggagaaacaa 1140
tggcctgttc gatgtctcta caaagccggg agagccaaat tcagtcaagg atggtacgaa 1200
ttcactctag agaacaactt aggagaagga gacgtctgtg tgtttgagct gctcagaacc 1260
agagatttgc ttttgaaagt gacagccttt cgagtcaacg agtacgtctg aacaaagcat 1320
tatggtgtga tcattctgga tttgcaagta caatgtcgtg taggagtatc ttaattttaa 1380
aacaactaaa aaactctctt ctggtctgtg tcattattgc gtcagtgtct cgttttttct 1440
ctcgggttta ctttgtgta tcgatgtgga taagtgtgtt ttacctcatt atatataacc 1500
tcttgagtgg

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

Met Pro Arg Pro Phe Phe His Lys Leu Ile Phe Ser Ser Thr Ile Gln
1 5 10 15
Glu Lys Arg Leu Arg Val Pro Asp Lys Phe Val Ser Lys Phe Lys Asp
20 25 30
Glu Leu Ser Val Ala Val Ala Leu Thr Val Pro Asp Gly His Val Trp
35 40 45
Arg Val Gly Leu Arg Lys Ala Asp Asn Lys Ile Trp Phe Gln Asp Gly
50 55 60
Trp Gln Glu Phe Val Asp Arg Tyr Ser Ile Arg Ile Asp Tyr Leu Leu
65 70 75 80
Ile Phe Arg Tyr Glu Gly Asn Ser Ala Phe Ser Val Tyr Ile Phe Asn
85 90 95
Leu Ser His Ser Glu Ile Asn Tyr His Ser Thr Gly Leu Met Asp Ser
100 105 110
Ala His Asn His Phe Lys Arg Ala Arg Leu Phe Glu Asp Leu Glu Asp
115 120 125
Glu Asp Ala Glu Val Ile Phe Pro Ser Ser Val Tyr Pro Ser Pro Leu
130 135 140
Pro Glu Ser Thr Val Pro Ala Asn Lys Gly Tyr Ala Ser Ser Ala Ile
145 150 155 160
Gln Thr Leu Phe Thr Gly Pro Val Lys Ala Glu Glu Pro Thr Pro Thr
165 170 175
Pro Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Lys Asn Ala Asp Pro
180 185 190

Glu Glu Ile Asn Ser Ser Ala Pro Arg Asp Asp Asp Pro Glu Asn Arg
195 200 205
Ser Lys Phe Tyr Glu Ser Ala Ser Ala Arg Lys Arg Thr Val Thr Ala
210 215 220
Glu Glu Arg Glu Arg Ala Ile Asn Ala Ala Lys Thr Phe Glu Pro Thr
225 230 235 240
Asn Pro Phe Phe Arg Val Val Leu Arg Pro Ser Tyr Leu Tyr Arg Gly
245 250 255
Cys Ile Met Tyr Leu Pro Ser Gly Phe Ala Glu Lys Tyr Leu Ser Gly
260 265 270
Ile Ser Gly Phe Ile Lys Val Gln Leu Ala Glu Lys Gln Trp Pro Val
275 280 285
Arg Cys Leu Tyr Lys Ala Gly Arg Ala Lys Phe Ser Gln Gly Trp Tyr
290 295 300
Glu Phe Thr Leu Glu Asn Asn Leu Gly Glu Gly Asp Val Cys Val Phe
305 310 315 320
Glu Leu Leu Arg Thr Arg Asp Phe Val Leu Lys Val Thr Ala Phe Arg
325 330 335
Val Asn Glu Tyr Val
340

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 1500087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

Met Asp Ser Ala His Asn His Phe Lys Arg Ala Arg Leu Phe Glu Asp
1 5 10 15
Leu Glu Asp Glu Asp Ala Glu Val Ile Phe Pro Ser Ser Val Tyr Pro
20 25 30
Ser Pro Leu Pro Glu Ser Thr Val Pro Ala Asn Lys Gly Tyr Ala Ser
35 40 45
Ser Ala Ile Gln Thr Leu Phe Thr Gly Pro Val Lys Ala Glu Glu Pro
50 55 60
Thr Pro Thr Pro Lys Ile Pro Lys Lys Arg Gly Arg Lys Lys Lys Asn
65 70 75 80
Ala Asp Pro Glu Glu Ile Asn Ser Ser Ala Pro Arg Asp Asp Asp Pro
85 90 95
Glu Asn Arg Ser Lys Phe Tyr Glu Ser Ala Ser Ala Arg Lys Arg Thr
100 105 110
Val Thr Ala Glu Glu Arg Glu Arg Ala Ile Asn Ala Ala Lys Thr Phe
115 120 125
Glu Pro Thr Asn Pro Phe Phe Arg Val Val Leu Arg Pro Ser Tyr Leu
130 135 140
Tyr Arg Gly Cys Ile Met Tyr Leu Pro Ser Gly Phe Ala Glu Lys Tyr
145 150 155 160
Leu Ser Gly Ile Ser Gly Phe Ile Lys Val Gln Leu Ala Glu Lys Gln
165 170 175
Trp Pro Val Arg Cys Leu Tyr Lys Ala Gly Arg Ala Lys Phe Ser Gln
180 185 190
Gly Trp Tyr Glu Phe Thr Leu Glu Asn Asn Leu Gly Glu Gly Asp Val
195 200 205
Cys Val Phe Glu Leu Leu Arg Thr Arg Asp Phe Val Leu Lys Val Thr
210 215 220
Ala Phe Arg Val Asn Glu Tyr Val

225

230

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

```
aaaataaaga accttgacaa cttctctaca acactcactt tttctctcta atgggtggaag      60
caagaagctt gaagaaacca atccaattgg gtaataaaga agatcaaaac cctagaaaat      120
tctactctcg attcatcttt aaagctctta tcctcaccgt gctctgcgcc gtctgtacctg      180
tcttcccttc tcagacacca gagcttgcta accaaacaag actcctcgag cttctccacc      240
ttgttttcgt cggtatcgca gtctcttacg gtctcttcag ccgcaggaac tacgacggag      300
gaggaggtgg aggaacaagc aatagtgatc acaacaaagc tgatcatagt aataataatt      360
cgcattcata tgtgcctaag attcttgaag taccctctgt ttttaacgtg ggtcacgaga      420
gtgaatctga accgtccgat gattcctccg gtgatcaacg taagtttcag acatggaaga      480
acaagtacca catgaaaatc cccgaggttg agactcgttt cgttgatcga gttagttcag      540
aaaacagaga gaagcctctg cttttgcccg ttcggagctt gaattattct cgtgtttctg      600
attcttccgg cgataattcc ggtcgatggg agaaagttag atctaagaga gaacttctga      660
agactcttgg cgatgataat agtgatgtgc ttccttctcc gattccatgg aggtcaagat      720
catcttcac ccatcatca tcatcaaagg aggttgaatc tctaccgtcc gttagaatc      780
tgactacagt tgaatcacag ccgttgatca agaactctgac accatcttct tctttctctt      840
ctccaagaaa gtcgaatcct atacctaata tcgcatctga gttccatcca tctccgccac      900
cgccctctcc gccgcgccca ccactaccgg cgttttataa ctctcgtcg agaaaagatc      960
atcccggaa ttacagggtt gagaggagag aatcatcagt tcacaagacg aaatttgtag      1020
gaggtgagtt tcactctccg ccgcctcctc ctccaccacc tccggtggag tattataagt      1080
cacctccgac aaaattcaga ctaagtaacg aacggagaaa gtccctcgag caaaagatgw      1140
aaagaaacgc tcctaaaaag gtttggtggt ccgatccaat cgtggaatcg aaggaacaag      1200
acacagagaa gaatgatcaa agaagtaact tggaagcaa ggcagtggaa gaatccgaga      1260
atggagaaca gagaagagga gaaaatgaaa tccacgacga ggttgagaag aagatagtag      1320
aggaagaagg agttagtgag atcaacaatg gaagtgcagt ggacaagaag gcagatgagt      1380
tcattgcaaa gttcagagaa cagattaggt tacaaagaat cgagtctatc aagagatcta      1440
ctaataagat ctctgcaaat tcttcgaggt agaactcatt atttattaat aataggtata      1500
cattttaagt atgttttggt aatcatcata aggttgtaat attaagggga acaaatattt      1560
ttgttacatt tattcagcca caaaaacagg attggag
```

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

```
Met Val Glu Ala Arg Ser Leu Lys Lys Pro Ile Gln Leu Gly Asn Lys
1           5           10           15
Glu Asp Gln Asn Pro Arg Lys Phe Tyr Ser Arg Phe Ile Phe Lys Ala
20           25           30
Leu Ile Leu Thr Val Leu Cys Ala Val Val Pro Val Phe Leu Ser Gln
35           40           45
Thr Pro Glu Leu Ala Asn Gln Thr Arg Leu Leu Glu Leu Leu His Leu
50           55           60
Val Phe Val Gly Ile Ala Val Ser Tyr Gly Leu Phe Ser Arg Arg Asn
```

65					70					75					80
Tyr	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Ser	Asn	Ser	Asp	His	Asn	Lys
				85					90					95	
Ala	Asp	His	Ser	Asn	Asn	Asn	Ser	His	Ser	Tyr	Val	Pro	Lys	Ile	Leu
			100					105					110		
Glu	Val	Ser	Ser	Val	Phe	Asn	Val	Gly	His	Glu	Ser	Glu	Ser	Glu	Pro
		115					120					125			
Ser	Asp	Asp	Ser	Ser	Gly	Asp	Gln	Arg	Lys	Phe	Gln	Thr	Trp	Lys	Asn
	130					135					140				
Lys	Tyr	His	Met	Lys	Ile	Pro	Glu	Val	Glu	Thr	Arg	Phe	Val	Asp	Arg
145					150					155					160
Val	Ser	Ser	Glu	Asn	Arg	Glu	Lys	Pro	Leu	Leu	Leu	Pro	Val	Arg	Ser
				165					170					175	
Leu	Asn	Tyr	Ser	Arg	Val	Ser	Asp	Ser	Ser	Gly	Asp	Asn	Ser	Gly	Arg
		180						185					190		
Trp	Glu	Lys	Val	Arg	Ser	Lys	Arg	Glu	Leu	Leu	Lys	Thr	Leu	Gly	Asp
	195						200					205			
Asp	Asn	Ser	Asp	Val	Leu	Pro	Ser	Pro	Ile	Pro	Trp	Arg	Ser	Arg	Ser
	210					215					220				
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Lys	Glu	Val	Glu	Ser	Leu	Pro	Ser
225						230				235					240
Val	Lys	Asn	Leu	Thr	Thr	Val	Glu	Ser	Gln	Pro	Leu	Ile	Lys	Asn	Leu
				245					250					255	
Thr	Pro	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Arg	Lys	Ser	Asn	Pro	Ile	Pro
			260					265					270		
Asn	Leu	Ala	Ser	Glu	Phe	His	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro
		275					280						285		
Pro	Pro	Pro	Leu	Pro	Ala	Phe	Tyr	Asn	Ser	Ser	Ser	Arg	Lys	Asp	His
	290					295					300				
Pro	Gly	Ile	Tyr	Arg	Val	Glu	Arg	Arg	Glu	Ser	Ser	Val	His	Lys	Thr
305					310					315					320
Lys	Phe	Ala	Gly	Gly	Glu	Phe	His	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				325					330					335	
Pro	Pro	Val	Glu	Tyr	Tyr	Lys	Ser	Pro	Pro	Thr	Lys	Phe	Arg	Leu	Ser
			340					345					350		
Asn	Glu	Arg	Arg	Lys	Ser	Ser	Glu	Gln	Lys	Met	Xaa	Arg	Asn	Ala	Pro
		355					360					365			
Lys	Lys	Val	Trp	Trp	Ser	Asp	Pro	Ile	Val	Glu	Ser	Lys	Glu	Gln	Asp
	370					375					380				
Thr	Glu	Lys	Asn	Asp	Gln	Arg	Ser	Asn	Leu	Gly	Ser	Lys	Ala	Val	Glu
385					390					395					400
Glu	Ser	Glu	Asn	Gly	Glu	Gln	Arg	Arg	Gly	Glu	Asn	Glu	Ile	His	Asp
			405						410					415	
Glu	Val	Glu	Lys	Lys	Ile	Val	Glu	Glu	Glu	Gly	Val	Ser	Glu	Ile	Asn
			420					425					430		
Asn	Gly	Ser	Asp	Val	Asp	Lys	Lys	Ala	Asp	Glu	Phe	Ile	Ala	Lys	Phe
	435						440					445			
Arg	Glu	Gln	Ile	Arg	Leu	Gln	Arg	Ile	Glu	Ser	Ile	Lys	Arg	Ser	Thr
	450					455					460				
Asn	Lys	Ile	Ser	Ala	Asn	Ser	Ser	Arg							
465					470										

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1500090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

```
Met Lys Ile Pro Glu Val Glu Thr Arg Phe Val Asp Arg Val Ser Ser
1          5          10          15
Glu Asn Arg Glu Lys Pro Leu Leu Leu Pro Val Arg Ser Leu Asn Tyr
20          25          30
Ser Arg Val Ser Asp Ser Ser Gly Asp Asn Ser Gly Arg Trp Glu Lys
35          40          45
Val Arg Ser Lys Arg Glu Leu Leu Lys Thr Leu Gly Asp Asp Asn Ser
50          55          60
Asp Val Leu Pro Ser Pro Ile Pro Trp Arg Ser Arg Ser Ser Ser Ser
65          70          75          80
Ser Ser Ser Ser Ser Lys Glu Val Glu Ser Leu Pro Ser Val Lys Asn
85          90          95
Leu Thr Thr Val Glu Ser Gln Pro Leu Ile Lys Asn Leu Thr Pro Ser
100         105         110
Ser Ser Phe Ser Ser Pro Arg Lys Ser Asn Pro Ile Pro Asn Leu Ala
115         120         125
Ser Glu Phe His Pro Ser Pro Pro Pro Pro Pro Pro Pro Pro Pro
130         135         140
Leu Pro Ala Phe Tyr Asn Ser Ser Ser Arg Lys Asp His Pro Gly Ile
145         150         155         160
Tyr Arg Val Glu Arg Arg Glu Ser Ser Val His Lys Thr Lys Phe Ala
165         170         175
Gly Gly Glu Phe His Pro Pro Pro Pro Pro Pro Pro Pro Pro Val
180         185         190
Glu Tyr Tyr Lys Ser Pro Pro Thr Lys Phe Arg Leu Ser Asn Glu Arg
195         200         205
Arg Lys Ser Ser Glu Gln Lys Met Xaa Arg Asn Ala Pro Lys Lys Val
210         215         220
Trp Trp Ser Asp Pro Ile Val Glu Ser Lys Glu Gln Asp Thr Glu Lys
225         230         235         240
Asn Asp Gln Arg Ser Asn Leu Gly Ser Lys Ala Val Glu Glu Ser Glu
245         250         255
Asn Gly Glu Gln Arg Arg Gly Glu Asn Glu Ile His Asp Glu Val Glu
260         265         270
Lys Lys Ile Val Glu Glu Glu Gly Val Ser Glu Ile Asn Asn Gly Ser
275         280         285
Asp Val Asp Lys Lys Ala Asp Glu Phe Ile Ala Lys Phe Arg Glu Gln
290         295         300
Ile Arg Leu Gln Arg Ile Glu Ser Ile Lys Arg Ser Thr Asn Lys Ile
305         310         315         320
Ser Ala Asn Ser Ser Arg
325
```

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..798

(D) OTHER INFORMATION: / Ceres Seq. ID 1500091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

```
ttgtcaaaag ctgattcttc gccttatggc atcgattttg caccttcgaa cggccaaccc      60
acgggaagat tcactaatgg tcgaaccatt tccgatattg tgggtgaagc cttaggagca      120
aatcaccac caccaccata tcttgaacca aacactgagg ctaacacaat tctcaatgga      180
atcaactatg cttctgtgtc tgctggaatc ttggacgaca ctggacttct ggttcatcgg      240
ggcgagttcc gctgagagaa caagtgahta attttgagaa gagtagagaa tatatggtaa      300
```

```
gcgtgattgg tgaaaatggt acaaaagaga tgttgaagaa tgcaatgttc acaatcacao 360
ttggatcaaa tgatatattg aattatattc aaccatcaat acctttcttc tctcaagaca 420
agctccccac tgaatgtcct acaagattcc atggtcctcc attttaacca cacatcttaa 480
gcgattgcat cagctaggag gtaggaagtt cgtgggtggt ggagtagggc cactcggttg 540
catacccttt gctcgagcgt tgaatttwat accagccgga aaatgctccg aacaagtcaa 600
ccaagtagtc cgaggttata acatgaagct tatacactct cttaagacat tgaacaatga 660
gttaagatcc gaagattaca acactacatt tgtctacgcc aactcttacg acctattctt 720
gaaactagtt ttgaactatc aactatttgg cttgaagaac gcagacaagc cgtgttgttg 780
cggctacttt ccaccgtt
```

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1500092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

```
Leu Ser Lys Ala Asp Ser Ser Pro Tyr Gly Ile Asp Phe Ala Pro Ser
1          5          10          15
Asn Gly Gln Pro Thr Gly Arg Phe Thr Asn Gly Arg Thr Ile Ser Asp
20          25          30
Ile Val Gly Glu Ala Leu Gly Ala Lys Ser Pro Pro Pro Pro Tyr Leu
35          40          45
Glu Pro Asn Thr Glu Ala Asn Thr Ile Leu Asn Gly Ile Asn Tyr Ala
50          55          60
Ser Gly Ala Ala Gly Ile Leu Asp Asp Thr Gly Leu Leu Val His Arg
65          70          75          80
Gly Glu Phe Arg
```

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1500093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

```
Met Ser Tyr Lys Ile Pro Trp Ser Ser Ile Leu Thr Thr His Leu Lys
1          5          10          15
Arg Leu His Gln Leu Gly Gly Arg Lys Phe Val Val Val Gly Val Gly
20          25          30
Pro Leu Gly Cys Ile Pro Phe Ala Arg Ala Leu Asn Xaa Ile Pro Ala
35          40          45
Gly Lys Cys Ser Glu Gln Val Asn Gln Val Val Arg Gly Tyr Asn Met
50          55          60
Lys Leu Ile His Ser Leu Lys Thr Leu Asn Asn Glu Leu Arg Ser Glu
65          70          75          80
Asp Tyr Asn Thr Thr Phe Val Tyr Ala Asn Ser Tyr Asp Leu Phe Leu
85          90          95
Lys Leu Val Leu Asn Tyr Gln Leu Phe Gly Leu Lys Asn Ala Asp Lys
100          105          110
Pro Cys Cys Gly Gly Tyr Phe Pro Pro
115          120
```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```
agttggagct cgaaccctt cttcatcttc ttcttctcct ccacctaacc aatgggagca      60
attgatctct ctttctcaca gagtcttctc ttcttctcgt cgcgttccaa tctttcctcc      120
tccacacacc gttccgtctc ttttttgccg ccgggaagca agtcacggtg tctgccgccg      180
ttgcgttcaa tgagtcatga cgacgacacg gcctcaaagg aggtgaagct atgggggtgga      240
aggttcgaag agagtgtcac tgagaaagtg gagaagttca ctgagtcaat ttcatttgat      300
aaggttctct acaagcagga cattatgggt agcaaagctc atgcttcaat gcttgctcac      360
caggggctaa taactgatag cgataaagat agcattttga gaggtcttga tgatattgag      420
agacaaattg aagcaaataa gtttgaatgg aggactgatc gagaagatgt gcatatgaac      480
attgaagcag ctcttactga tcttattggt gaacctgcaa agaaacttca tactgcaagg      540
agcagaaatg accaagttgc tactgacttc aggccttgggt gtcgtgatgc tatcgataca      600
attattgtca aaatcagaaa tcttcagaga gcacttggtg aactggcttt gaagaatgag      660
gctttgattg ttcttggtta tactcatctt caaagagctc agcctgtttt actcccacac      720
gttctcttaa cttttgtaga gcagctcgaa cgtgatgctg gtcgttatgt ggactgtcga      780
gcaaggctaa atttctcccc cctgggagct tgtgctttgg ctggaactgg tctgcctatt      840
gataggttta tgactgcaa tgctcttgga tttaccgaac caatgagaaa cagtatcgat      900
gcagtctcag accgagactt cgtgctggag ttcttatata caaatgcaa caccggtatt      960
catttatcac ggcttggaag agagtgggta ctgtgggctt ccgaggagtt tgggttcctg      1020
actccaagtg attctgtgtc aaccggaagt agtataatgc cacagaagaa aaatccagac      1080
ccaatggaac ttgtcagagg aaaatccgca agagtcatag gcgatctggt cactgtctta      1140
acactgtgca aaggacttcc ccttgcttac aacagagatt ttcaagaaga caaagagccg      1200
atgttcgata gtaccaagac aataatggga atgatcgatg tatctgcaga atttgctcag      1260
aatgttacat tcaacgaaga cagaatcaag aaaagtcttc ccgcaggaca tcttgatgcg      1320
actactctcg ctgattatct tgtgaagaag gggatgcctt ttaggtcatc tcatgacata      1380
gttggaaaac tagttggagt ttgcgtctca aaaggctgtg aacttcagaa cttaagtctt      1440
gaagagatga aaaagctgag cctgtgtttt gaag
```

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

```
Met Gly Ala Ile Asp Leu Ser Phe Ser Gln Ser Leu Leu Phe Ser Ser
1           5           10           15
Ser Arg Ser Asn Leu Ser Ser Ser Thr His Arg Ser Val Ser Phe Leu
20           25           30
Pro Pro Gly Ser Lys Ser Arg Cys Leu Pro Pro Leu Arg Ser Met Ser
35           40           45
His Asp Asp Asp Thr Ala Ser Lys Glu Val Lys Leu Trp Gly Gly Arg
50           55           60
Phe Glu Glu Ser Val Thr Glu Lys Val Glu Lys Phe Thr Glu Ser Ile
65           70           75           80
Ser Phe Asp Lys Val Leu Tyr Lys Gln Asp Ile Met Gly Ser Lys Ala
85           90           95
```

His	Ala	Ser	Met	Leu	Ala	His	Gln	Gly	Leu	Ile	Thr	Asp	Ser	Asp	Lys
			100					105					110		
Asp	Ser	Ile	Leu	Arg	Gly	Leu	Asp	Asp	Ile	Glu	Arg	Gln	Ile	Glu	Ala
		115					120					125			
Asn	Lys	Phe	Glu	Trp	Arg	Thr	Asp	Arg	Glu	Asp	Val	His	Met	Asn	Ile
	130					135					140				
Glu	Ala	Ala	Leu	Thr	Asp	Leu	Ile	Gly	Glu	Pro	Ala	Lys	Lys	Leu	His
145					150					155					160
Thr	Ala	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr	Asp	Phe	Arg	Leu	Trp
				165					170					175	
Cys	Arg	Asp	Ala	Ile	Asp	Thr	Ile	Ile	Val	Lys	Ile	Arg	Asn	Leu	Gln
			180					185					190		
Arg	Ala	Leu	Val	Glu	Leu	Ala	Leu	Lys	Asn	Glu	Ala	Leu	Ile	Val	Pro
		195					200					205			
Gly	Tyr	Thr	His	Leu	Gln	Arg	Ala	Gln	Pro	Val	Leu	Leu	Pro	His	Val
	210				215						220				
Leu	Leu	Thr	Phe	Val	Glu	Gln	Leu	Glu	Arg	Asp	Ala	Gly	Arg	Tyr	Val
225					230					235					240
Asp	Cys	Arg	Ala	Arg	Leu	Asn	Phe	Ser	Pro	Leu	Gly	Ala	Cys	Ala	Leu
				245					250					255	
Ala	Gly	Thr	Gly	Leu	Pro	Ile	Asp	Arg	Phe	Met	Thr	Ala	Asn	Ala	Leu
			260				265						270		
Gly	Phe	Thr	Glu	Pro	Met	Arg	Asn	Ser	Ile	Asp	Ala	Val	Ser	Asp	Arg
		275				280						285			
Asp	Phe	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Asn	Ala	Asn	Thr	Gly	Ile	His
	290					295					300				
Leu	Ser	Arg	Leu	Gly	Glu	Glu	Trp	Val	Leu	Trp	Ala	Ser	Glu	Glu	Phe
305					310					315					320
Gly	Phe	Met	Thr	Pro	Ser	Asp	Ser	Val	Ser	Thr	Gly	Ser	Ser	Ile	Met
				325					330					335	
Pro	Gln	Lys	Lys	Asn	Pro	Asp	Pro	Met	Glu	Leu	Val	Arg	Gly	Lys	Ser
			340					345					350		
Ala	Arg	Val	Ile	Gly	Asp	Leu	Val	Thr	Val	Leu	Thr	Leu	Cys	Lys	Gly
		355					360					365			
Leu	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Phe	Gln	Glu	Asp	Lys	Glu	Pro	Met
370						375					380				
Phe	Asp	Ser	Thr	Lys	Thr	Ile	Met	Gly	Met	Ile	Asp	Val	Ser	Ala	Glu
385					390						395				400
Phe	Ala	Gln	Asn	Val	Thr	Phe	Asn	Glu	Asp	Arg	Ile	Lys	Lys	Ser	Leu
				405					410					415	
Pro	Ala	Gly	His	Leu	Asp	Ala	Thr	Thr	Leu	Ala	Asp	Tyr	Leu	Val	Lys
			420					425				430			
Lys	Gly	Met	Pro	Phe	Arg	Ser	Ser	His	Asp	Ile	Val	Gly	Lys	Leu	Val
		435					440					445			
Gly	Val	Cys	Val	Ser	Lys	Gly	Cys	Glu	Leu	Gln	Asn	Leu	Ser	Leu	Glu
	450					455					460				
Glu	Met	Lys	Lys	Leu	Ser	Pro	Val	Phe	Glu						
465					470										

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

Met Ser His Asp Asp Asp Thr Ala Ser Lys Glu Val Lys Leu Trp Gly

1		5		10		15
Gly	Arg	Phe	Glu	Ser	Val	Thr
		20			25	
Ser	Ile	Ser	Phe	Asp	Lys	Val
		35			40	
Lys	Ala	His	Ala	Ser	Met	Leu
		50			55	
Asp	Lys	Asp	Ser	Ile	Leu	Arg
		65			70	
Glu	Ala	Asn	Lys	Phe	Glu	Trp
				85		
Asn	Ile	Glu	Ala	Leu	Thr	Asp
		100			105	
Leu	His	Thr	Ala	Arg	Ser	Arg
		115			120	
Leu	Trp	Cys	Arg	Asp	Ala	Ile
		130			135	
Leu	Gln	Arg	Ala	Leu	Val	Glu
		145			150	
Val	Pro	Gly	Tyr	Thr	His	Leu
				165		
His	Val	Leu	Leu	Thr	Phe	Val
		180			185	
Tyr	Val	Asp	Cys	Arg	Ala	Arg
		195			200	
Ala	Leu	Ala	Gly	Thr	Gly	Leu
		210			215	
Ala	Leu	Gly	Phe	Thr	Glu	Pro
		225			230	
Asp	Arg	Asp	Phe	Val	Leu	Glu
				245		
Ile	His	Leu	Ser	Arg	Leu	Gly
		260			265	
Glu	Phe	Gly	Phe	Met	Thr	Pro
		275			280	
Ile	Met	Pro	Gln	Lys	Lys	Asn
		290			295	
Lys	Ser	Ala	Arg	Val	Ile	Gly
		305			310	
Lys	Gly	Leu	Pro	Leu	Ala	Tyr
				325		
Pro	Met	Phe	Asp	Ser	Thr	Lys
				340		
Ala	Glu	Phe	Ala	Gln	Asn	Val
		355			360	
Ser	Leu	Pro	Ala	Gly	His	Leu
		370			375	
Val	Lys	Lys	Gly	Met	Pro	Phe
		385			390	
Leu	Val	Gly	Val	Cys	Val	Ser
				405		
Leu	Glu	Glu	Met	Lys	Lys	Leu
				420		

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..383
(D) OTHER INFORMATION: / Ceres Seq. ID 1500100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

Met	Gly	Ser	Lys	Ala	His	Ala	Ser	Met	Leu	Ala	His	Gln	Gly	Leu	Ile
1				5					10					15	
Thr	Asp	Ser	Asp	Lys	Asp	Ser	Ile	Leu	Arg	Gly	Leu	Asp	Asp	Ile	Glu
			20					25				30			
Arg	Gln	Ile	Glu	Ala	Asn	Lys	Phe	Glu	Trp	Arg	Thr	Asp	Arg	Glu	Asp
		35					40					45			
Val	His	Met	Asn	Ile	Glu	Ala	Ala	Leu	Thr	Asp	Leu	Ile	Gly	Glu	Pro
	50					55				60					
Ala	Lys	Lys	Leu	His	Thr	Ala	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr
65				70					75					80	
Asp	Phe	Arg	Leu	Trp	Cys	Arg	Asp	Ala	Ile	Asp	Thr	Ile	Ile	Val	Lys
			85					90						95	
Ile	Arg	Asn	Leu	Gln	Arg	Ala	Leu	Val	Glu	Leu	Ala	Leu	Lys	Asn	Glu
			100				105						110		
Ala	Leu	Ile	Val	Pro	Gly	Tyr	Thr	His	Leu	Gln	Arg	Ala	Gln	Pro	Val
	115						120					125			
Leu	Leu	Pro	His	Val	Leu	Leu	Thr	Phe	Val	Glu	Gln	Leu	Glu	Arg	Asp
	130					135				140					
Ala	Gly	Arg	Tyr	Val	Asp	Cys	Arg	Ala	Arg	Leu	Asn	Phe	Ser	Pro	Leu
145				150						155				160	
Gly	Ala	Cys	Ala	Leu	Ala	Gly	Thr	Gly	Leu	Pro	Ile	Asp	Arg	Phe	Met
			165					170						175	
Thr	Ala	Asn	Ala	Leu	Gly	Phe	Thr	Glu	Pro	Met	Arg	Asn	Ser	Ile	Asp
			180					185					190		
Ala	Val	Ser	Asp	Arg	Asp	Phe	Val	Leu	Glu	Phe	Leu	Tyr	Thr	Asn	Ala
	195						200					205			
Asn	Thr	Gly	Ile	His	Leu	Ser	Arg	Leu	Gly	Glu	Glu	Trp	Val	Leu	Trp
	210					215				220					
Ala	Ser	Glu	Glu	Phe	Gly	Phe	Met	Thr	Pro	Ser	Asp	Ser	Val	Ser	Thr
225				230						235				240	
Gly	Ser	Ser	Ile	Met	Pro	Gln	Lys	Lys	Asn	Pro	Asp	Pro	Met	Glu	Leu
			245						250					255	
Val	Arg	Gly	Lys	Ser	Ala	Arg	Val	Ile	Gly	Asp	Leu	Val	Thr	Val	Leu
			260					265					270		
Thr	Leu	Cys	Lys	Gly	Leu	Pro	Leu	Ala	Tyr	Asn	Arg	Asp	Phe	Gln	Glu
	275					280						285			
Asp	Lys	Glu	Pro	Met	Phe	Asp	Ser	Thr	Lys	Thr	Ile	Met	Gly	Met	Ile
	290					295					300				
Asp	Val	Ser	Ala	Glu	Phe	Ala	Gln	Asn	Val	Thr	Phe	Asn	Glu	Asp	Arg
305				310						315				320	
Ile	Lys	Lys	Ser	Leu	Pro	Ala	Gly	His	Leu	Asp	Ala	Thr	Thr	Leu	Ala
			325					330						335	
Asp	Tyr	Leu	Val	Lys	Lys	Gly	Met	Pro	Phe	Arg	Ser	Ser	His	Asp	Ile
		340					345						350		
Val	Gly	Lys	Leu	Val	Gly	Val	Cys	Val	Ser	Lys	Gly	Cys	Glu	Leu	Gln
	355					360						365			
Asn	Leu	Ser	Leu	Glu	Glu	Met	Lys	Lys	Leu	Ser	Pro	Val	Phe	Glu	
	370					375					380				

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..904

(D) OTHER INFORMATION: / Ceres Seq. ID 1500101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

actcttactc	tggtctcgct	acagaatctc	ctgggaaaaa	aaaaagaaac	ttgatccacc	60
cgaattcccc	aaatcttcac	aatttctgga	aactctctcg	atcgtgaagc	agaaaagtga	120
ggttccaaat	gggttctggt	tcgggtcaaa	cccgaattac	aacgatgaac	ctctcgctct	180
caacagcaga	gaagaaccct	aatttctgct	cggcgcttct	caattctaag	aacgcaattt	240
cagatacttt	aggggtctct	tccaaatgca	gtacattcct	caggggtcaa	tttcaaagaa	300
tacatttttc	ttggctacaa	cacactcgac	ctttgagaaa	acgaacagta	tttggtcacg	360
tgagctgcgt	catgccggtt	acggaagaga	atgtggagag	agtgttagac	gaagtacgac	420
catctcta	ggccgacgga	ggaaacgtgg	cggtgcacga	aatcgacgga	cttgtggtgg	480
ttttaagct	acaaggagct	tgtggttcgt	gtcctagctc	atcaatgacg	ttgaagatgg	540
gaatcgagag	tcgtcttcga	gacaagattc	cagagatcat	gtccgttgag	cagtttcttg	600
aatccgagac	aggaggttta	gagctgaacg	atgagaacat	tgagaagggt	ctctctgagt	660
taaggcgta	cctatccggt	actggaggtg	gggggcttga	gttagttgag	attgatgggt	720
acgtggtcaa	ggttcgactc	actggaccag	ctgctggagt	catgactgtt	cgtgtcgcgt	780
tgactcaaaa	actgagggaa	acaattcctt	ctataggtgc	agtccagctt	ctagagtgc	840
attaaccttt	ttattttgta	acttatatac	aaggcctatt	tttgattcaa	tatatattat	900
ttcc						

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1500102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

Met	Gly	Ser	Val	Ser	Gly	Gln	Thr	Arg	Ile	Thr	Thr	Met	Asn	Leu	Ser
1				5					10					15	
Leu	Ser	Thr	Ala	Glu	Lys	Asn	Pro	Asn	Phe	Cys	Ser	Ala	Leu	Leu	Asn
			20					25					30		
Ser	Lys	Asn	Ala	Ile	Ser	Asp	Thr	Leu	Gly	Val	Ser	Ser	Lys	Cys	Ser
		35					40					45			
Thr	Phe	Leu	Arg	Gly	Gln	Phe	Gln	Arg	Ile	His	Phe	Ser	Trp	Leu	Gln
	50				55					60					
His	Thr	Arg	Pro	Leu	Arg	Lys	Arg	Thr	Val	Phe	Gly	His	Val	Ser	Cys
65					70					75				80	
Val	Met	Pro	Leu	Thr	Glu	Glu	Asn	Val	Glu	Arg	Val	Leu	Asp	Glu	Val
				85					90					95	
Arg	Pro	Ser	Leu	Met	Ala	Asp	Gly	Gly	Asn	Val	Ala	Leu	His	Glu	Ile
			100					105					110		
Asp	Gly	Leu	Val	Val	Val	Leu	Lys	Leu	Gln	Gly	Ala	Cys	Gly	Ser	Cys
		115					120					125			
Pro	Ser	Ser	Ser	Met	Thr	Leu	Lys	Met	Gly	Ile	Glu	Ser	Arg	Leu	Arg
		130				135					140				
Asp	Lys	Ile	Pro	Glu	Ile	Met	Ser	Val	Glu	Gln	Phe	Leu	Glu	Ser	Glu
145					150					155				160	
Thr	Gly	Gly	Leu	Glu	Leu	Asn	Asp	Glu	Asn	Ile	Glu	Lys	Val	Leu	Ser
			165						170					175	
Glu	Leu	Arg	Pro	Tyr	Leu	Ser	Gly	Thr	Gly	Gly	Gly	Gly	Leu	Glu	Leu
			180					185					190		
Val	Glu	Ile	Asp	Gly	Tyr	Val	Val	Lys	Val	Arg	Leu	Thr	Gly	Pro	Ala
		195					200					205			
Ala	Gly	Val	Met	Thr	Val	Arg	Val	Ala	Leu	Thr	Gln	Lys	Leu	Arg	Glu
	210					215					220				
Thr	Ile	Pro	Ser	Ile	Gly	Ala	Val	Gln	Leu	Leu	Glu				
225					230						235				

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1500103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

Met Asn Leu Ser Leu Ser Thr Ala Glu Lys Asn Pro Asn Phe Cys Ser
1 5 10 15
Ala Leu Leu Asn Ser Lys Asn Ala Ile Ser Asp Thr Leu Gly Val Ser
20 25 30
Ser Lys Cys Ser Thr Phe Leu Arg Gly Gln Phe Gln Arg Ile His Phe
35 40 45
Ser Trp Leu Gln His Thr Arg Pro Leu Arg Lys Arg Thr Val Phe Gly
50 55 60
His Val Ser Cys Val Met Pro Leu Thr Glu Glu Asn Val Glu Arg Val
65 70 75 80
Leu Asp Glu Val Arg Pro Ser Leu Met Ala Asp Gly Gly Asn Val Ala
85 90 95
Leu His Glu Ile Asp Gly Leu Val Val Val Leu Lys Leu Gln Gly Ala
100 105 110
Cys Gly Ser Cys Pro Ser Ser Ser Met Thr Leu Lys Met Gly Ile Glu
115 120 125
Ser Arg Leu Arg Asp Lys Ile Pro Glu Ile Met Ser Val Glu Gln Phe
130 135 140
Leu Glu Ser Glu Thr Gly Gly Leu Glu Leu Asn Asp Glu Asn Ile Glu
145 150 155 160
Lys Val Leu Ser Glu Leu Arg Pro Tyr Leu Ser Gly Thr Gly Gly Gly
165 170 175
Gly Leu Glu Leu Val Glu Ile Asp Gly Tyr Val Val Lys Val Arg Leu
180 185 190
Thr Gly Pro Ala Ala Gly Val Met Thr Val Arg Val Ala Leu Thr Gln
195 200 205
Lys Leu Arg Glu Thr Ile Pro Ser Ile Gly Ala Val Gln Leu Leu Glu
210 215 220

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

Met Pro Leu Thr Glu Glu Asn Val Glu Arg Val Leu Asp Glu Val Arg
1 5 10 15
Pro Ser Leu Met Ala Asp Gly Gly Asn Val Ala Leu His Glu Ile Asp
20 25 30
Gly Leu Val Val Val Leu Lys Leu Gln Gly Ala Cys Gly Ser Cys Pro
35 40 45
Ser Ser Ser Met Thr Leu Lys Met Gly Ile Glu Ser Arg Leu Arg Asp

50	55	60
Lys Ile Pro Glu Ile Met Ser Val Glu Gln Phe Leu Glu Ser Glu Thr		
65	70	75
Gly Gly Leu Glu Leu Asn Asp Glu Asn Ile Glu Lys Val Leu Ser Glu		80
	85	90
Leu Arg Pro Tyr Leu Ser Gly Thr Gly Gly Gly Gly Leu Glu Leu Val		95
	100	105
Glu Ile Asp Gly Tyr Val Val Lys Val Arg Leu Thr Gly Pro Ala Ala		110
	115	120
Gly Val Met Thr Val Arg Val Ala Leu Thr Gln Lys Leu Arg Glu Thr		125
	130	135
Ile Pro Ser Ile Gly Ala Val Gln Leu Leu Glu		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1640
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

acatggtcctt gttctttctc tctccttctt ttctcatctt gcggttccc tttctctctc	60
tatcgccaca atgatcatta ccaaccaaac tgattgaaac tcatttggtc tctctctctc	120
aaatccactc tctctctttc ttttctcttc tcctctctgt gtctctatcg ccatggctga	180
tgataaggag atgcctgctg ctgtagttga tggacatgat caagtcactg gtcattat	240
ttccaccaca atcgggtggca aaaaagggtga accaaaacag acaattagtt acatggcgga	300
sgagttggtg gtacaggctc gttcgggatc gttttccaag caaaatgttt ggagactgga	360
gaaaccgtgg cgataaagaa ggttttgcaa gatagaagat acaagaaccg agaacttcag	420
ttgatgcgtg tgatggatca tccgaatgtg gtttggttga agcattgctt cttttcgact	480
acaagtaaag acgagctttt cttgaacttg gttatggagt atgtccctga gagcttgat	540
cgagttctga aacattatag tagtgcaaac caaagaatgc ctcttgctta tgttaaactt	600
tacatgtatc agatcttccg gggacttgct tacattcaca atgttgctgg agtttgctac	660
agagatctaa agcctcaaaa tcttctggtt gatectctta ctcatcaagt caaaatctgt	720
gactttggca gtgcgaaaca gctcgtaaaa ggtgaagcca acatttctta catctgctca	780
cgattctacc gtgcaccga gctcatattt ggtgccactg agtacacaac ttctattgat	840
atctggctctg ctggttggtg tcttgctgag cttcttcttg gtcagccatt atttcccgga	900
gaaaatgctg tggatcagct cgttgaaatt ataaaagttc ttggtacacc aactcgagaa	960
gaaatccgtt gtatgaatcc acattacaca gatttcaggt ttccacagat aaaggcacat	1020
ccctggcaca agatcttcca caaaaggatg cccccagaag cgattgattt tgcataaagg	1080
ctgcttcaat actctccaag tctaagatgc acagcgctcg aagcttgctg acatccgttc	1140
tttgatgaac tcagagaagc whmccaaacg ctcgtttmcc aaatggacgg cctttcccgc	1200
ctctcttcaa cttcaaacaa gaagtagctg gatcatcacc tgaactggtc acaagttga	1260
ttccagacca tatcaagaga caattgggtc taagcttctt gaatcaatct ggaacttaaa	1320
agggatcctg caaaagacaa ctactttttt atatataatg taccattaca cgagccacaa	1380
ggtcgtgatt gaaggcaaac gtggaggaca caattcaaag tttttcctcc tcaaactcgt	1440
tcagacaaag ccagctgcta gcaaaaccaa ctacccaaat ctgcgaaaac aaaaactctc	1500
cagtgttgta tctgcttatt tctcttctct tttcaagttt ggtgaaaaac acagtctcct	1560
ctttgcttca tttcttcttt ctttccccct tatgtaaagt agtttagtca gaagtttttt	1620
tatatagtaa agtttgggcg	

(2) INFORMATION FOR SEQ ID NO:1364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..267

(D) OTHER INFORMATION: / Ceres Seq. ID 1500106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

Met	Arg	Val	Met	Asp	His	Pro	Asn	Val	Val	Cys	Leu	Lys	His	Cys	Phe
1			5						10					15	
Phe	Ser	Thr	Thr	Ser	Lys	Asp	Glu	Leu	Phe	Leu	Asn	Leu	Val	Met	Glu
			20					25					30		
Tyr	Val	Pro	Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser	Ser	Ala
			35				40					45			
Asn	Gln	Arg	Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr	Gln	Ile
	50					55					60				
Phe	Arg	Gly	Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys	His	Arg
65					70					75					80
Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His	Gln	Val
				85					90					95	
Lys	Ile	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly	Glu	Ala
			100					105					110		
Asn	Ile	Ser	Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Leu	Ile
	115						120					125			
Phe	Gly	Ala	Thr	Glu	Tyr	Thr	Ser	Ile	Asp	Ile	Trp	Ser	Ala	Gly	
	130					135				140					
Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Glu
145					150					155					160
Asn	Ala	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly	Thr	Pro
				165						170					175
Thr	Arg	Glu	Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp	Phe	Arg
			180					185					190		
Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His	Lys	Arg
	195						200					205			
Met	Pro	Pro	Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln	Tyr	Ser
	210					215					220				
Pro	Ser	Leu	Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro	Phe	Phe
225					230					235					240
Asp	Glu	Leu	Arg	Glu	Xaa	Xaa	Gln	Thr	Leu	Val	Xaa	Gln	Met	Asp	Gly
				245					250					255	
Leu	Ser	Arg	Leu	Ser	Ser	Thr	Ser	Asn	Lys	Lys					
			260					265							

(2) INFORMATION FOR SEQ ID NO:1365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..264

(D) OTHER INFORMATION: / Ceres Seq. ID 1500107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

Met	Asp	His	Pro	Asn	Val	Val	Cys	Leu	Lys	His	Cys	Phe	Phe	Ser	Thr
1				5					10					15	
Thr	Ser	Lys	Asp	Glu	Leu	Phe	Leu	Asn	Leu	Val	Met	Glu	Tyr	Val	Pro
			20					25					30		
Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser	Ser	Ala	Asn	Gln	Arg
			35				40					45			
Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr	Gln	Ile	Phe	Arg	Gly
	50					55					60				
Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys	His	Arg	Asp	Leu	Lys
65				70						75				80	
Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His	Gln	Val	Lys	Ile	Cys

				85					90					95			
Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly	Glu	Ala	Asn	Ile	Ser		
			100					105					110				
Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Leu	Ile	Phe	Gly	Ala		
		115					120					125					
Thr	Glu	Tyr	Thr	Thr	Ser	Ile	Asp	Ile	Trp	Ser	Ala	Gly	Cys	Val	Leu		
	130					135					140						
Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Glu	Asn	Ala	Val		
145					150					155					160		
Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly	Thr	Pro	Thr	Arg	Glu		
			165					170						175			
Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp	Phe	Arg	Phe	Pro	Gln		
		180						185					190				
Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His	Lys	Arg	Met	Pro	Pro		
	195						200					205					
Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln	Tyr	Ser	Pro	Ser	Leu		
	210					215					220						
Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro	Phe	Phe	Asp	Glu	Leu		
225					230					235					240		
Arg	Glu	Xaa	Xaa	Gln	Thr	Leu	Val	Xaa	Gln	Met	Asp	Gly	Leu	Ser	Arg		
			245					250						255			
Leu	Ser	Ser	Thr	Ser	Asn	Lys	Lys										
			260														

(2) INFORMATION FOR SEQ ID NO:1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1500108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

Met	Glu	Tyr	Val	Pro	Glu	Ser	Leu	Tyr	Arg	Val	Leu	Lys	His	Tyr	Ser		
1			5					10						15			
Ser	Ala	Asn	Gln	Arg	Met	Pro	Leu	Val	Tyr	Val	Lys	Leu	Tyr	Met	Tyr		
		20					25					30					
Gln	Ile	Phe	Arg	Gly	Leu	Ala	Tyr	Ile	His	Asn	Val	Ala	Gly	Val	Cys		
	35				40						45						
His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Val	Asp	Pro	Leu	Thr	His		
	50				55					60							
Gln	Val	Lys	Ile	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val	Lys	Gly		
65				70				75						80			
Glu	Ala	Asn	Ile	Ser	Tyr	Ile	Cys	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu		
		85						90					95				
Leu	Ile	Phe	Gly	Ala	Thr	Glu	Tyr	Thr	Thr	Ser	Ile	Asp	Ile	Trp	Ser		
	100						105					110					
Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Leu	Phe	Pro		
	115					120					125						
Gly	Glu	Asn	Ala	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu	Gly		
	130				135						140						
Thr	Pro	Thr	Arg	Glu	Glu	Ile	Arg	Cys	Met	Asn	Pro	His	Tyr	Thr	Asp		
145				150				155						160			
Phe	Arg	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	His	Lys	Ile	Phe	His		
		165						170					175				
Lys	Arg	Met	Pro	Pro	Glu	Ala	Ile	Asp	Phe	Ala	Ser	Arg	Leu	Leu	Gln		
	180							185					190				
Tyr	Ser	Pro	Ser	Leu	Arg	Cys	Thr	Ala	Leu	Glu	Ala	Cys	Ala	His	Pro		
	195						200					205					

Phe Phe Asp Glu Leu Arg Glu Xaa Xaa Gln Thr Leu Val Xaa Gln Met
210 215 220
Asp Gly Leu Ser Arg Leu Ser Ser Thr Ser Asn Lys Lys
225 230 235

(2) INFORMATION FOR SEQ ID NO:1367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1841
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

cattaggatt ttgaatttcc aaatacat	ttcagaaaaa aagaattaaa agatcccatt	60
gttgttatcc tcacagtaaa tgcttttgct	tgagagagag tctgttagag gttttttggt	120
tgtttctgtt tccttctgtc acccagaaaa	ctaaaaagca acaaaattca agaagagaga	180
gagagagata gcctcaaaac caagtcctaa	ccattgttga tagaagagaa agcttttctt	240
ttcttggtgc ttatggtgaa agaattgaa	agagagagga ggagaagtaa gaagcagaga	300
aagtgtttag agcttttgcg gttcctttct	ctccaagttt atatcttcat cggtttcaca	360
agttcactta aaaagttgaa aagagtcttt	cttcttcaac tattgtaaat gcgaaatgga	420
tcgaagagat gcaatgggat tatccgggtc	aggttcttac tatatccata gaggattacc	480
cgggtcgggt cctccaacgt ttcatggatc	accacagcaa cagcaaggtc ttcgtcactt	540
acctaataca aactctccat tcgggtcagg	ctccactggt ttcggatctc cttctttaca	600
cggtgatcct tctctggcaa cagcagccgg	aggagccgga gctcttcctc atcatatcgg	660
cgtaaatatg attgctcctc ctccacctcc	cagtgaact ccgatgaaac gaaagagagg	720
acggcctaga aaatacggtc aagacggctc	tgtttctttg gctctgtcgt cttcctctgt	780
ttcgaccatt actcccaaca actctaaca	acgcggccgt ggtcgacctc cgggctccgg	840
caagaacacag agaattggctt ccggttggtg	actgatgcct tcacttcttg gaatgagctt	900
cacgccacat gttatcgcggt tttcaatagg	agaagatatt gcatcaaagg ttatagcttt	960
ctctcaacaa ggtccgagag ccatttgcgt	tttatctgca agtgggtgcag tctctactgc	1020
aacacttatt caaccatcag catctcccgg	agccattaaa tacgagggcc ggtttgaaat	1080
cctagcggtta tcaacatctt atatagtggc	aactgatgga agcttccgta accgaactgg	1140
aaacttatcg gtttgcgttg ctagccccga	tgggcgtgtg attggcgggtg ccattgggtg	1200
gcctttaata gctgcaagtc ctgttcagggt	tattgtaggg agctttatat gggcagctcc	1260
aaagatcaag agcaagaaac gagaagaaga	agcttctgaa gttgttcaag aaactgatga	1320
tcaccacggt ctggacaata ataacaacac	gatttcgcct gtccctcagc agcagccaaa	1380
ccaaaacctg atttgggtcaa caggttcaag	gcaaattgat atgcgtcatg ctcatgctga	1440
tattgattta atgcgcgggt gatgatagcg	agaaagaact ctgtgtatat aaagcatgga	1500
atctaggaag aagaagaagg aatataagct	aacctctgaa caaaagtatg tggaaatgtt	1560
agggaanaag attaactcta ttagtgtacc	tctcatatct ctaagcttgt ttggttttac	1620
tgtttctgtg actctgaaga ttgacagagt	tcctttcttt ctctgtttta gattgttcag	1680
tctttatgta atttgcttgc aattctgatt	ctacagctta gattcagtac attgtgtaga	1740
agtttacatg ggaacctgaa aattgggcat	ttcatgggcc ttcatatgat ccaatttatt	1800
ttcatcaaat ttgtattagt acataattaa	ttttgttttt t	

(2) INFORMATION FOR SEQ ID NO:1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

Met Asp Arg Arg Asp Ala Met Gly Leu Ser Gly Ser Gly Ser Tyr Tyr
1 5 10 15

Ile His Arg Gly Leu Pro Gly Ser Gly Pro Pro Thr Phe His Gly Ser
20 25 30
Pro Gln Gln Gln Gln Gly Leu Arg His Leu Pro Asn Gln Asn Ser Pro
35 40 45
Phe Gly Ser Gly Ser Thr Gly Phe Gly Ser Pro Ser Leu His Gly Asp
50 55 60
Pro Ser Leu Ala Thr Ala Ala Gly Gly Ala Gly Ala Leu Pro His His
65 70 75 80
Ile Gly Val Asn Met Ile Ala Pro Pro Pro Pro Pro Ser Glu Thr Pro
85 90 95
Met Lys Arg Lys Arg Gly Arg Pro Arg Lys Tyr Gly Gln Asp Gly Ser
100 105 110
Val Ser Leu Ala Leu Ser Ser Ser Val Ser Thr Ile Thr Pro Asn
115 120 125
Asn Ser Asn Lys Arg Gly Arg Gly Arg Pro Pro Gly Ser Gly Lys Lys
130 135 140
Gln Arg Met Ala Ser Val Gly Glu Leu Met Pro Ser Ser Ser Gly Met
145 150 155 160
Ser Phe Thr Pro His Val Ile Ala Val Ser Ile Gly Glu Asp Ile Ala
165 170 175
Ser Lys Val Ile Ala Phe Ser Gln Gln Gly Pro Arg Ala Ile Cys Val
180 185 190
Leu Ser Ala Ser Gly Ala Val Ser Thr Ala Thr Leu Ile Gln Pro Ser
195 200 205
Ala Ser Pro Gly Ala Ile Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala
210 215 220
Leu Ser Thr Ser Tyr Ile Val Ala Thr Asp Gly Ser Phe Arg Asn Arg
225 230 235 240
Thr Gly Asn Leu Ser Val Ser Leu Ala Ser Pro Asp Gly Arg Val Ile
245 250 255
Gly Gly Ala Ile Gly Gly Pro Leu Ile Ala Ala Ser Pro Val Gln Val
260 265 270
Ile Val Gly Ser Phe Ile Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys
275 280 285
Arg Glu Glu Glu Ala Ser Glu Val Val Gln Glu Thr Asp Asp His His
290 295 300
Val Leu Asp Asn Asn Asn Asn Thr Ile Ser Pro Val Pro Gln Gln Gln
305 310 315 320
Pro Asn Gln Asn Leu Ile Trp Ser Thr Gly Ser Arg Gln Met Asp Met
325 330 335
Arg His Ala His Ala Asp Ile Asp Leu Met Arg Gly
340 345

(2) INFORMATION FOR SEQ ID NO:1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

Met Gly Leu Ser Gly Ser Gly Ser Tyr Ile His Arg Gly Leu Pro
1 5 10 15
Gly Ser Gly Pro Pro Thr Phe His Gly Ser Pro Gln Gln Gln Gln Gly
20 25 30
Leu Arg His Leu Pro Asn Gln Asn Ser Pro Phe Gly Ser Gly Ser Thr
35 40 45
Gly Phe Gly Ser Pro Ser Leu His Gly Asp Pro Ser Leu Ala Thr Ala

50	55	60
Ala Gly Gly Ala Gly	Ala Leu Pro His His	Ile Gly Val Asn Met Ile
65	70	75
Ala Pro Pro Pro Pro	Pro Ser Glu Thr Pro	Met Lys Arg Lys Arg Gly
85	90	95
Arg Pro Arg Lys Tyr Gly	Gln Asp Gly Ser Val	Ser Leu Ala Leu Ser
100	105	110
Ser Ser Ser Val Ser Thr	Ile Thr Pro Asn Asn	Ser Asn Lys Arg Gly
115	120	125
Arg Gly Arg Pro Pro Gly	Ser Gly Lys Lys Gln	Arg Met Ala Ser Val
130	135	140
Gly Glu Leu Met Pro Ser	Ser Ser Gly Met Ser	Phe Thr Pro His Val
145	150	155
Ile Ala Val Ser Ile Gly	Glu Asp Ile Ala Ser	Lys Val Ile Ala Phe
165	170	175
Ser Gln Gln Gly Pro Arg	Ala Ile Cys Val Leu	Ser Ala Ser Gly Ala
180	185	190
Val Ser Thr Ala Thr Leu	Ile Gln Pro Ser Ala	Ser Pro Gly Ala Ile
195	200	205
Lys Tyr Glu Gly Arg Phe	Glu Ile Leu Ala Leu	Ser Thr Ser Tyr Ile
210	215	220
Val Ala Thr Asp Gly Ser	Phe Arg Asn Arg Thr	Gly Asn Leu Ser Val
225	230	235
Ser Leu Ala Ser Pro Asp	Gly Arg Val Ile Gly	Gly Ala Ile Gly Gly
245	250	255
Pro Leu Ile Ala Ala Ser	Pro Val Gln Val Ile	Val Gly Ser Phe Ile
260	265	270
Trp Ala Ala Pro Lys Ile	Lys Ser Lys Arg Glu	Glu Glu Ala Ser
275	280	285
Glu Val Val Gln Glu Thr	Asp Asp His His Val	Leu Asp Asn Asn Asn
290	295	300
Asn Thr Ile Ser Pro Val	Pro Gln Gln Gln Pro	Asn Gln Asn Leu Ile
305	310	315
Trp Ser Thr Gly Ser Arg	Gln Met Asp Met Arg	His Ala His Ala Asp
325	330	335
Ile Asp Leu Met Arg Gly		
340		

(2) INFORMATION FOR SEQ ID NO:1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..264
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

Met Ile Ala Pro Pro Pro Pro Pro	Ser Glu Thr Pro Met Lys Arg Lys
1	15
Arg Gly Arg Pro Arg Lys Tyr Gly	Gln Asp Gly Ser Val Ser Leu Ala
20	30
Leu Ser Ser Ser Ser Val Ser Thr	Ile Thr Pro Asn Asn Ser Asn Lys
35	45
Arg Gly Arg Gly Arg Pro Pro Gly	Ser Gly Lys Lys Gln Arg Met Ala
50	60
Ser Val Gly Glu Leu Met Pro Ser Ser	Ser Gly Met Ser Phe Thr Pro
65	80
His Val Ile Ala Val Ser Ile Gly	Glu Asp Ile Ala Ser Lys Val Ile
85	95

Ala Phe Ser Gln Gln Gly Pro Arg Ala Ile Cys Val Leu Ser Ala Ser
100 105 110
Gly Ala Val Ser Thr Ala Thr Leu Ile Gln Pro Ser Ala Ser Pro Gly
115 120 125
Ala Ile Lys Tyr Glu Gly Arg Phe Glu Ile Leu Ala Leu Ser Thr Ser
130 135 140
Tyr Ile Val Ala Thr Asp Gly Ser Phe Arg Asn Arg Thr Gly Asn Leu
145 150 155 160
Ser Val Ser Leu Ala Ser Pro Asp Gly Arg Val Ile Gly Gly Ala Ile
165 170 175
Gly Gly Pro Leu Ile Ala Ala Ser Pro Val Gln Val Ile Val Gly Ser
180 185 190
Phe Ile Trp Ala Ala Pro Lys Ile Lys Ser Lys Lys Arg Glu Glu Glu
195 200 205
Ala Ser Glu Val Val Gln Glu Thr Asp Asp His His Val Leu Asp Asn
210 215 220
Asn Asn Asn Thr Ile Ser Pro Val Pro Gln Gln Gln Pro Asn Gln Asn
225 230 235 240
Leu Ile Trp Ser Thr Gly Ser Arg Gln Met Asp Met Arg His Ala His
245 250 255
Ala Asp Ile Asp Leu Met Arg Gly
260

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1270
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

atctacaact	ttcattcttc	cactacat	ctctccttga	gtatcttctt	atcctat	60
ccaaattcca	aaacaattca	caaaatggct	acatgctggc	ctgagccgat	tgtttccg	120
caatccttgt	cccaaaccgg	tgtaccaact	gtaccaaacc	gctatgtgaa	gccggctcat	180
cagagaccgg	tctttaacac	cacccaatcc	gatgctggga	tagaaatccc	tgttctagac	240
atgaacgacg	tttgggggaa	accagagggg	ctaaggctcg	tgaggagcgc	gtgtgaggag	300
tgggggtttct	tccaaatggg	gaaccatggg	gtgacccact	cgttgatgga	gagagtgaga	360
ggagcgtggc	gagagttctt	cgagctaccg	ctagaggaga	aacggaagta	tgcaaaactca	420
ccggacacgt	acgaggggata	tgggaagccgc	cttgggggttg	tgagagatgc	taaattagat	480
tggagtgatt	atttcttctt	caattacttg	ccttcttcca	taagaaaccc	ttccaagtgg	540
ccatactcag	cctcctaaga	tcagagaatt	gatcgaaaag	tacggagaag	aagtgagaaa	600
actgtgcgaa	aggctaacag	agacgttgct	agagagttta	ggtttaaaac	caaacaagct	660
catgcaggct	ttaggaggag	gcgacaaagt	cggagcttct	ctgaggacaa	acttctaccc	720
aaaatgccct	cagccgcagc	tcacttttagg	tctctcttct	cattctgacc	ctggaggcat	780
caccattctt	ctcccggaag	agaaggtcgc	tggccttcag	gtccgctcgtg	gtgatggctg	840
ggtcaccatt	aaatcagtc	ctaattgctt	gatcggttaac	attggagatc	aacttcagat	900
acttagcaat	ggaatttaca	aaagcgtgga	acatcaagtg	atcggttaatt	ccggtatgga	960
acgagtctct	ttggcattct	tctataaccc	gagaagtgat	atcccgggtg	gaccaatcga	1020
agaactagta	actgcaaacc	gacctgctct	ttataaacca	atcaggttcg	acgagtaccg	1080
ttctctgata	aggcaaaagg	gtccttgttg	aaaaaaccaa	gtcgactcac	tgttattaac	1140
tagataataa	ttgataaaca	ttccaagtat	tatctgttat	tcctatgtcc	ttgatatagt	1200
cgttactaaa	taatatgtaa	accgtatctt	cactttttct	tatttatattg	ctgctctctc	1260
ttgaggtttg						

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..185
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500116
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

Ile	Tyr	Asn	Phe	His	Ser	Ser	Thr	Thr	Phe	Leu	Ser	Leu	Ser	Ile	Phe
1				5					10					15	
Leu	Ser	Tyr	Phe	Pro	Asn	Ser	Lys	Thr	Ile	His	Lys	Met	Ala	Thr	Cys
			20					25					30		
Trp	Pro	Glu	Pro	Ile	Val	Ser	Val	Gln	Ser	Leu	Ser	Gln	Thr	Gly	Val
		35					40					45			
Pro	Thr	Val	Pro	Asn	Arg	Tyr	Val	Lys	Pro	Ala	His	Gln	Arg	Pro	Val
		50				55					60				
Phe	Asn	Thr	Thr	Gln	Ser	Asp	Ala	Gly	Ile	Glu	Ile	Pro	Val	Leu	Asp
65					70					75				80	
Met	Asn	Asp	Val	Trp	Gly	Lys	Pro	Glu	Gly	Leu	Arg	Leu	Val	Arg	Ser
			85						90					95	
Ala	Cys	Glu	Glu	Trp	Gly	Phe	Phe	Gln	Met	Val	Asn	His	Gly	Val	Thr
			100					105					110		
His	Ser	Leu	Met	Glu	Arg	Val	Arg	Gly	Ala	Trp	Arg	Glu	Phe	Phe	Glu
		115					120					125			
Leu	Pro	Leu	Glu	Glu	Lys	Arg	Lys	Tyr	Ala	Asn	Ser	Pro	Asp	Thr	Tyr
	130					135					140				
Glu	Gly	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Val	Arg	Asp	Ala	Lys	Leu	Asp
145					150					155				160	
Trp	Ser	Asp	Tyr	Phe	Phe	Leu	Asn	Tyr	Leu	Pro	Ser	Ser	Ile	Arg	Asn
			165						170					175	
Pro	Ser	Lys	Trp	Pro	Tyr	Ser	Ala	Ser							
			180					185							

(2) INFORMATION FOR SEQ ID NO:1373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500117
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

Met	Ala	Thr	Cys	Trp	Pro	Glu	Pro	Ile	Val	Ser	Val	Gln	Ser	Leu	Ser
1				5					10					15	
Gln	Thr	Gly	Val	Pro	Thr	Val	Pro	Asn	Arg	Tyr	Val	Lys	Pro	Ala	His
			20					25					30		
Gln	Arg	Pro	Val	Phe	Asn	Thr	Thr	Gln	Ser	Asp	Ala	Gly	Ile	Glu	Ile
		35					40					45			
Pro	Val	Leu	Asp	Met	Asn	Asp	Val	Trp	Gly	Lys	Pro	Glu	Gly	Leu	Arg
	50					55					60				
Leu	Val	Arg	Ser	Ala	Cys	Glu	Glu	Trp	Gly	Phe	Phe	Gln	Met	Val	Asn
65					70					75				80	
His	Gly	Val	Thr	His	Ser	Leu	Met	Glu	Arg	Val	Arg	Gly	Ala	Trp	Arg
			85					90						95	
Glu	Phe	Phe	Glu	Leu	Pro	Leu	Glu	Glu	Lys	Arg	Lys	Tyr	Ala	Asn	Ser
			100					105					110		
Pro	Asp	Thr	Tyr	Glu	Gly	Tyr	Gly	Ser	Arg	Leu	Gly	Val	Val	Arg	Asp
		115					120						125		
Ala	Lys	Leu	Asp	Trp	Ser	Asp	Tyr	Phe	Phe	Leu	Asn	Tyr	Leu	Pro	Ser
	130						135						140		

Ser Ile Arg Asn Pro Ser Lys Trp Pro Tyr Ser Ala Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

```
Met Gln Ala Leu Gly Gly Gly Asp Lys Val Gly Ala Ser Leu Arg Thr
1      5      10      15
Asn Phe Tyr Pro Lys Cys Pro Gln Pro Gln Leu Thr Leu Gly Leu Ser
20      25      30
Ser His Ser Asp Pro Gly Gly Ile Thr Ile Leu Leu Pro Asp Glu Lys
35      40      45
Val Ala Gly Leu Gln Val Arg Arg Gly Asp Gly Trp Val Thr Ile Lys
50      55      60
Ser Val Pro Asn Ala Leu Ile Val Asn Ile Gly Asp Gln Leu Gln Ile
65      70      75      80
Leu Ser Asn Gly Ile Tyr Lys Ser Val Glu His Gln Val Ile Val Asn
85      90      95
Ser Gly Met Glu Arg Val Ser Leu Ala Phe Phe Tyr Asn Pro Arg Ser
100     105     110
Asp Ile Pro Val Gly Pro Ile Glu Leu Val Thr Ala Asn Arg Pro
115     120     125
Ala Leu Tyr Lys Pro Ile Arg Phe Asp Glu Tyr Arg Ser Leu Ile Arg
130     135     140
Gln Lys Gly Pro Cys Gly Lys Asn Gln Val Asp Ser Leu Leu Leu Thr
145     150     155     160
Arg
```

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1756
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

```
gctctgattc attcacaaat aacaatcctc tcttcgtttt tgtttttctt ttggatccaa      60
agctctctta aatctgtaaa tcaacaatgg ccgccaccac tgagaatctc cctcaactca      120
aatccgccgt cgatggcctt actgagatga gtgagagtga gaagagcgga ttcacagcc      180
tggtttcacg ttacctgagc ggtgaggcac aacacattga gtggagtaag atccagactc      240
ctaccgatga aatcgttgtt ccctacgaga aaatgacccc tgtctcccaa gatgttgccg      300
agaccaagaa tctgttggac aaacttgttg tgttgaagct taatggagggt cttggaacaa      360
caatgggatg cactggcccg aagtccgtta tcgaagtctg tgatggtttg acatttcttg      420
atctgattgt tatccagatt gagaatctca acaacaagta tggctgcaag gttccgttag      480
ttctcatgaa ctcgtttaat acacatgatg acagacataa gattgtggaa aagtacacca      540
actcaaatgt tgacattcac acttttaacc agagcaaata tccccgtgtt gtggcagatg      600
agtttgtgcc atggcccagc aagggaaaga ccgacaagga gggctggtat cctcccggtc      660
atggtgatgt attcccagcc ctcatgaaca gtggaaagct cgatactttc ttatcacagg      720
gtaaggaata tgtgtttgtt gccaatcag acaactggg tgccatcggt gacttaacaa      780
```

```
tcttgaagca tttgatccag aacaagaacg aatactgcat ggaggttaca cccaaaacct 840
tagctgatgt aaagggggga actctcattt cttatgaagg caaagtccag cttctggaga 900
ttgctcagtt tcttgatgaa catgtcaatg agttcaaatac aattgagaag ttcaagatat 960
tcaacacaaa caacctatgg gtttaacttga aggccatcaa aaagcttggt gaagctgatg 1020
cacttaaaat ggagatcatt ccaaaccctaa aggaagtgtga tggagtcaaa gttcttcaac 1080
tggaactgc agcgggtgct gcgataaggt tctttgacaa cgctatcggt gttaatgtac 1140
ctcgtcacg gttcttgcca gtgaaggcaa gttcagactt gctgctcgtc cagtctgac 1200
tctacacctt agttgatggc tttgtcactc gaaacaaagc tagaactaac ccctcgaacc 1260
cgtcaattga attgggaccc gagttcaaga aggtggctac tttcttgagc cggtttaagt 1320
ccattcctag tatagtcgag ctgcacagcc ttaaggtgtc tgggtgatgtc tggtttggtc 1380
cttccattgt tctcaagggc aaggtgactg tggcgccaaa atccgggtgtg aagcttgaaa 1440
ttccggacag ggccgtggtc gagaacaaga acatcaatgg tccagaagac ctctgaataa 1500
aacaaattca agtcttcttc cctctctcat ggaagacaca tcttgatact cctttaattg 1560
gtgtgaaaag atcacaagtg gcacagcaaa gcaagtttat gaagaaagaa taaataatgt 1620
ttctttttct ttttgacgt tagcaagtc ttttctctt tggactttat ttttaatttg 1680
ctctttgaat tttccaaaa catcacattt atatgttcga ttataatttg gttctatcca 1740
caatcatttt tctttt
```

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..469

(D) OTHER INFORMATION: / Ceres Seq. ID 1500132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

```
Met Ala Ala Thr Thr Glu Asn Leu Pro Gln Leu Lys Ser Ala Val Asp
1          5          10          15
Gly Leu Thr Glu Met Ser Glu Ser Glu Lys Ser Gly Phe Ile Ser Leu
20        25        30
Val Ser Arg Tyr Leu Ser Gly Glu Ala Gln His Ile Glu Trp Ser Lys
35        40        45
Ile Gln Thr Pro Thr Asp Glu Ile Val Val Pro Tyr Glu Lys Met Thr
50        55        60
Pro Val Ser Gln Asp Val Ala Glu Thr Lys Asn Leu Leu Asp Lys Leu
65        70        75        80
Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr Met Gly Cys Thr
85        90        95
Gly Pro Lys Ser Val Ile Glu Val Arg Asp Gly Leu Thr Phe Leu Asp
100       105       110
Leu Ile Val Ile Gln Ile Glu Asn Leu Asn Asn Lys Tyr Gly Cys Lys
115       120       125
Val Pro Leu Val Leu Met Asn Ser Phe Asn Thr His Asp Asp Arg His
130       135       140
Lys Ile Val Glu Lys Tyr Thr Asn Ser Asn Val Asp Ile His Thr Phe
145       150       155       160
Asn Gln Ser Lys Tyr Pro Arg Val Val Ala Asp Glu Phe Val Pro Trp
165       170       175
Pro Ser Lys Gly Lys Thr Asp Lys Glu Gly Trp Tyr Pro Pro Gly His
180       185       190
Gly Asp Val Phe Pro Ala Leu Met Asn Ser Gly Lys Leu Asp Thr Phe
195       200       205
Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn Ser Asp Asn Leu
210       215       220
Gly Ala Ile Val Asp Leu Thr Ile Leu Lys His Leu Ile Gln Asn Lys
225       230       235       240
Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp Val Lys
245       250       255
```

Gly Gly Thr Leu Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu Glu Ile
260 265 270
Ala Gln Phe Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile Glu Lys
275 280 285
Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys Ala Ile
290 295 300
Lys Lys Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile Pro Asn
305 310 315 320
Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr Ala Ala
325 330 335
Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly Val Asn Val Pro
340 345 350
Arg Ser Arg Phe Leu Pro Val Lys Ala Ser Ser Asp Leu Leu Leu Val
355 360 365
Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Phe Val Thr Arg Asn Lys
370 375 380
Ala Arg Thr Asn Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro Glu Phe
385 390 395 400
Lys Lys Val Ala Thr Phe Leu Ser Arg Phe Lys Ser Ile Pro Ser Ile
405 410 415
Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Trp Phe Gly Ser
420 425 430
Ser Ile Val Leu Lys Gly Lys Val Thr Val Ala Ala Lys Ser Gly Val
435 440 445
Lys Leu Glu Ile Pro Asp Arg Ala Val Val Glu Asn Lys Asn Ile Asn
450 455 460
Gly Pro Glu Asp Leu
465

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1500133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

Met Ser Glu Ser Glu Lys Ser Gly Phe Ile Ser Leu Val Ser Arg Tyr
1 5 10 15
Leu Ser Gly Glu Ala Gln His Ile Glu Trp Ser Lys Ile Gln Thr Pro
20 25 30
Thr Asp Glu Ile Val Val Pro Tyr Glu Lys Met Thr Pro Val Ser Gln
35 40 45
Asp Val Ala Glu Thr Lys Asn Leu Leu Asp Lys Leu Val Val Leu Lys
50 55 60
Leu Asn Gly Gly Leu Gly Thr Thr Met Gly Cys Thr Gly Pro Lys Ser
65 70 75 80
Val Ile Glu Val Arg Asp Gly Leu Thr Phe Leu Asp Leu Ile Val Ile
85 90 95
Gln Ile Glu Asn Leu Asn Asn Lys Tyr Gly Cys Lys Val Pro Leu Val
100 105 110
Leu Met Asn Ser Phe Asn Thr His Asp Asp Arg His Lys Ile Val Glu
115 120 125
Lys Tyr Thr Asn Ser Asn Val Asp Ile His Thr Phe Asn Gln Ser Lys
130 135 140
Tyr Pro Arg Val Val Ala Asp Glu Phe Val Pro Trp Pro Ser Lys Gly
145 150 155 160
Lys Thr Asp Lys Glu Gly Trp Tyr Pro Pro Gly His Gly Asp Val Phe

				165					170					175	
Pro	Ala	Leu	Met	Asn	Ser	Gly	Lys	Leu	Asp	Thr	Phe	Leu	Ser	Gln	Gly
			180					185					190		
Lys	Glu	Tyr	Val	Phe	Val	Ala	Asn	Ser	Asp	Asn	Leu	Gly	Ala	Ile	Val
		195					200					205			
Asp	Leu	Thr	Ile	Leu	Lys	His	Leu	Ile	Gln	Asn	Lys	Asn	Glu	Tyr	Cys
	210					215					220				
Met	Glu	Val	Thr	Pro	Lys	Thr	Leu	Ala	Asp	Val	Lys	Gly	Gly	Thr	Leu
225					230					235					240
Ile	Ser	Tyr	Glu	Gly	Lys	Val	Gln	Leu	Leu	Glu	Ile	Ala	Gln	Phe	Pro
			245						250					255	
Asp	Glu	His	Val	Asn	Glu	Phe	Lys	Ser	Ile	Glu	Lys	Phe	Lys	Ile	Phe
		260						265					270		
Asn	Thr	Asn	Asn	Leu	Trp	Val	Asn	Leu	Lys	Ala	Ile	Lys	Lys	Leu	Val
		275					280					285			
Glu	Ala	Asp	Ala	Leu	Lys	Met	Glu	Ile	Ile	Pro	Asn	Pro	Lys	Glu	Val
	290					295					300				
Asp	Gly	Val	Lys	Val	Leu	Gln	Leu	Glu	Thr	Ala	Ala	Gly	Ala	Ala	Ile
305					310					315					320
Arg	Phe	Phe	Asp	Asn	Ala	Ile	Gly	Val	Asn	Val	Pro	Arg	Ser	Arg	Phe
			325						330					335	
Leu	Pro	Val	Lys	Ala	Ser	Ser	Asp	Leu	Leu	Val	Gln	Ser	Asp	Leu	
		340						345				350			
Tyr	Thr	Leu	Val	Asp	Gly	Phe	Val	Thr	Arg	Asn	Lys	Ala	Arg	Thr	Asn
		355					360					365			
Pro	Ser	Asn	Pro	Ser	Ile	Glu	Leu	Gly	Pro	Glu	Phe	Lys	Lys	Val	Ala
	370					375					380				
Thr	Phe	Leu	Ser	Arg	Phe	Lys	Ser	Ile	Pro	Ser	Ile	Val	Glu	Leu	Asp
385					390					395				400	
Ser	Leu	Lys	Val	Ser	Gly	Asp	Val	Trp	Phe	Gly	Ser	Ser	Ile	Val	Leu
			405						410				415		
Lys	Gly	Lys	Val	Thr	Val	Ala	Ala	Lys	Ser	Gly	Val	Lys	Leu	Glu	Ile
			420					425					430		
Pro	Asp	Arg	Ala	Val	Val	Glu	Asn	Lys	Asn	Ile	Asn	Gly	Pro	Glu	Asp
		435					440					445			
Leu															

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1500134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

Met	Thr	Pro	Val	Ser	Gln	Asp	Val	Ala	Glu	Thr	Lys	Asn	Leu	Leu	Asp
1				5					10					15	
Lys	Leu	Val	Val	Leu	Lys	Leu	Asn	Gly	Gly	Leu	Gly	Thr	Thr	Met	Gly
		20						25					30		
Cys	Thr	Gly	Pro	Lys	Ser	Val	Ile	Glu	Val	Arg	Asp	Gly	Leu	Thr	Phe
	35					40						45			
Leu	Asp	Leu	Ile	Val	Ile	Gln	Ile	Glu	Asn	Leu	Asn	Asn	Lys	Tyr	Gly
	50					55				60					
Cys	Lys	Val	Pro	Leu	Val	Leu	Met	Asn	Ser	Phe	Asn	Thr	His	Asp	Asp
65					70					75				80	
Arg	His	Lys	Ile	Val	Glu	Lys	Tyr	Thr	Asn	Ser	Asn	Val	Asp	Ile	His
			85					90						95	


```

Thr Phe Asn Gln Ser Lys Tyr Pro Arg Val Val Ala Asp Glu Phe Val
      100      105      110
Pro Trp Pro Ser Lys Gly Lys Thr Asp Lys Glu Gly Trp Tyr Pro Pro
      115      120      125
Gly His Gly Asp Val Phe Pro Ala Leu Met Asn Ser Gly Lys Leu Asp
      130      135      140
Thr Phe Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn Ser Asp
      145      150      155      160
Asn Leu Gly Ala Ile Val Asp Leu Thr Ile Leu Lys His Leu Ile Gln
      165      170      175
Asn Lys Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp
      180      185      190
Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Lys Val Gln Leu Leu
      195      200      205
Glu Ile Ala Gln Phe Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile
      210      215      220
Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys
      225      230      235      240
Ala Ile Lys Lys Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile
      245      250      255
Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr
      260      265      270
Ala Ala Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly Val Asn
      275      280      285
Val Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Ser Ser Asp Leu Leu
      290      295      300
Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Phe Val Thr Arg
      305      310      315      320
Asn Lys Ala Arg Thr Asn Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro
      325      330      335
Glu Phe Lys Lys Val Ala Thr Phe Leu Ser Arg Phe Lys Ser Ile Pro
      340      345      350
Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Trp Phe
      355      360      365
Gly Ser Ser Ile Val Leu Lys Gly Lys Val Thr Val Ala Ala Lys Ser
      370      375      380
Gly Val Lys Leu Glu Ile Pro Asp Arg Ala Val Val Glu Asn Lys Asn
      385      390      395      400
Ile Asn Gly Pro Glu Asp Leu
      405

```

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1210
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

attaaaaatgg cagttcaagc tcaacacccat tcctccaatc tcctcttcct caataaaaaga	60
aacgggaaaag agaaagaaca tagtaatttt acattacaat cacaagcagc tggagatttt	120
cttgatcaaaa ccaatatggtt attcaacaat ggaagttcta atcagagaaa aagaagaaga	180
gaaacgaaca atcatcagtt attacctatg cagtctcatc agtttcctca agttatagac	240
ttatctctat tacacaacta caatcatcca ccgtcgaata tggttcatac aggactccga	300
ttatttttcog gcgaagatca ggcacaaaag attagtcacc tgtctgaaga tgtttttgct	360
gcacatatca ataggcaaag cgaagaactt gatgagtttc ttcatgcccc gccggaggag	420
ctacggcgta cattagcgga gaagaggaag atgcactata aagcgcttct tggcgccgtg	480
gaagagtcgt tgggttcgtaa gctgagggag aaagaggtag agatagagag agccacgcgc	540

```
cgtcacaatg agctgggtggc acgtgactcg cagctgagag cggaggtgca agtatggcaa 600
gagagagcta aagcgcacga agacgccgcc gcgtcgctgc agtctcagct ccagcaagcc 660
gttaaccaat gcgccggtgg atgtgtatcg gcgcaggata gtagagcggc ggaggaagg 720
ctattatgca ccacaatcag cggagtgatg gacgccgagt cgggtgtacgt ggatccggag 780
agagtaaagc ggccgaattg caaagcttgc cgggaaagag aggcaacggt ggttgtgttg 840
ccgtgtcggc atctgagcat ctgcccggga tgtgaccgga cagcttttagc ttgcccgttg 900
tgtctcacgt tgcggaattc aagtgttgaa gctatctttt gctaaatggg cctaattcaa 960
gcccattagg ttgttatcgt aaatagaact tagtaggtaa cacaaatata aatttcattg 1020
gtatatgata taccgtatat cgaatccact agctattaag gaagccctct aaattttaca 1080
acaaaagaag tttttttttt tttttttact tttcattact tgggattctt tacacagata 1140
tgggatatgg aaatgttgct attcgtacaa aatagttaac taagctaaga aaccattttt 1200
tggggggccc
```

(2) INFORMATION FOR SEQ ID NO:1380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

```
Ile Lys Met Ala Val Gln Ala Gln His His Ser Ser Asn Leu Leu Phe
1           5           10           15
Leu Asn Lys Arg Asn Gly Lys Glu Lys Glu His Ser Asn Phe Thr Leu
20           25           30
Gln Ser Gln Ala Ala Gly Asp Phe Leu Asp Gln Thr Asn Met Leu Phe
35           40           45
Asn Asn Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Glu Thr Asn Asn
50           55           60
His Gln Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln Val Ile Asp
65           70           75           80
Leu Ser Leu Leu His Asn Tyr Asn His Pro Pro Ser Asn Met Val His
85           90           95
Thr Gly Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln Lys Ile Ser
100          105          110
His Leu Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg Gln Ser Glu
115          120          125
Glu Leu Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu Arg Arg Thr
130          135          140
Leu Ala Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu Gly Ala Val
145          150          155          160
Glu Glu Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val Glu Ile Glu
165          170          175
Arg Ala Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp Ser Gln Leu
180          185          190
Arg Ala Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala His Glu Asp
195          200          205
Ala Ala Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val Asn Gln Cys
210          215          220
Ala Gly Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala Glu Glu Gly
225          230          235          240
Leu Leu Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu Ser Val Tyr
245          250          255
Val Asp Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala Cys Arg Glu
260          265          270
Arg Glu Ala Thr Val Val Val Leu Pro Cys Arg His Leu Ser Ile Cys
275          280          285
Pro Gly Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys Leu Thr Leu
```

290 295 300
Arg Asn Ser Ser Val Glu Ala Ile Phe Cys
305 310
(2) INFORMATION FOR SEQ ID NO:1381:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..312
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500137
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:
Met Ala Val Gln Ala Gln His His Ser Ser Asn Leu Leu Phe Leu Asn
1 5 10 15
Lys Arg Asn Gly Lys Glu Lys Glu His Ser Asn Phe Thr Leu Gln Ser
20 25 30
Gln Ala Ala Gly Asp Phe Leu Asp Gln Thr Asn Met Leu Phe Asn Asn
35 40 45
Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Glu Thr Asn Asn His Gln
50 55 60
Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln Val Ile Asp Leu Ser
65 70 75 80
Leu Leu His Asn Tyr Asn His Pro Pro Ser Asn Met Val His Thr Gly
85 90 95
Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln Lys Ile Ser His Leu
100 105 110
Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg Gln Ser Glu Glu Leu
115 120 125
Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu Arg Arg Thr Leu Ala
130 135 140
Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu Gly Ala Val Glu Glu
145 150 155 160
Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val Glu Ile Glu Arg Ala
165 170 175
Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp Ser Gln Leu Arg Ala
180 185 190
Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala His Glu Asp Ala Ala
195 200 205
Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val Asn Gln Cys Ala Gly
210 215 220
Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala Glu Glu Gly Leu Leu
225 230 235 240
Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu Ser Val Tyr Val Asp
245 250 255
Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala Cys Arg Glu Arg Glu
260 265 270
Ala Thr Val Val Val Leu Pro Cys Arg His Leu Ser Ile Cys Pro Gly
275 280 285
Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys Leu Thr Leu Arg Asn
290 295 300
Ser Ser Val Glu Ala Ile Phe Cys
305 310
(2) INFORMATION FOR SEQ ID NO:1382:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..269
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

```
Met Leu Phe Asn Asn Gly Ser Ser Asn Gln Arg Lys Arg Arg Arg Glu
1          5          10          15
Thr Asn Asn His Gln Leu Leu Pro Met Gln Ser His Gln Phe Pro Gln
20          25          30
Val Ile Asp Leu Ser Leu Leu His Asn Tyr Asn His Pro Ser Asn
35          40          45
Met Val His Thr Gly Leu Arg Leu Phe Ser Gly Glu Asp Gln Ala Gln
50          55          60
Lys Ile Ser His Leu Ser Glu Asp Val Phe Ala Ala His Ile Asn Arg
65          70          75          80
Gln Ser Glu Glu Leu Asp Glu Phe Leu His Ala Gln Ala Glu Glu Leu
85          90          95
Arg Arg Thr Leu Ala Glu Lys Arg Lys Met His Tyr Lys Ala Leu Leu
100         105         110
Gly Ala Val Glu Glu Ser Leu Val Arg Lys Leu Arg Glu Lys Glu Val
115         120         125
Glu Ile Glu Arg Ala Thr Arg Arg His Asn Glu Leu Val Ala Arg Asp
130         135         140
Ser Gln Leu Arg Ala Glu Val Gln Val Trp Gln Glu Arg Ala Lys Ala
145         150         155         160
His Glu Asp Ala Ala Ala Ser Leu Gln Ser Gln Leu Gln Gln Ala Val
165         170         175
Asn Gln Cys Ala Gly Gly Cys Val Ser Ala Gln Asp Ser Arg Ala Ala
180         185         190
Glu Glu Gly Leu Leu Cys Thr Thr Ile Ser Gly Val Asp Asp Ala Glu
195         200         205
Ser Val Tyr Val Asp Pro Glu Arg Val Lys Arg Pro Asn Cys Lys Ala
210         215         220
Cys Arg Glu Arg Glu Ala Thr Val Val Val Leu Pro Cys Arg His Leu
225         230         235         240
Ser Ile Cys Pro Gly Cys Asp Arg Thr Ala Leu Ala Cys Pro Leu Cys
245         250         255
Leu Thr Leu Arg Asn Ser Ser Val Glu Ala Ile Phe Cys
260         265
```

(2) INFORMATION FOR SEQ ID NO:1383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..719
(D) OTHER INFORMATION: / Ceres Seq. ID 1500149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

```
gttgatatatg cggatctcca ttcaccaatc gccttcctgt cgccctcccg ctcgggtcgg      60
cgaacgcgat ctgttcccca acctccgcag ccgctccacc gtccctccact ccggctgccc      120
aatcgaccgg ccccgatcca gatcaggagc tgagggatgg acgcgaacag gcgccagagt      180
gggatccagc agttgctggc tgcggascag gaggctcagc aaattgtgaa tgcccgctag      240
agctgccaag tcagcgaggc tcaggcaagc aaaagaggag gctgagcggg aaatagccga      300
ataccgtgcc cagatggagg ctgagtttca gaggaaggtt gcagagagca gggcgactc      360
cggtgcaaac gtcaagcgtc tcgaggaaga aacggcggcg aagatcgagc aactcaccca      420
gcaggccgca agcatctccc cggatgtcat tcagatgctt ctgcggcatg tcaccaccgt      480
caagaactga ggagtgctgt tcccgaacta tgctcgcaga cttgtaccgt cgatctattt      540
```

```
atttttgtca agagtgagag tgggtaggaa taatatgcc gcttgtatcc ataattcctg 600
ttcgtaaacta cggaataagc cgccgcagct ttagcggcaa acgtgactag tactgtcaga 660
acctaccatt gttatttggg acaattggta aataatattg ttttaaactg gatttttcg
```

(2) INFORMATION FOR SEQ ID NO:1384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

```
Leu Tyr Met Arg Ile Ser Ile His Gln Ser Pro Ser Cys Arg Pro Pro
1          5          10          15
Ala Arg Leu Gly Glu Arg Asp Leu Phe Pro Asn Leu Arg Ser Arg Ser
20          25          30
Thr Val Leu His Ser Gly Cys Arg Ile Asp Pro Pro Arg Ser Arg Ser
35          40          45
Gly Ala Glu Gly Trp Thr Arg Thr Gly Ala Arg Val Gly Ser Ser Ser
50          55          60
Cys Trp Leu Arg Xaa Arg Arg Leu Ser Lys Leu
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

```
Cys Ile Cys Gly Ser Pro Phe Thr Asn Arg Leu Pro Val Ala Leu Pro
1          5          10          15
Leu Gly Ser Ala Asn Ala Ile Cys Ser Pro Thr Ser Ala Ala Ala Pro
20          25          30
Pro Ser Ser Thr Pro Ala Ala Glu Ser Thr Arg Pro Asp Pro Asp Gln
35          40          45
Glu Leu Arg Asp Gly Arg Glu Gln Ala Pro Glu Trp Asp Pro Ala Val
50          55          60
Ala Gly Cys Gly Xaa Gly Gly Ser Ala Asn Cys Glu Cys Pro Leu Glu
65          70          75          80
Leu Pro Ser Gln Arg Gly Ser Gly Lys Gln Lys Arg Arg Leu Ser Gly
85          90          95
Lys
```

(2) INFORMATION FOR SEQ ID NO:1386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

```
Met Pro Ala Arg Ala Ala Lys Ser Ala Arg Leu Arg Gln Ala Lys Glu
1           5           10           15
Glu Ala Glu Arg Glu Ile Ala Glu Tyr Arg Ala Gln Met Glu Ala Glu
20           25           30
Phe Gln Arg Lys Val Ala Glu Ser Ser Gly Asp Ser Gly Ala Asn Val
35           40           45
Lys Arg Leu Glu Glu Glu Thr Ala Ala Lys Ile Glu Gln Leu Thr Gln
50           55           60
Gln Ala Ala Ser Ile Ser Pro Asp Val Ile Gln Met Leu Leu Arg His
65           70           75           80
Val Thr Thr Val Lys Asn
85
```

(2) INFORMATION FOR SEQ ID NO:1387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1500153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

```
cttcgggtcc tgcattttgt tgtccctct ccgtagcgga gacgttcgtt cactttctct 60
ctctcgccct ccgtttgccc cgcgtgcgct ctgtgtcgct ccctctcttg tgaggagtga 120
ggacgactgg ggcgaccgcc gccgcgcgcg ccgccctacg ccagatgccc aggtaggggc 180
cattcgctag ctcttcttcg tgcccttcgc cggcgacgag cattcaccag ttgctgatgc 240
aaggctttca aaagttaaac agtctcactt gatgcaaaag caacacaatc actctaaagg 300
tttgatcag tcatttcaga gcatgggttc gcggtttcca tcccatcagc taagcaatgg 360
cttgatgtc tctggccgac ctgagcaacc taaagagaag gccccagtca tttgctcctc 420
ggctatgcgt acactggcgg ggacataaag aaatctggag
```

(2) INFORMATION FOR SEQ ID NO:1388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1500154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

```
Phe Arg Ser Cys Ile Leu Leu Ser Pro Leu Arg Ser Gly Asp Val Arg
1           5           10           15
Ser Leu Ser Leu Ser Arg Leu Pro Phe Ala Pro Arg Ala Leu Cys Val
20           25           30
Ala Pro Ser Leu Val Arg Ser Glu Asp Asp Trp Gly Asp Arg Arg Arg
35           40           45
Arg Arg Arg Pro Thr Pro Asp Ala Gln Val Gly Ala Ile Arg
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:1389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

```
Met Gln Lys Gln His Asn His Ser Lys Gly Leu Asp Gln Ser Phe Gln
1          5          10          15
Ser Met Gly Ser Arg Phe Pro Ser His Gln Leu Ser Asn Gly Leu Tyr
          20          25          30
Val Ser Gly Arg Pro Glu Gln Pro Lys Glu Lys Ala Pro Val Ile Cys
          35          40          45
Ser Ser Ala Met Arg Thr Leu Ala Gly Thr
          50          55
```

(2) INFORMATION FOR SEQ ID NO:1390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

```
Met Gly Ser Arg Phe Pro Ser His Gln Leu Ser Asn Gly Leu Tyr Val
1          5          10          15
Ser Gly Arg Pro Glu Gln Pro Lys Glu Lys Ala Pro Val Ile Cys Ser
          20          25          30
Ser Ala Met Arg Thr Leu Ala Gly Thr
          35          40
```

(2) INFORMATION FOR SEQ ID NO:1391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..522
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

```
aaaacaactg tgtaaagtgc tgaagattgc attttggaga gtcgagtttc aaatagaatc      60
gtgagataga gagtgaaca gggacaatct gagtgacgta cattatattg acagcrtgcc      120
tggctgtrca ggaggcctac ctggtgacgt cgaggaagta cagcccgggtg cccaggaacc      180
agctgctgag cccgctgatc gtgcacgacg gccgcctcgt gcagcgcccg acgcgctcg      240
tcgcgctcgt caccttcctc tggatgccgt tcggcttcgc gctggcgctc atgcgcgtgt      300
acatcaacct gccgtgccc gagcgcacgc tctactacac ctacaagctc atgggcatca      360
rgctcgctgt caagddcacc ccgccgccgc cgccaagaa gggccacccg ggcgtcctct      420
tcgtctgcaa ccaccgcacc gtgctcgacc ccgtcgaggt ggccgtrgcg ctgcgccgca      480
aggtcagctg cgtcacctac agsatctcca agttctccga gc
```

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

Met Pro Phe Gly Phe Ala Leu Ala Leu Met Arg Val Tyr Ile Asn Leu
1 5 10 15
Pro Leu Pro Glu Arg Ile Val Tyr Tyr Thr Tyr Lys Leu Met Gly Ile
20 25 30
Xaa Leu Val Val Lys Xaa Thr Pro Pro Pro Pro Pro Lys Lys Gly His
35 40 45
Pro Gly Val Leu Phe Val Cys Asn His Arg Thr Val Leu Asp Pro Val
50 55 60
Glu Val Ala Xaa Ala Leu Arg Arg Lys Val Ser Cys Val Thr Tyr Xaa
65 70 75 80
Ile Ser Lys Phe Ser Glu
85

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1500159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

Met Arg Val Tyr Ile Asn Leu Pro Leu Pro Glu Arg Ile Val Tyr Tyr
1 5 10 15
Thr Tyr Lys Leu Met Gly Ile Xaa Leu Val Val Lys Xaa Thr Pro Pro
20 25 30
Pro Pro Pro Lys Lys Gly His Pro Gly Val Leu Phe Val Cys Asn His
35 40 45
Arg Thr Val Leu Asp Pro Val Glu Val Ala Xaa Ala Leu Arg Arg Lys
50 55 60
Val Ser Cys Val Thr Tyr Xaa Ile Ser Lys Phe Ser Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1500160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

Met Gly Ile Xaa Leu Val Val Lys Xaa Thr Pro Pro Pro Pro Pro Lys
1 5 10 15
Lys Gly His Pro Gly Val Leu Phe Val Cys Asn His Arg Thr Val Leu
20 25 30
Asp Pro Val Glu Val Ala Xaa Ala Leu Arg Arg Lys Val Ser Cys Val
35 40 45
Thr Tyr Xaa Ile Ser Lys Phe Ser Glu
50 55

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..508
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500165
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

```
atatatgtga atcctaactg tacactgtct gaagtggacg aacggctctg gcttcggcgt      60
gttacgtgta tagtaggccc cttttgaacg aacggcgcg ggcggggcca ccaccagcat      120
ctgcggcagg gagaatcgcg ttggttcgac gcaaacgcta cccggcgccc ccttgccctt      180
ggggccggct attttaccgc acccgttctc ccctctctac cgcagatcag atcacactcg      240
tagagagaag gaaaaaatc cccaaacct agctcccgat ctcgatggcg aaccctcgcg      300
tcttcttcga catgaccgtc ggcgcgcccc cgcggggccc gatcgtgatg gagctgtacg      360
ccaacgaggt gcccaagacc gcggagaact tccgcgcgct gtgcacgggc gagaagggcg      420
tgggcaagtc cggaagccg ctccactaca agggctccac cttccaccgc gtcatccccg      480
arttcatgtg ccagggcggc gacttcac
```

(2) INFORMATION FOR SEQ ID NO:1396:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..74
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500166
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

```
Met Ala Asn Pro Arg Val Phe Phe Asp Met Thr Val Gly Gly Ala Pro
1          5          10          15
Ala Gly Arg Ile Val Met Glu Leu Tyr Ala Asn Glu Val Pro Lys Thr
          20          25          30
Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys
          35          40          45
Ser Gly Lys Pro Leu His Tyr Lys Gly Ser Thr Phe His Arg Val Ile
          50          55          60
Pro Xaa Phe Met Cys Gln Gly Gly Asp Phe
65          70
```

(2) INFORMATION FOR SEQ ID NO:1397:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..65
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500167
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

```
Met Thr Val Gly Gly Ala Pro Ala Gly Arg Ile Val Met Glu Leu Tyr
1          5          10          15
Ala Asn Glu Val Pro Lys Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr
          20          25          30
Gly Glu Lys Gly Val Gly Lys Ser Gly Lys Pro Leu His Tyr Lys Gly
          35          40          45
Ser Thr Phe His Arg Val Ile Pro Xaa Phe Met Cys Gln Gly Gly Asp
          50          55          60
Phe
65
```

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

Met Glu Leu Tyr Ala Asn Glu Val Pro Lys Thr Ala Glu Asn Phe Arg
1 5 10 15
Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys Ser Gly Lys Pro Leu
20 25 30
His Tyr Lys Gly Ser Thr Phe His Arg Val Ile Pro Xaa Phe Met Cys
35 40 45
Gln Gly Gly Asp Phe
50

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

acgatattaa ccgaccaaaa taagctagtgt gtagcagttg gaggggtaac agcacttgct 60
gcagggatat acacaacaag ggagggtgca agagtagtct ggggctatgt tgatcgatt 120
ctgggtcagc catcactgat aagggagtca tcacgtggga aatatccctg gtctggtttc 180
ctctcacgtg ctacaagtac cctgactagc aaactgaaga atggaagcaa cctaggggaag 240
gacagaaatg gggtttggtga tgttattcta aatccttctc tccagaagag agtgaagcag 300
cttgctaatt ccacagccaa taaaaaactt catcaagctc ctttcaggaa catgcttttc 360
tatgggcctc ctggcacagg gaaaaccatg gcagcacgag aacttgctcg caattctgga 420
ttagattatg cactaatgac tggtggagat gttgcaccat tgggatcaca agcagtcacc 480
aagattcatc agttggttga ctgggcg

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

Thr Ile Leu Thr Asp Gln Asn Lys Leu Val Ala Val Gly Gly Val
1 5 10 15
Thr Ala Leu Ala Ala Gly Ile Tyr Thr Thr Arg Glu Gly Ala Arg Val
20 25 30
Val Trp Gly Tyr Val Asp Arg Ile Leu Gly Gln Pro Ser Leu Ile Arg
35 40 45
Glu Ser Ser Arg Gly Lys Tyr Pro Trp Ser Gly Phe Leu Ser Arg Ala
50 55 60

Thr Ser Thr Leu Thr Ser Lys Leu Lys Asn Gly Ser Asn Leu Gly Lys
65 70 75 80
Asp Arg Asn Gly Phe Gly Asp Val Ile Leu Asn Pro Ser Leu Gln Lys
85 90 95
Arg Val Lys Gln Leu Ala Asn Ala Thr Ala Asn Thr Lys Leu His Gln
100 105 110
Ala Pro Phe Arg Asn Met Leu Phe Tyr Gly Pro Pro Gly Thr Gly Lys
115 120 125
Thr Met Ala Ala Arg Glu Leu Ala Arg Asn Ser Gly Leu Asp Tyr Ala
130 135 140
Leu Met Thr Gly Gly Asp Val Ala Pro Leu Gly Ser Gln Ala Val Thr
145 150 155 160
Lys Ile His Gln Leu Phe Asp Trp Ala
165

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

aaaagccagg attcctctgc tcttcctggt tagggtttcc ccctctctct gtccttgccg	60
gatgcgatgg cgattccgcc gcggactcct tccccgccgc catcgtggtc gcgctctgta	120
accgagaccg ttcggggggtc ccaccagttc accgtacggg gctactccct cgccaagggc	180
atgggccccg gccgctacct cgccagcgac gtcttcgccg tcggaggata ccactgggcc	240
gtctacctct accccgacgg caagaacgcc gaggacaact ccaactacgt ctccgttttc	300
gtcgccctcg cttccgacgg catcgacgtc cgagccctct tcgagctcac cctcctcgac	360
cagtycgcm gcggtgcma caaggttcac tcgcacttg accgctcgct caagttcggc	420
ccatacacc tcaagtacag gggatccatg tggggttaca agcgcttcta caaaagaaca	480
ctcttggaag aatctgattt cttaaagaat gattgcctag tgatgaactg cacagt	

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

Lys Pro Gly Phe Leu Cys Ser Ser Cys Leu Gly Phe Pro Pro Leu Ser
1 5 10 15
Ala Pro Ala Gly Cys Asp Gly Asp Ser Ala Ala Asp Ser Phe Pro Ala
20 25 30
Ala Ile Val Val Ala Leu Cys Asn Arg Asp Arg Ser Gly Val Pro Pro
35 40 45
Val His Arg Thr Gly Leu Leu Pro Arg Gln Gly His Gly Pro Arg Pro
50 55 60
Leu Pro Arg Gln Arg Arg Leu Arg Arg Arg Arg Ile Pro Leu Gly Arg
65 70 75 80
Leu Pro Leu Pro Arg Arg Gln Glu Arg Arg Gly Gln Leu Gln Leu Arg
85 90 95
Leu Arg Phe Arg Arg Pro Arg Phe Arg Arg His Arg Arg Pro Ser Pro
100 105 110

Leu Arg Ala His Pro Pro Arg Pro Xaa Arg Xaa Arg Leu Xaa Gln Gly
115 120 125
Ser Leu Ala Leu
130

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

Met Ala Ile Pro Pro Arg Thr Pro Ser Pro Pro Pro Ser Trp Ser Arg
1 5 10 15
Ser Val Thr Glu Thr Val Arg Gly Ser His Gln Phe Thr Val Arg Gly
20 25 30
Tyr Ser Leu Ala Lys Gly Met Gly Pro Gly Arg Tyr Leu Ala Ser Asp
35 40 45
Val Phe Ala Val Gly Gly Tyr His Trp Ala Val Tyr Leu Tyr Pro Asp
50 55 60
Gly Lys Asn Ala Glu Asp Asn Ser Asn Tyr Val Ser Val Phe Val Ala
65 70 75 80
Leu Ala Ser Asp Gly Ile Asp Val Arg Ala Leu Phe Glu Leu Thr Leu
85 90 95
Leu Asp Gln Xaa Gly Xaa Gly Cys Xaa Lys Val His Ser His Phe Asp
100 105 110
Arg Ser Leu Lys Phe Gly Pro Tyr Thr Leu Lys Tyr Arg Gly Ser Met
115 120 125
Trp Gly Tyr Lys Arg Phe Tyr Lys Arg Thr Leu Leu Glu Glu Ser Asp
130 135 140
Phe Leu Lys Asn Asp Cys Leu Val Met Asn Cys Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

Met Gly Pro Gly Arg Tyr Leu Ala Ser Asp Val Phe Ala Val Gly Gly
1 5 10 15
Tyr His Trp Ala Val Tyr Leu Tyr Pro Asp Gly Lys Asn Ala Glu Asp
20 25 30
Asn Ser Asn Tyr Val Ser Val Phe Val Ala Leu Ala Ser Asp Gly Ile
35 40 45
Asp Val Arg Ala Leu Phe Glu Leu Thr Leu Leu Asp Gln Xaa Gly Xaa
50 55 60
Gly Cys Xaa Lys Val His Ser His Phe Asp Arg Ser Leu Lys Phe Gly
65 70 75 80
Pro Tyr Thr Leu Lys Tyr Arg Gly Ser Met Trp Gly Tyr Lys Arg Phe
85 90 95
Tyr Lys Arg Thr Leu Leu Glu Glu Ser Asp Phe Leu Lys Asn Asp Cys

100
Leu Val Met Asn Cys Thr
115

105

110

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..540
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

ggccacacct tccgtccccc ggcctccgct cgcctcgccg cccgcctgtc cctgtctgtc	60
tctctctctc ctgctgagt cgccgccagc catgaacaac ctccctacgg attcctttga	120
gctcccccg cgggactcct caagagatgc agacattgaa atgggaatgc atcaagctga	180
tgcttcagac aacttaaaag atttcttgaa gaaggtcgat acaattgaga gtttaattgc	240
aaagctgaca aatctattga ataagctaca gactgcaaat gaggaatcca aagcagttac	300
aaaagcaagt tccatgaaag caattaagca gcggatggag aaagatatg atgaagtggg	360
gaaaattgct cgtcaggcga agacaaaagt tgatgaattg gaaaaagaca acttatcaaa	420
taggcaaaaa cctggatgtg gaaaaggttc tgccgtggac cgatcaagag agcaaamtac	480
tggagcagtg aaaaagaaat tgaaggagcg gatggatgac tttcagacct tgagagaagc	540

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

Ala Thr Pro Ser Val Pro Arg Pro Pro Leu Ala Ser Pro Pro Ala Cys	
1	5 10 15
Pro Cys Leu Ser Leu Ser Leu Leu Ala Glu Ser Pro Pro Ala Met Asn	
	20 25 30
Asn Leu Leu Thr Asp Ser Phe Glu Leu Pro Arg Arg Asp Ser Ser Arg	
	35 40 45
Asp Ala Asp Ile Glu Met Gly Met His Gln Ala Asp Ala Ser Asp Asn	
	50 55 60
Leu Lys Asp Phe Leu Lys Lys Val Asp Thr Ile Glu Ser Leu Ile Ala	
65	70 75 80
Lys Leu Thr Asn Leu Leu Asn Lys Leu Gln Thr Ala Asn Glu Glu Ser	
	85 90 95
Lys Ala Val Thr Lys Ala Ser Ser Met Lys Ala Ile Lys Gln Arg Met	
	100 105 110
Glu Lys Asp Ile Asp Glu Val Gly Lys Ile Ala Arg Gln Ala Lys Thr	
	115 120 125
Lys Val Asp Glu Leu Glu Lys Asp Asn Leu Ser Asn Arg Gln Lys Pro	
	130 135 140
Gly Cys Gly Lys Gly Ser Ala Val Asp Arg Ser Arg Glu Gln Xaa Thr	
145	150 155 160
Gly Ala Val Lys Lys Lys Leu Lys Glu Arg Met Asp Asp Phe Gln Thr	
	165 170 175
Leu Arg Glu	

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

```
Met Asn Asn Leu Leu Thr Asp Ser Phe Glu Leu Pro Arg Arg Asp Ser
1          5          10          15
Ser Arg Asp Ala Asp Ile Glu Met Gly Met His Gln Ala Asp Ala Ser
          20          25          30
Asp Asn Leu Lys Asp Phe Leu Lys Lys Val Asp Thr Ile Glu Ser Leu
          35          40          45
Ile Ala Lys Leu Thr Asn Leu Leu Asn Lys Leu Gln Thr Ala Asn Glu
          50          55          60
Glu Ser Lys Ala Val Thr Lys Ala Ser Ser Met Lys Ala Ile Lys Gln
65          70          75          80
Arg Met Glu Lys Asp Ile Asp Glu Val Gly Lys Ile Ala Arg Gln Ala
          85          90          95
Lys Thr Lys Val Asp Glu Leu Glu Lys Asp Asn Leu Ser Asn Arg Gln
          100          105          110
Lys Pro Gly Cys Gly Lys Gly Ser Ala Val Asp Arg Ser Arg Glu Gln
          115          120          125
Xaa Thr Gly Ala Val Lys Lys Lys Leu Lys Glu Arg Met Asp Asp Phe
130          135          140
Gln Thr Leu Arg Glu
145
```

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

```
Met Gly Met His Gln Ala Asp Ala Ser Asp Asn Leu Lys Asp Phe Leu
1          5          10          15
Lys Lys Val Asp Thr Ile Glu Ser Leu Ile Ala Lys Leu Thr Asn Leu
          20          25          30
Leu Asn Lys Leu Gln Thr Ala Asn Glu Glu Ser Lys Ala Val Thr Lys
          35          40          45
Ala Ser Ser Met Lys Ala Ile Lys Gln Arg Met Glu Lys Asp Ile Asp
          50          55          60
Glu Val Gly Lys Ile Ala Arg Gln Ala Lys Thr Lys Val Asp Glu Leu
65          70          75          80
Glu Lys Asp Asn Leu Ser Asn Arg Gln Lys Pro Gly Cys Gly Lys Gly
          85          90          95
Ser Ala Val Asp Arg Ser Arg Glu Gln Xaa Thr Gly Ala Val Lys Lys
          100          105          110
Lys Leu Lys Glu Arg Met Asp Asp Phe Gln Thr Leu Arg Glu
          115          120          125
```

(2) INFORMATION FOR SEQ ID NO:1409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1473 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1473
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500190
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

```
agaaagaaga agataacaca atgctcttct tcttattctt cttctactta ctcttatctt      60
catcctccga tctagtcttc gccgaccgtc gtgtactcca cgaaccattc ttccctatag      120
attcgccacc accgtcacca ccatcaccac caccacttcc taaactacca ttctcttcaa      180
ccactcctcc atcttcatca gacccaaatg cttctccttt cttcccttta tacccttcat      240
ctccaccacc accttctcca gcctccttcg cttcttttcc ggcgaatata tcatctctaa      300
tcgtccctca cgccactaaa tccccaccta actccaaaaa actccttata gtcgctatct      360
ccgccgtttc ctccgctgct ttagtcgctc tacttatcgc tttactctat tggcgaagaa      420
gcaaacgtaa ccaagatctt aacttctccg atgatagcaa aacatacacc accgacagta      480
gccgccgtgt ctaccctcct cctccggcaa cggcgccctc aacacgacgc aatgcgaggg      540
ctagaagtaa acagaggacc accacgagct ccaccaataa caacagctct gagtttcttt      600
acttaggaac aatggtgaat caaagaggaa tcgatgaaca atctcttagt aataatggat      660
caagctcaag aaaacttgaa tctccagatc ttcaaccact tcctccattg atgaaacgaa      720
gtttccgttt aaatccagat gttggttcaa tcggagaaga agatgaagaa gatgagtttt      780
actctccacg tggctcacia agcgggagag aaccgttaaa ccgggtcgga cttccggggtc      840
aaaatcctag atctgttaac aatgacacta tctcttgctc atcttcaagc tctggttcac      900
caggaagatc aacatttatc agtatctctc cttcaatgag tcctaagaga tctgaaccaa      960
aaccgccggt tatctccaca ccagaaccgg cggagttaac cgattataga tttgttcggt      1020
ctccgtcact gtcgttagct tctttatcgt cgggattgaa aaactccgat gaagtaggat      1080
tgaatcaaat cttagatctc ccgacggtta catctctaac aacttcaccg gagaataaca      1140
aaaaagagaa ctctccatta tcacttactt caacttcacc ggaacgacga ccaaagata      1200
caccagaagc ttacttgaga tctccgtcgc attcttctgc ttctacatca ccgtatagat      1260
gttttcagaa atctccggag gtcttaccgg cgtttatgag taatctccgg caaggtttgc      1320
aatctcagtt actatcttct ctttctaact ctcattggag acaaggtttc ctttaagcagt      1380
tagatgcatt acgttctcgt tcaccgtcgt cgtcttcttc ttctgtttgt tcttcaccgg      1440
agaaagcttc tcataagtca ccagttacat ctc
```

(2) INFORMATION FOR SEQ ID NO:1410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 490 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..490
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

```
Lys Glu Glu Asp Asn Thr Met Leu Phe Phe Leu Phe Phe Tyr Leu
1          5          10          15
Leu Leu Ser Ser Ser Ser Asp Leu Val Phe Ala Asp Arg Arg Val Leu
20          25          30
His Glu Pro Phe Phe Pro Ile Asp Ser Pro Pro Pro Ser Pro Pro Ser
35          40          45
Pro Pro Pro Leu Pro Lys Leu Pro Phe Ser Ser Thr Thr Pro Pro Ser
50          55          60
Ser Ser Asp Pro Asn Ala Ser Pro Phe Phe Pro Leu Tyr Pro Ser Ser
65          70          75          80
Pro Pro Pro Pro Ser Pro Ala Ser Phe Ala Ser Phe Pro Ala Asn Ile
85          90          95
Ser Ser Leu Ile Val Pro His Ala Thr Lys Ser Pro Pro Asn Ser Lys
```

	100		105		110
Lys	Leu	Leu	Ile	Val	Ala
	115		120		125
Ala	Leu	Leu	Ile	Ala	Leu
	130		135		140
Asp	Leu	Asn	Phe	Ser	Asp
145		150		155	160
Arg	Arg	Val	Tyr	Pro	Pro
	165		170		175
Asn	Ala	Glu	Ala	Arg	Ser
	180		185		190
Asn	Asn	Ser	Glu	Phe	Leu
	195		200		205
Gly	Ile	Asp	Glu	Gln	Ser
	210		215		220
Leu	Glu	Ser	Pro	Asp	Leu
225		230		235	240
Phe	Arg	Leu	Asn	Pro	Asp
	245		250		255
Asp	Glu	Phe	Tyr	Ser	Pro
	260		265		270
Asn	Arg	Val	Gly	Leu	Pro
	275		280		285
Thr	Ile	Ser	Cys	Ser	Ser
	290		295		300
Phe	Ile	Ser	Ile	Ser	Pro
305		310		315	320
Pro	Pro	Val	Ile	Ser	Thr
	325		330		335
Phe	Val	Arg	Ser	Pro	Ser
	340		345		350
Lys	Asn	Ser	Asp	Glu	Val
	355		360		365
Val	Thr	Ser	Leu	Thr	Thr
	370		375		380
Pro	Leu	Ser	Ser	Thr	Ser
385		390		395	400
Pro	Glu	Ala	Tyr	Leu	Arg
	405		410		415
Pro	Tyr	Arg	Cys	Phe	Gln
	420		425		430
Ser	Asn	Leu	Arg	Gln	Gly
	435		440		445
Asn	Ser	His	Gly	Gly	Gln
	450		455		460
Ser	Arg	Ser	Pro	Ser	Ser
465		470		475	480
Lys	Ala	Ser	His	Lys	Ser
	485		490		

(2) INFORMATION FOR SEQ ID NO:1411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..484
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

Met	Leu	Phe	Phe	Leu	Phe	Phe	Phe	Tyr	Leu	Leu	Leu	Ser	Ser	Ser	Ser	1	5	10	15
Asp	Leu	Val	Phe	Ala	Asp	Arg	Arg	Val	Leu	His	Glu	Pro	Phe	Phe	Pro	20	25	30	
Ile	Asp	Ser	Pro	Pro	Pro	Ser	Pro	Pro	Ser	Pro	Pro	Pro	Leu	Pro	Lys	35	40	45	
Leu	Pro	Phe	Ser	Ser	Thr	Thr	Pro	Pro	Ser	Ser	Ser	Asp	Pro	Asn	Ala	50	55	60	
Ser	Pro	Phe	Phe	Pro	Leu	Tyr	Pro	Ser	Ser	Pro	Pro	Pro	Pro	Ser	Pro	65	70	75	80
Ala	Ser	Phe	Ala	Ser	Phe	Pro	Ala	Asn	Ile	Ser	Ser	Leu	Ile	Val	Pro	85	90	95	
His	Ala	Thr	Lys	Ser	Pro	Pro	Asn	Ser	Lys	Lys	Leu	Leu	Ile	Val	Ala	100	105	110	
Ile	Ser	Ala	Val	Ser	Ser	Ala	Ala	Leu	Val	Ala	Leu	Leu	Ile	Ala	Leu	115	120	125	
Leu	Tyr	Trp	Arg	Arg	Ser	Lys	Arg	Asn	Gln	Asp	Leu	Asn	Phe	Ser	Asp	130	135	140	
Asp	Ser	Lys	Thr	Tyr	Thr	Thr	Asp	Ser	Ser	Arg	Val	Tyr	Pro	Pro		145	150	155	160
Pro	Pro	Ala	Thr	Ala	Pro	Pro	Thr	Arg	Arg	Asn	Ala	Glu	Ala	Arg	Ser	165	170	175	
Lys	Gln	Arg	Thr	Thr	Ser	Ser	Thr	Asn	Asn	Asn	Ser	Ser	Glu	Phe		180	185	190	
Leu	Tyr	Leu	Gly	Thr	Met	Val	Asn	Gln	Arg	Gly	Ile	Asp	Glu	Gln	Ser	195	200	205	
Leu	Ser	Asn	Asn	Gly	Ser	Ser	Ser	Arg	Lys	Leu	Glu	Ser	Pro	Asp	Leu	210	215	220	
Gln	Pro	Leu	Pro	Pro	Leu	Met	Lys	Arg	Ser	Phe	Arg	Leu	Asn	Pro	Asp	225	230	235	240
Val	Gly	Ser	Ile	Gly	Glu	Glu	Asp	Glu	Glu	Asp	Glu	Phe	Tyr	Ser	Pro	245	250	255	
Arg	Gly	Ser	Gln	Ser	Gly	Arg	Glu	Pro	Leu	Asn	Arg	Val	Gly	Leu	Pro	260	265	270	
Gly	Gln	Asn	Pro	Arg	Ser	Val	Asn	Asn	Asp	Thr	Ile	Ser	Cys	Ser	Ser	275	280	285	
Ser	Ser	Ser	Gly	Ser	Pro	Gly	Arg	Ser	Thr	Phe	Ile	Ser	Ile	Ser	Pro	290	295	300	
Ser	Met	Ser	Pro	Lys	Arg	Ser	Glu	Pro	Lys	Pro	Pro	Val	Ile	Ser	Thr	305	310	315	320
Pro	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Tyr	Arg	Phe	Val	Arg	Ser	Pro	Ser	325	330	335	
Leu	Ser	Leu	Ala	Ser	Leu	Ser	Ser	Gly	Leu	Lys	Asn	Ser	Asp	Glu	Val	340	345	350	
Gly	Leu	Asn	Gln	Ile	Phe	Arg	Ser	Pro	Thr	Val	Thr	Ser	Leu	Thr	Thr	355	360	365	
Ser	Pro	Glu	Asn	Asn	Lys	Lys	Glu	Asn	Ser	Pro	Leu	Ser	Ser	Thr	Ser	370	375	380	
Thr	Ser	Pro	Glu	Arg	Arg	Pro	Asn	Asp	Thr	Pro	Glu	Ala	Tyr	Leu	Arg	385	390	395	400
Ser	Pro	Ser	His	Ser	Ser	Ala	Ser	Thr	Ser	Pro	Tyr	Arg	Cys	Phe	Gln	405	410	415	
Lys	Ser	Pro	Glu	Val	Leu	Pro	Ala	Phe	Met	Ser	Asn	Leu	Arg	Gln	Gly	420	425	430	
Leu	Gln	Ser	Gln	Leu	Leu	Ser	Ser	Pro	Ser	Asn	Ser	His	Gly	Gly	Gln	435	440	445	
Gly	Phe	Leu	Lys	Gln	Leu	Asp	Ala	Leu	Arg	Ser	Arg	Ser	Pro	Ser	Ser	450	455	460	
Ser	Ser	Ser	Ser	Val	Cys	Ser	Ser	Pro	Glu	Lys	Ala	Ser	His	Lys	Ser	465	470	475	480
Pro	Val	Thr	Ser																

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met Val Asn Gln Arg Gly Ile Asp Glu Gln Ser Leu Ser Asn Asn Gly
1 5 10 15
Ser Ser Ser Arg Lys Leu Glu Ser Pro Asp Leu Gln Pro Leu Pro Pro
20 25 30
Leu Met Lys Arg Ser Phe Arg Leu Asn Pro Asp Val Gly Ser Ile Gly
35 40 45
Glu Glu Asp Glu Glu Asp Glu Phe Tyr Ser Pro Arg Gly Ser Gln Ser
50 55 60
Gly Arg Glu Pro Leu Asn Arg Val Gly Leu Pro Gly Gln Asn Pro Arg
65 70 75 80
Ser Val Asn Asn Asp Thr Ile Ser Cys Ser Ser Ser Ser Ser Gly Ser
85 90 95
Pro Gly Arg Ser Thr Phe Ile Ser Ile Ser Pro Ser Met Ser Pro Lys
100 105 110
Arg Ser Glu Pro Lys Pro Pro Val Ile Ser Thr Pro Glu Pro Ala Glu
115 120 125
Leu Thr Asp Tyr Arg Phe Val Arg Ser Pro Ser Leu Ser Leu Ala Ser
130 135 140
Leu Ser Ser Gly Leu Lys Asn Ser Asp Glu Val Gly Leu Asn Gln Ile
145 150 155 160
Phe Arg Ser Pro Thr Val Thr Ser Leu Thr Thr Ser Pro Glu Asn Asn
165 170 175
Lys Lys Glu Asn Ser Pro Leu Ser Ser Thr Ser Thr Ser Pro Glu Arg
180 185 190
Arg Pro Asn Asp Thr Pro Glu Ala Tyr Leu Arg Ser Pro Ser His Ser
195 200 205
Ser Ala Ser Thr Ser Pro Tyr Arg Cys Phe Gln Lys Ser Pro Glu Val
210 215 220
Leu Pro Ala Phe Met Ser Asn Leu Arg Gln Gly Leu Gln Ser Gln Leu
225 230 235 240
Leu Ser Ser Pro Ser Asn Ser His Gly Gly Gln Gly Phe Leu Lys Gln
245 250 255
Leu Asp Ala Leu Arg Ser Arg Ser Pro Ser Ser Ser Ser Ser Val
260 265 270
Cys Ser Ser Pro Glu Lys Ala Ser His Lys Ser Pro Val Thr Ser
275 280 285

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

```
gccatttttr gtgartgcgc cctttccctt cctccccaga tccccgtccc cgttttccac      60
ttttgcctcc gcccgaattc ggataacaaa cccctccgcc tcgtcgcgtc tcctcccagc      120
cgagccgata cggtagagag agggagargg agggactgar ggaggaggag ctgggttccg      180
gtcccggccg cccggccgnc ntgcgcgatt cgattgcagc tctcgtcccc gggcggcgtc      240
caggatggtg cggggcaaga cgcagatgaa gcggatagag aaccggacca gccgccaggt      300
caccttctcc aagcgccgca acggcctgct caagaaggcg ttcgarctct ccgtcctctg      360
cramgccgag gtcgccctcg tmgctctctc cmcgcgcggc aagctctacg aattcgccag      420
cggaagtrcg cagaaaacga ttgaacgtta tagaacatac acaaaggata atgtcagcaa      480
caagacagtg cagcaggata ttg
```

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1500199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

```
Ala Ile Phe Xaa Xaa Cys Ala Leu Ser Leu Pro Pro Gln Ile Pro Val
1           5           10           15
Pro Val Phe His Phe Cys Leu Arg Pro Asn Ser Asp Asn Lys Pro Leu
          20           25           30
Arg Leu Val Ala Ser Pro Pro Ser Arg Ala Asp Pro Val Glu Arg Gly
          35           40           45
Arg Xaa Arg Asp
          50
```

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1500200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

```
Met Val Arg Gly Lys Thr Gln Met Lys Arg Ile Glu Asn Pro Thr Ser
1           5           10           15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
          20           25           30
Phe Xaa Leu Ser Val Leu Cys Xaa Ala Glu Val Ala Leu Xaa Val Phe
          35           40           45
Ser Xaa Arg Gly Lys Leu Tyr Glu Phe Ala Ser Gly Ser Xaa Gln Lys
          50           55           60
Thr Ile Glu Arg Tyr Arg Thr Tyr Thr Lys Asp Asn Val Ser Asn Lys
          65           70           75           80
Thr Val Gln Gln Asp Ile
          85
```

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1500201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

```
Met Lys Arg Ile Glu Asn Pro Thr Ser Arg Gln Val Thr Phe Ser Lys
 1             5             10             15
Arg Arg Asn Gly Leu Leu Lys Lys Ala Phe Xaa Leu Ser Val Leu Cys
          20          25          30
Xaa Ala Glu Val Ala Leu Xaa Val Phe Ser Xaa Arg Gly Lys Leu Tyr
          35          40          45
Glu Phe Ala Ser Gly Ser Xaa Gln Lys Thr Ile Glu Arg Tyr Arg Thr
          50          55          60
Tyr Thr Lys Asp Asn Val Ser Asn Lys Thr Val Gln Gln Asp Ile
65             70             75
```

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..892
(D) OTHER INFORMATION: / Ceres Seq. ID 1500202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

```
atcctcggca tccgtcccgc tttgcccttg tttaattcca aaggtttcat tttctgcagg      60
gataacattt gtvvggggtg gtgagccggc cggccctata gaatcctgct cctgctcctg      120
cgcccgcccc cttttcatgt tgctttccct ttctctctct tcttctcctt caccctaccg      180
gctcacctcc tatattagccg tccgaattgc ttgtcagcat cttcccagct tcttcttctt      240
cttccaaccg cgctacgctc tcttgcccc ggtgctcgct tggattcttc tctcttcata      300
ggaaggaagg attggctacc gagatattcc tactagtcca gggctgtagt gcacctgcgc      360
cgcttggttt attctgcagc cataaccagt accagtacct ccagcctgav ccggtgagga      420
gaggagatag agagagcgag cgggagcggn gagcagagga ggagggccat ggaaggcgac      480
agcttctccg gcggcgccat ggccaacggc ggcggcggcg gcggcagcgg cggcgggcag      540
gtgggtggacg ggaagctgat ccacacgttc cacaggagct tcgtgcagggt gcagagcctg      600
ctggaccaga accggatgct catcagcgag atcaaccaga accacgagtc ccgcgcgcgt      660
gntmstccgc tgctgttgct gcgggataga tatagcgctt ccacttaatt tcttctgtct      720
tttccggttt cttcttcttc tctggttccc gctgcttgta ttgtattgta tctagtatgt      780
atcgctgtcc atccctccgg cgggctctga gatgtacct cattctcct cgtgtaccgc      840
tctcgatgca gatgataccg gggcatgtga atgaacagag ctggttccga cc
```

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1500203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

```
Ser Ser Ala Ser Val Pro Leu Cys Pro Cys Leu Ile Pro Lys Val Ser
 1             5             10             15
Phe Ser Ala Gly Ile Thr Phe Xaa Gly Gly Gly Glu Pro Ala Gly Pro
          20          25          30
Ile Glu Ser Cys Ser Cys Ser Cys Ala Arg Pro Leu Phe Met Leu Leu
          35          40          45
Ser Leu Ser Ser Ser Ser Ser Ser Ser Pro His Arg Leu Thr Ser Tyr
50             55             60
```

Leu Ala Val Arg Ile Ala Cys Gln His Leu Pro Ser Phe Phe Phe Phe
65 70 75 80
Phe Gln Pro Arg Tyr Ala Leu Leu Ser Pro Val Leu Ala Trp Ile Leu
85 90 95
Leu Ser Ser

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

Met Glu Gly Asp Ser Xaa Ser Gly Gly Ala Met Ala Asn Gly Gly Gly
1 5 10 15
Gly Gly Gly Ser Gly Gly Gly Gln Val Asp Gly Lys Leu Ile His
20 25 30
Thr Phe His Arg Ser Phe Val Gln Val Gln Ser Leu Leu Asp Gln Asn
35 40 45
Arg Met Leu Ile Ser Glu Ile Asn Gln Asn His Glu Ser Arg Ala Arg
50 55 60
Xaa Xaa Pro Leu Leu Leu Leu Arg Asp Arg Tyr Ser Ala Ser Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

Met Ala Asn Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gln Val Val
1 5 10 15
Asp Gly Lys Leu Ile His Thr Phe His Arg Ser Phe Val Gln Val Gln
20 25 30
Ser Leu Leu Asp Gln Asn Arg Met Leu Ile Ser Glu Ile Asn Gln Asn
35 40 45
His Glu Ser Arg Ala Arg Xaa Xaa Pro Leu Leu Leu Leu Arg Asp Arg
50 55 60
Tyr Ser Ala Ser Thr
65

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..756
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

ataggggttct	aagcctcggc	cgtttcttcg	tctccacagc	tcccgcgcgc	gcggaccagc	60
gcgtcactct	accgggttcc	ggcgtotccc	cgtaccgcga	gcgcggcatc	catggcggas	120
agacggaaaag	ggctttcttg	aagcagccca	agggtgtttct	ctgttccaag	aaggccacca	180
aggtaaaca	acctggcaag	ggaggaaa	gattctggaa	gaacattggc	cttggtttca	240
agacacccag	ggaagccatt	gaaggaacct	acattgataa	gaagtgtcca	ttcaccggca	300
ctgtgtctat	caggggtcgc	atcatcgccg	gaacatgcca	cagtgttaag	atgaatagga	360
ccatcattgt	tcgttagaat	tatcttctac	tcgtcaagaa	gtaccagagg	tatgagaaga	420
gacactccaa	catccctgcg	cacatttcac	catgcttccg	tgtaaggaa	ggagatcatg	480
tgatcattgg	ccagtgcagg	ccagtgtcga	agactgntaa	ggttcaatgt	gggtcaaagt	540
attcctgcag	gttcgaagag	tggagcagtg	aagaaagctt	tactgcccgc	ttaagatcat	600
gacgagttca	tcatccatgg	cccggaaaag	ctctgtgtta	taacgttttg	atgctgccta	660
ttagcctttt	tccccgtaac	tactatatgt	gtacttgtaa	ttggacttga	attacatcca	720
gaacttgaaa	tcctgaaaaa	aaatcataac	cctttg			

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

Met	Asn	Arg	Thr	Ile	Ile	Val	Arg	Arg	Asn	Tyr	Leu	His	Phe	Val	Lys
1			5						10					15	
Lys	Tyr	Gln	Arg	Tyr	Glu	Lys	Arg	His	Ser	Asn	Ile	Pro	Ala	His	Ile
		20						25					30		
Ser	Pro	Cys	Phe	Arg	Val	Lys	Glu	Gly	Asp	His	Val	Ile	Ile	Gly	Gln
		35					40					45			
Cys	Arg	Pro	Val	Ser	Lys	Thr	Xaa	Lys	Val	Gln	Cys	Gly	Gln	Ser	Tyr
		50				55				60					
Ser	Cys	Arg	Phe	Glu	Glu	Trp	Ser	Ser	Glu	Glu	Ser	Phe	His	Cys	Arg
65					70				75					80	
Leu	Arg	Ser													

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1034
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

gtgtctctta	tttctttgtg	tgtttggttg	ctggaaaggg	agtggacttt	tacaacttct	60
catgtcccta	ttgttgggag	ggttcggagt	ccggatcggg	atttgccaca	accagattgt	120
tcaacactcg	gaaggctcac	caaatcgctc	tacgcttctg	cttccctctc	cacgaggtga	180
ggaaacccta	gcgactgacc	atggcggttg	tcccgcgcac	cgcacgggtg	gccttcctct	240
ctaccccgcg	gtcgtactcc	gccgcgcgcg	ctgcgggcgc	ctcccccagc	tcccagcgc	300
catacggggg	cgcgccccca	ccggcgatgt	cgaagaggnc	cgagttcgtg	gtctccaagg	360
ttgatgacct	gatgaactgg	gcgcgtaagg	gctcgatttg	gccatgacc	tttgggctcg	420
cctgctgcr	ggtcgagatg	atgcacgccg	gcgcgtcccg	ctacgacttc	gaccgggttc	480
ggcgtcatct	tccgtccctc	gccgcgcmag	tccgattgca	tgatcgtcgc	cggcacgytc	540
accaacaaaa	tggctccagc	cctccgcaag	gtttatgacc	aaatgcctga	gcctagatgg	600
gttattttcaa	tgggcagctg	tgccaacggt	ggtggatact	accattactc	ctactctgtt	660

```
gtacgtggat gtgaccgtat agtccccgtg gacatctacg tccctgggtg cccaccaact 720
gctgaggcac tgctgtacgg tgttcttcag ctccaaaaga agatcaacag gcgtaaggat 780
ttccttcact ggtggaccaa gtgaagcatg cttctgctgt tgctcgcttg ctacgtttct 840
ttgcaactga cctacctgtc ttatctgaaa taaggacgga ctttgctcgg attcacaaat 900
ttgttggtgcc tggaaggatg tatgccacgg ttgtgacgaa catataactt gtgtacttgg 960
agtcagttcg cctgtaatgg acaccagacc tgctgtgaat ctgtttttaa gcttccattg 1020
taatacagca atac
```

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

```
Cys Leu Leu Phe Leu Cys Val Phe Gly Cys Trp Lys Gly Ser Gly Leu
1          5          10          15
Leu Gln Leu Leu Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile
20          25          30
Gly Ile Cys His Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn
35          40          45
Arg Pro Thr Leu Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala
50          55          60
Thr Asp His Gly Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu
65          70          75          80
Tyr Pro Ala Val Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp
85          90          95
Leu Pro Ser Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu
100         105         110
Xaa Arg Val Arg Gly Leu Gln Gly
115         120
```

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

```
Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile Gly Ile Cys His
1          5          10          15
Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu
20          25          30
Leu Leu Pro Pro Pro Arg Gly Glu Thr Leu Ala Thr Asp His Gly
35          40          45
Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val
50          55          60
Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser Ala
65          70          75          80
Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu Xaa Arg Val Arg
85          90          95
Gly Leu Gln Gly
100
```

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

```
Met Ala Leu Leu Pro Arg Thr Ala Arg Leu Ala Phe Leu Ser Thr Pro
1          5          10          15
Arg Ser Tyr Ser Ala Ala Ala Ala Ala Gly Ala Ser Pro Thr Ser Pro
          20          25          30
Ala Pro Tyr Gly Gly Ala Pro Pro Pro Ala Met Ser Lys Arg Xaa Glu
          35          40          45
Phe Val Val Ser Lys Val Asp Asp Leu Met Asn Trp Ala Arg Lys Gly
          50          55          60
Ser Ile Trp Pro Met Thr Phe Gly Leu Ala Cys Cys Xaa Val Glu Met
65          70          75          80
Met His Ala Gly Ala Ser Arg Tyr Asp Phe Asp Arg Val Arg Arg His
          85          90          95
Leu Pro Ser Leu Ala Ala Xaa Val Arg Leu His Asp Arg Arg Arg His
          100         105         110
Xaa His Gln Gln Asn Gly Ser Ser Pro Pro Gln Gly Leu
          115         120         125
```

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

```
aaccacacca ctgcavcgcg cgcgacggcc caccgctccg ccgctgcccg cccgccgcca      60
tgcgaggggat cctctcctct tcctccgctc tcctccggcg agccggcgcc cagctctcgc      120
gcacggactg cagtagcccc tcagcgctccg cgacctctcc tctccgccgc tccccctctc      180
agaatgggaa aagagacaca ttttggttcg tttggttcaa aggtcgttcg gtatcaacca      240
cagttgatat gcagttagac tatgagagtg atccccctct tgacgataca aaagctattg      300
agaaggagtc atcacttaat gttgctggtt ctcaactcgc aattgacttc gatagagact      360
ctaatttatg twtgagcgca ttttcccgtg caaggaaagc atctgtagtc tctactggtt      420
ctcttaagct tgamctcgct ctcggcggtg gaggattacc gaaggtagaa tgggtggagat      480
atatgggaaa gaagcatctg ggaagacaac actcgcgctt catgttatta aggaagctc
```

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:


```

Pro His His Ser Xaa Ala Arg Asp Gly Pro Pro Leu Arg Arg Cys Pro
1          5          10          15
Pro Ala Ala Met Arg Gly Ile Leu Ser Ser Ser Ala Leu Arg
          20          25          30
Arg Ala Gly Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala
          35          40          45
Ser Ala Thr Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg
          50          55          60
Asp Thr Phe Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr
          65          70          75          80
Val Asp Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr
          85          90          95
Lys Ala Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu
          100         105         110
Ala Ile Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser
          115         120         125
Arg Ala Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa
          130         135         140
Leu Ala Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr
          145         150         155         160
Met Gly Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu
          165         170         175
Arg Lys Leu

```

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

```

Met Arg Gly Ile Leu Ser Ser Ser Ser Ala Leu Leu Arg Arg Ala Gly
1          5          10          15
Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala Ser Ala Thr
          20          25          30
Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg Asp Thr Phe
          35          40          45
Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr Val Asp Met
          50          55          60
Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala Ile
          65          70          75          80
Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile Asp
          85          90          95
Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala Arg
          100         105         110
Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala Leu
          115         120         125
Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly Lys
          130         135         140
Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys Leu
          145         150         155         160

```

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..97
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500249
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

```
Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala
1          5          10          15
Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile
20          25          30
Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala
35          40          45
Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala
50          55          60
Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly
65          70          75          80
Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys
85          90          95
Leu
```

(2) INFORMATION FOR SEQ ID NO:1431:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 749 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..749
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500250
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

```
agccgactgg gactgagaag aaacctccaa acacctacct ctctacgaac tacctgccgc 60
cggaaaaccc tagagcgctc gaccatggat cgcagcagc cggagcctgt cagttacctc 120
tgccgagatt gcgactgag aacaccctga agcccggaga tgtcatccag tgccgtgaat 180
gtggctaccg catcctctac aagaagcggg agccacattc acggcactgg aagacctctg 240
agggtgaact gcgggccacc gccacctaga gatggatccg caccaagagc accaaggggt 300
ggtggtggtg gcggcgcgcg cagcagcttt gtcgattcag ggaacaaggt atacgtgggg 360
aaccttgcat ggggcgttga caactcgact ctggagaacc tattcagtga gcaaggacag 420
gtgctggatg ctaaggatcat ctacgacagg gatagcggca ggtcaagggg gtttggtttc 480
gtcacctatg gctctgccga ggagggtcaac aatgccatat caaaccttga tggcatagac 540
ttggatggtg gacagatccg agtcacgggt gcagaatcaa agcccaggcg tgaattttga 600
gattttgtta aggtggttta gaggtcaata gcgtgtgttc acaagttcta gttttagcgc 660
tctattcttt ctccgatatg agtaacaaga agatgctgat aatgagagac tggaagtga 720
actgctgtcc acaggaagat atttttccc
```

(2) INFORMATION FOR SEQ ID NO:1432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..146
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500251
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

```
Met Ser Ser Ser Ala Val Asn Val Ala Thr Ala Ser Ser Thr Arg Ser
```

1 5 10 15
Gly Ser His Ile His Gly Thr Gly Arg Pro Leu Arg Val Asn Cys Gly
20 25 30
Pro Pro Pro Arg Asp Gly Ser Ala Pro Arg Ala Pro Arg Gly Gly
35 40 45
Gly Gly Gly Gly Gly Gly Ser Phe Val Asp Ser Gly Asn Lys Val
50 55 60
Tyr Val Gly Asn Leu Ala Trp Gly Val Asp Asn Ser Thr Leu Glu Asn
65 70 75 80
Leu Phe Ser Glu Gln Gly Gln Val Leu Asp Ala Lys Val Ile Tyr Asp
85 90 95
Arg Asp Ser Gly Arg Ser Arg Gly Phe Gly Phe Val Thr Tyr Gly Ser
100 105 110
Ala Glu Glu Val Asn Asn Ala Ile Ser Asn Leu Asp Gly Ile Asp Leu
115 120 125
Asp Gly Arg Gln Ile Arg Val Thr Val Ala Glu Ser Lys Pro Arg Arg
130 135 140
Glu Phe
145

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met Asp Pro His Gln Glu His Gln Gly Val Val Val Val Ala Ala Ala
1 5 10 15
Ala Ala Ala Leu Ser Ile Gln Gly Thr Arg Tyr Thr Trp Gly Thr Leu
20 25 30
His Gly Ala Leu Thr Thr Arg Leu Trp Arg Thr Tyr Ser Val Ser Lys
35 40 45
Asp Arg Cys Trp Met Leu Arg Ser Ser Thr Thr Gly Ile Ala Ala Gly
50 55 60
Gln Gly Gly Leu Val Ser Ser Pro Met Ala Leu Pro Arg Arg Ser Thr
65 70 75 80
Met Pro Tyr Gln Thr Leu Met Ala
85

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

ctctctctct ctctctcttc tcgtctctct tctcctctcc gatcttctct gtgacctctt 60
tcttcttcga tttccttttg gtttcttctc cgaatcgccg gagaaaaaaa cccttctttg 120
aatctaaaga gactgttttt ttgaagctat tgactgattg attgataagg aagaataagc 180
attgatcgat ctgaattttg ggtacaagat gtcgagattc agagacagga cggaggattt 240
caaggattct gttcgggaagt ccgctgtttc gataggttat aatgagtcta aagtggcatc 300
aacaatggcg tcttttatta tacataagcc aaaggagaga tcgcctttca cgaaagctgc 360

```
tttcaaaacg cttgatagca tcaaggagtt ggaactgttt atgttgaagc atcgaaagga 420
ttatgttgat ctgcaccgga ctacagaaca ggaaaaggat agtattgaac aagaagttgc 480
tgcttttatt aaagcttgca aagaacagat cgatattctc ataaacagta ttagaaatga 540
agaagcaaac tccaaaggat ggcttggcct ccccgagat aacttcaatg ctgattctat 600
agcacacaaa catggagtgg ttttgattct gagtgagaaa cttcattcag tcactgcca 660
gtttgatcag cttagagcta ctcgtttcca agatattata aacagagcta tgccgagaag 720
aaaacctaag agggtcataa aggaagctac cccaattaat acaactctgg gaaattcgga 780
gtccatagaa cgggatgaaa tccaggccca acctcgtaga ttacaacaac aacaacttct 840
agacgatgaa acacaagccc ttcaggtaga gctaagtaat ctttttagatg gtgctaggca 900
gacagaaact aagatgggtg agatgtctgc attaaaccac ttgatggcaa ctcattgtct 960
gcagcaagcc caacagatag agtttcttta tgaccaggca gttgaggcaa caaagaacgt 1020
ggagcttgga aacaaagagc tttctcaagc aatccaacga aacagcagca gcagaacctt 1080
tctcttactg tttttcttcg tccttacttt ctccgtcttg ttcttggtt ggtacagtta 1140
aaaaaccatt ctccaacaac aacttcacac agtttttga gattttgatt gttactata 1200
aattatgaaa aattggaaat gggtttaaat gttaaaacaa aaataatgag
```

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

```
Met Ser Arg Phe Arg Asp Arg Thr Glu Asp Phe Lys Asp Ser Val Arg
1          5          10          15
Lys Ser Ala Val Ser Ile Gly Tyr Asn Glu Ser Lys Val Ala Ser Thr
20          25          30
Met Ala Ser Phe Ile Ile His Lys Pro Lys Glu Arg Ser Pro Phe Thr
35          40          45
Lys Ala Ala Phe Lys Thr Leu Asp Ser Ile Lys Glu Leu Glu Leu Phe
50          55          60
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
65          70          75          80
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
85          90          95
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
100         105         110
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
115         120         125
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
130         135         140
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
145         150         155         160
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
165         170         175
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
180         185         190
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
195         200         205
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
210         215         220
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
225         230         235         240
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
245         250         255
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
260         265         270
```

Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
275 280 285
Arg Thr Phe Leu Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu
290 295 300
Phe Leu Asp Trp Tyr Ser
305 310

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

Met Ala Ser Phe Ile Ile His Lys Pro Lys Glu Arg Ser Pro Phe Thr
1 5 10 15
Lys Ala Ala Phe Lys Thr Leu Asp Ser Ile Lys Glu Leu Glu Leu Phe
20 25 30
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
35 40 45
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
50 55 60
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
65 70 75 80
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
85 90 95
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
100 105 110
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
115 120 125
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
130 135 140
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
145 150 155 160
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
165 170 175
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
180 185 190
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
195 200 205
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
210 215 220
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
225 230 235 240
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
245 250 255
Arg Thr Phe Leu Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu
260 265 270
Phe Leu Asp Trp Tyr Ser
275

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
1 5 10 15
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
20 25 30
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
35 40 45
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
50 55 60
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
65 70 75 80
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
85 90 95
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
100 105 110
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
115 120 125
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
130 135 140
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
145 150 155 160
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
165 170 175
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
180 185 190
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
195 200 205
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
210 215 220
Arg Thr Phe Leu Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu
225 230 235 240
Phe Leu Asp Trp Tyr Ser
245

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

agagtcccag cgacctgtag cctcctctct cgcgcgacct cgctctcgcc tcgccgcctc 60
cgacccgcag cagcgccctcc attgctctct ctcacgagtc cggcggttcc agtggggggc 120
attcatggcg gggcagtcgc accgcgacct ctccatcttc tcgccctccg aggtggagtt 180
cgtggctgag gatgagattg tcgaaatcgt ccccaacatc cgcatggacg ccctcaacat 240
gatctgcggg gatttcgggc ccttcttccc ccagattccc accaagggtc ctctctggct 300
cgctgtcgcg ctcaagaagc gtasaagtgc accatccgca ccccggaactg gatgactgtt 360
gaccgcttga cacaggtatt ggaagcggaa agagagtcgc cacgagaatt ccagccatta 420
ccattccact atattgaaat ttctaagctt ctgtttgatc atgctcgtga tgacatctca 480
gatgcatacc tggaagatc tctaattgag gacatcagag atgtcagat

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1500284
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:
Arg Val Pro Ala Thr Cys Ser Leu Leu Ser Pro Ser Thr Ser Leu Ser
1 5 10 15
Pro Arg Arg Leu Arg Pro Ala Ala Ala Pro Pro Leu Leu Ser Leu Thr
20 25 30
Ser Pro Gly Val Pro Val Gly Gly Ile His Gly Gly Ala Val Arg Pro
35 40 45
Ala Pro Leu His Leu Leu Ala Leu Arg Gly Gly Val Arg Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1500285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

Glu Ser Gln Arg Pro Val Ala Ser Ser Leu Arg Arg Pro Arg Ser Arg
1 5 10 15
Leu Ala Ala Ser Asp Pro Gln Gln Arg Leu His Cys Ser Leu Ser Arg
20 25 30
Val Pro Ala Phe Gln Trp Gly Ala Phe Met Ala Gly Gln Ser Asp Pro
35 40 45
His Leu Ser Ile Phe Ser Pro Ser Glu Val Glu Phe Val Ala Glu Asp
50 55 60
Glu Ile Val Glu Ile Val Pro Asn Ile Arg Met Asp Ala Leu Asn Met
65 70 75 80
Ile Cys Gly Asp Phe Gly Pro Phe Phe Pro Gln Ile Pro Thr Lys Val
85 90 95
Pro Leu Trp Leu Ala Val Ala Leu Lys Lys Arg Xaa Ser Ala Pro Ser
100 105 110
Ala Pro Arg Thr Gly
115

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1500286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu
1 5 10 15
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile
20 25 30

Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe
35 40 45
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys
50 55 60
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

tactacatgc aatttgggaa atgtaaat	60
ttt caatcagctt gtatatcaa tcattcaaaa	120
gacatacttt caagtvgrtg gcatccagca gaatgcccat tctacatgaa aactaggaca	180
tgccaatttg gatcagcttg tgagttttat caccctaaaag atcggvgctc cttcaagang	240
rctgggaaca ggcaggcgcc ctaccagccg ccgaabgccc tgacgtgctg tggcasacga	300
catgtaccct gcrntcgccg cagargcgcc ggcggcgcca ggtctcggc gctcgaracg	360
ggcaccaagc tctacatctc caacctggac tttrgggttt cgaacgacga tatcaaggag	420
ctgttctctg agctaggtga tctgaagcgt ttttcgataa tatatgadcg aagtrggagg	
tctaaggga cagctgaagt tg	

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Tyr Tyr Met Gln Phe Gly Lys Cys Lys Phe Gln Ser Ala Cys Ile Phe	
1 5 10 15	
Asn His Ser Lys Asp Ile Leu Ser Ser Xaa Trp His Pro Ala Glu Cys	
20 25 30	
Pro Phe Tyr Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu	
35 40 45	
Phe Tyr His Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg	
50 55 60	
Gln Ala Pro Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg	
65 70 75 80	
His Val Pro Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Gly Arg Val Ser	
85 90 95	
Ala Leu Xaa Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa	
100 105 110	
Val Ser Asn Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu	
115 120 125	
Lys Arg Phe Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr	
130 135 140	
Ala Glu Val	
145	

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..145
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

```
Met Gln Phe Gly Lys Cys Lys Phe Gln Ser Ala Cys Ile Phe Asn His
1          5          10          15
Ser Lys Asp Ile Leu Ser Ser Xaa Trp His Pro Ala Glu Cys Pro Phe
          20          25          30
Tyr Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu Phe Tyr
          35          40          45
His Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg Gln Ala
          50          55          60
Pro Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg His Val
65          70          75          80
Pro Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Gly Arg Val Ser Ala Leu
          85          90          95
Xaa Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa Val Ser
          100          105          110
Asn Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu Lys Arg
          115          120          125
Phe Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr Ala Glu
130          135          140
Val
145
```

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500301
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

```
Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu Phe Tyr His
1          5          10          15
Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg Gln Ala Pro
          20          25          30
Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg His Val Pro
          35          40          45
Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Gly Arg Val Ser Ala Leu Xaa
          50          55          60
Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa Val Ser Asn
65          70          75          80
Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu Lys Arg Phe
          85          90          95
Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr Ala Glu Val
100          105          110
```

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

aacttggccc	caaatcgtgg	agtggaaacc	ctactcgtcc	ccttccgcat	cgccgccc	60
ttccccacc	caattcccac	tctccgctcg	acagatccat	acatgatggg	agaggccaag	120
gagaacgacg	tttatgagga	ggagctcctg	gactacgagg	aggacgacga	caagacggtc	180
gatggctccg	ctgctaagcc	caccggagag	gtcgcaaaga	agggctacgt	cgggatccac	240
agttccgggt	tcagagactt	cctgctcaag	ccagagctgc	tccgtgctat	ccaggattgt	300
ggttttragc	atccttccga	agtgaacac	gagtgtatcc	ctcaagccat	tcttggaatg	360
gatgtcatct	gtcaagctaa	atctgggatg	gggaaaactg	ctgtttttgt	cctttcatcc	420
ctccaacaaa	ttgaccctgt	tgcgggtcag	gtagcagcac	ttgtactgtg	ccacacaarg	480
gaactggctt	atcagatatg	c				

(2) INFORMATION FOR SEQ ID NO:1447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..167
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Asn	Leu	Ala	Pro	Asn	Arg	Gly	Val	Glu	Thr	Leu	Leu	Val	Pro	Phe	Arg	
1			5					10						15		
Ile	Ala	Ala	Gln	Phe	Pro	His	Pro	Ile	Pro	Thr	Leu	Arg	Ser	Thr	Asp	
			20					25					30			
Pro	Tyr	Met	Met	Gly	Glu	Ala	Lys	Glu	Asn	Asp	Val	Tyr	Glu	Glu	Glu	
			35				40					45				
Leu	Leu	Asp	Tyr	Glu	Glu	Asp	Asp	Lys	Thr	Val	Asp	Gly	Ser	Ala		
			50			55				60						
Ala	Lys	Pro	Thr	Gly	Glu	Val	Ala	Lys	Lys	Gly	Tyr	Val	Gly	Ile	His	
65				70						75				80		
Ser	Ser	Gly	Phe	Arg	Asp	Phe	Leu	Leu	Lys	Pro	Glu	Leu	Leu	Arg	Ala	
			85					90						95		
Ile	Gln	Asp	Cys	Gly	Phe	Xaa	His	Pro	Ser	Glu	Val	Gln	His	Glu	Cys	
			100					105					110			
Ile	Pro	Gln	Ala	Ile	Leu	Gly	Met	Asp	Val	Ile	Cys	Gln	Ala	Lys	Ser	
			115				120					125				
Gly	Met	Gly	Lys	Thr	Ala	Val	Phe	Val	Leu	Ser	Ser	Leu	Gln	Gln	Ile	
			130			135						140				
Asp	Pro	Val	Ala	Gly	Gln	Val	Ala	Ala	Leu	Val	Leu	Cys	His	Thr	Xaa	
145				150						155					160	
Glu	Leu	Ala	Tyr	Gln	Ile	Cys										

(2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1500307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

Met Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu
1 5 10 15
Asp Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys
20 25 30
Pro Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser
35 40 45
Gly Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln
50 55 60
Asp Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro
65 70 75 80
Gln Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met
85 90 95
Gly Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro
100 105 110
Val Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu
115 120 125
Ala Tyr Gln Ile Cys
130

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1500308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu Asp
1 5 10 15
Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys Pro
20 25 30
Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser Gly
35 40 45
Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln Asp
50 55 60
Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro Gln
65 70 75 80
Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met Gly
85 90 95
Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro Val
100 105 110
Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu Ala
115 120 125
Tyr Gln Ile Cys
130

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1500313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

atcatcatcg	tattcacctg	tgtcctttct	ttcattgaca	cttgccagtt	tacatcgaca	60
aacaaaagaa	atcagaatgg	atttctcagg	gagattcctt	gtcatcttcg	ttaccttctt	120
ctttctccct	cctctgtctt	cagctgggag	ctacgattct	ggttcgggtc	tcgagtcact	180
cgctcgcggg	atgcttcatt	cagccaagga	tcctgagttc	ttcgagtggg	tgagaggaat	240
taggagaaag	attcatgaga	acccagagac	agggtttcag	gagttcaaaa	cgagtcaact	300
cgttcgagac	gagcttgact	cgcttgagg	gaagtataag	tatcctgtgg	cgaagactgg	360
cgctgctcrt	tggatcggat	cctgttcgaa	acctgttttc	ggacttagag	ccgacatgga	420
cgcacttccg	gttacaggga	attagtggaa	tgggaatcsa	aaagtaaagt	agatggaaag	480
atgcatgctt	gtggatcatg	tactcatgtt	gctatgcttc	ttggtgctgc	taagcttctt	540
caaaccacaa	aacacctcat	caagggggaca	gtaaaacttg	tgtttcaacc	aggcgaggaa	600
ggttatgcag	gtgcttatga	aatgctaaaa	gacgagattc	tagacgactt	msatgggata	660
ctcagtgttc	atgtctttcc	atcgatccca	tcaggtggta	ttggttctag	gcctgggacc	720
gttcttgtag	gtgcaggatt	gtttacagtc	acgggttcacg	gtcaaggtag	ccacgcagct	780
acaccgcact	tctctaaara	cccggttctt	gcagcttctt	ccgctgttgt	tgccttgcaa	840
cagattgttt	cgcgggaaact	ggatccactc	gaagctgggtg	tggttacagt	tggatatatt	900
gaaggagggtc	atgctcaaaa	cgtaataaccg	cagagtgcga	aattttggagg	tactttcaga	960
magcttaagc	aacgatgggc	ttctatttat	ccaaagacgg	atcaaagaga	tttcagaggc	1020
acaagcatcg	gtataccgat	gcaaagcaga	agtaaacttc	gaagagaaaa	agccgtcgct	1080
tcacmccggt	aatgaataac	gacgaggggt	tatacbgagc	acggtaaaaa	agtagcggaa	1140
gcatgatttg	gaaagaataa	cttccatgat	ttcccgggtg	caatggggagg	agaggatttc	1200
agcntttctt	actcaaaaaga	cntaaggctg	cgattttcgt	gctggggata	aagaatgaga	1260
cgctaggcgc	tggttaagccg	cttactcgcg	cttacttctt	tggtgatgaa	gaagctcttc	1320
ctgttggggc	tgctcttcac	gcagctatgg	ccgtttctta	tttgacgaa	catgscata	1380
gccatgaaga	agagggttaag	agtgaattat	agaaggtgtt	gggagaaaaat	cagcttatat	1440
tagtcatcat	ctatttgtat	ttgaacttga	aagttagggtg	aggttaggtt	tcgggttggg	1500
aagaatgttt	gttaatagtc	acgagaaaacc	aaccactttc			

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..203

(D) OTHER INFORMATION: / Ceres Seq. ID 1500314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

Met	His	Ala	Cys	Gly	His	Asp	Thr	His	Val	Ala	Met	Leu	Leu	Gly	Ala
1			5						10					15	
Ala	Lys	Leu	Leu	Gln	Thr	Thr	Lys	His	Leu	Ile	Lys	Gly	Thr	Val	Lys
		20						25				30			
Leu	Val	Phe	Gln	Pro	Gly	Glu	Glu	Gly	Tyr	Ala	Gly	Ala	Tyr	Glu	Met
		35				40					45				
Leu	Lys	Asp	Glu	Ile	Leu	Asp	Asp	Xaa	Xaa	Gly	Ile	Leu	Ser	Val	His
	50				55					60					
Val	Phe	Pro	Ser	Ile	Pro	Ser	Gly	Gly	Ile	Gly	Ser	Arg	Pro	Gly	Thr
65			70						75					80	
Val	Leu	Ala	Gly	Ala	Gly	Leu	Phe	Thr	Val	Thr	Val	His	Gly	Gln	Gly
		85						90					95		
Ser	His	Ala	Ala	Thr	Pro	His	Phe	Ser	Lys	Xaa	Pro	Val	Leu	Ala	Ala
	100						105					110			
Ser	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Val	Ser	Arg	Glu	Leu	Asp	
	115				120					125					
Pro	Leu	Glu	Ala	Gly	Val	Val	Thr	Val	Gly	Tyr	Ile	Glu	Gly	Gly	His
	130				135					140					
Ala	Gln	Asn	Val	Ile	Pro	Gln	Ser	Ala	Lys	Phe	Gly	Gly	Thr	Phe	Arg
145			150					155						160	
Xaa	Leu	Lys	Gln	Arg	Trp	Ala	Ser	Ile	Tyr	Pro	Lys	Thr	Asp	Gln	Arg
		165						170						175	

Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser Lys
180 185 190
Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg
195 200

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

Met Leu Leu Gly Ala Ala Lys Leu Leu Gln Thr Thr Lys His Leu Ile
1 5 10 15
Lys Gly Thr Val Lys Leu Val Phe Gln Pro Gly Glu Glu Gly Tyr Ala
20 25 30
Gly Ala Tyr Glu Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly
35 40 45
Ile Leu Ser Val His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly
50 55 60
Ser Arg Pro Gly Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr
65 70 75 80
Val His Gly Gln Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa
85 90 95
Pro Val Leu Ala Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val
100 105 110
Ser Arg Glu Leu Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr
115 120 125
Ile Glu Gly Gly His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe
130 135 140
Gly Gly Thr Phe Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro
145 150 155 160
Lys Thr Asp Gln Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met
165 170 175
Gln Ser Arg Ser Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg
180 185 190

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly Ile Leu Ser Val
1 5 10 15
His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly Ser Arg Pro Gly
20 25 30
Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr Val His Gly Gln
35 40 45
Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa Pro Val Leu Ala

50	55	60
Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val Ser Arg Glu Leu		
65	70	75
Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr Ile Glu Gly Gly		80
	85	90
His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe Gly Gly Thr Phe		95
	100	105
Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro Lys Thr Asp Gln		110
	115	120
Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser		125
	130	135
Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

gcttgctcgc taacaatcag tgaactgaac accttccgcc tcccgggtctc ctccctgccc	60
ggtgctgaag aaccctgccca tcccgggaac tggatcgatc tgccgccaac tctgaaaatc	120
catccgatcc atctctgtcg tccaagtcta ctccccgatg gacattatct accaggacag	180
cagttgtctt gccctagagc aggcgctaca tgatgaaggc gtgggaccaa tcgacctacc	240
tttcatgctt ctcagggccca tcacaaaaga tttctctgat actcaactaa ttggcagggg	300
tgggttcgga gaggtttaca aggtatgcat ggggtatttg gcacctgaat ttctgagcag	360
caatgcaatc acattcaagg cggacatata cagtctargt gttataatca ctgagattct	420
gacgggggca taargratgc accartgttg acaaaggkgc ttgaaarctg gacggacatg	480
tttcagacat taggaagc	

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

Ala Cys Ser Leu Thr Ile Ser Glu Leu Asn Thr Phe Arg Leu Pro Val	
1	5
Ser Ser Leu Pro Gly Ala Glu Glu Pro Cys His Pro Arg Asn Trp Ile	10
	15
20	25
Asp Leu Pro Pro Thr Leu Lys Ile His Pro Ile His Leu Cys Arg Pro	30
	35
35	40
Ser Leu Leu Pro Asp Gly His Tyr Leu Pro Gly Gln Gln Leu Ser Cys	45
	50
50	55
Pro Arg Ala Gly Ala Thr	60
65	70

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..91
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

Met	Asp	Ile	Ile	Tyr	Gln	Asp	Ser	Ser	Cys	Leu	Ala	Leu	Glu	Gln	Ala
1				5					10					15	
Leu	His	Asp	Glu	Gly	Val	Gly	Pro	Ile	Asp	Leu	Pro	Phe	Met	Leu	Leu
			20					25					30		
Arg	Ala	Ile	Thr	Lys	Asp	Phe	Ser	Asp	Thr	Gln	Leu	Ile	Gly	Arg	Gly
		35					40					45			
Gly	Phe	Gly	Glu	Val	Tyr	Lys	Val	Cys	Met	Gly	Tyr	Leu	Ala	Pro	Glu
	50					55				60					
Phe	Leu	Ser	Ser	Asn	Ala	Ile	Thr	Phe	Lys	Ala	Asp	Ile	Tyr	Ser	Leu
65				70						75					80
Xaa	Val	Ile	Ile	Thr	Glu	Ile	Leu	Thr	Gly	Ala					
				85					90						

(2) INFORMATION FOR SEQ ID NO:1457:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..62
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

Met	Leu	Leu	Arg	Ala	Ile	Thr	Lys	Asp	Phe	Ser	Asp	Thr	Gln	Leu	Ile
1				5					10					15	
Gly	Arg	Gly	Gly	Phe	Gly	Glu	Val	Tyr	Lys	Val	Cys	Met	Gly	Tyr	Leu
			20					25					30		
Ala	Pro	Glu	Phe	Leu	Ser	Ser	Asn	Ala	Ile	Thr	Phe	Lys	Ala	Asp	Ile
		35					40					45			
Tyr	Ser	Leu	Xaa	Val	Ile	Ile	Thr	Glu	Ile	Leu	Thr	Gly	Ala		
	50					55						60			

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..368
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

tcacactctg	cccagctaag	ctaagctccc	tccgtccatc	ggcatggcga	ctaccactac	60
taccatcctc	ctcctcctcc	tcgtcgcagc	cacagccgtc	tcggcgggccg	acctctccgt	120
gtaccacaac	gtgcaccgcg	cgtcccgcgc	cccgtcgcag	tccatcatcg	cgctcgccccg	180
cgccgacgac	gcgcggctcc	tcttcctctc	atccaaggcg	gcctcgctcg	gcggcgctcac	240
ctccgctccc	gtcgcctccg	gccagactcc	gcmctcgtag	gtmgtccgcg	cggggctcgg	300
caccccggtc	cagcagctgc	tcctcgcgct	cgacaccagc	gccgacgcca	cctggtcgcga	360
ctgcgcgc						

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

Thr Leu Cys Pro Ala Lys Leu Ser Ser Leu Arg Pro Ser Ala Trp Arg
1 5 10 15
Leu Pro Leu Leu Pro Ser Ser Ser Ser Ser Ser Ser Gln Pro Gln Pro
20 25 30
Ser Arg Arg Pro Thr Ser Pro Cys Thr Thr Thr Cys Thr Arg Arg Pro
35 40 45
Arg Pro Arg Ser Ser Pro Ser Ser Arg Ser Pro Ala Pro Thr Thr Arg
50 55 60
Gly Ser Ser Ser Ser His Pro Arg Arg Pro Arg Pro Ala Ala Ser Pro
65 70 75 80
Pro Leu Pro Ser Pro Pro Ala Arg Leu Arg Xaa Arg Thr Xaa Ser Ala
85 90 95
Arg Gly Ser Ala Pro Arg Ser Ser Ser Cys Ser Ser Arg Ser Thr Pro
100 105 110
Ala Pro Thr Pro Pro Gly Arg Thr Ala Arg
115 120

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500369
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

Met Ala Thr Thr Thr Thr Thr Ile Leu Leu Leu Leu Val Ala Ala
1 5 10 15
Thr Ala Val Ser Ala Ala Asp Leu Ser Val Tyr His Asn Val His Pro
20 25 30
Pro Ser Pro Ser Pro Leu Glu Ser Ile Ile Ala Leu Ala Arg Ala Asp
35 40 45
Asp Ala Arg Leu Leu Phe Leu Ser Ser Lys Ala Ala Ser Ser Gly Gly
50 55 60
Val Thr Ser Ala Pro Val Ala Ser Gly Gln Thr Pro Xaa Ser Tyr Xaa
65 70 75 80
Val Arg Ala Gly Leu Gly Thr Pro Val Gln Gln Leu Leu Leu Ala Leu
85 90 95
Asp Thr Ser Ala Asp Ala Thr Trp Ser His Cys Ala
100 105

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1500370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

```
atcctctagc tctctctctc tctcttctct cacacacaca cacagtcaca gacaccacct 60
tcacttagac tgtgctagta ggtagcggcc gcgtaaatgga gcaggagctc agccttgagc 120
tcacctcct ccacctctcg gcctcgccgc cggagccacc gggctacttc gtctgcatgt 180
actgogaccg caagttcttc agctcgagc ctctcggtgg ccaccagaac gcgcacaagt 240
acgagcgcas ctggccaagc gccgcaggga gatagccgcc gccctgcgcg cgcacggggc 300
ggcgcgccacc gcmacgggcg cyccggagga cgacgmcgyc gccgcgatgg gctctcgca 360
tgtccccgcc aggccacaag gcacgggtac cggagtcgtc gtcgttgaag atgagagtgc 420
aaccaggatg atgggacaag cagaaggctc ctgctgctga tgacgasstc ccgcgaccgc 480
gtcgtcgagc aacatgaaga ggtcgtcgga gtacggctac ggcgtcgagg agctggatct 540
ctccctcagg ctttgattgg ttctcttcc tcctccacyn nnanatataa ttgcgcccg 600
tngctnagat aattcgatct ttgtggtcag tgcaatcatc tgtttcgcgt gcgtggatc 660
tcagtgtctg atccgtcact ttcttctca tgtagttgtt gtgcagttat attcttccat 720
ccgatgatgg aacctatcgg caagaactat tgtcggccca tcctgctatc caaagggcgt 780
gggtattggg gtgctctttt cggttttctg ccttgagtct tctttgtgcg atctaaattc 840
gcagcttgtt ttttccaaa cggcggaaac agttttgccg caatttcggt tggaccttt 900
tcaagtgact ctaaattggg c
```

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

```
Met Glu Gln Glu Ser Leu Glu Leu Thr Leu Leu His Pro Ser Ala
1          5          10          15
Ser Pro Pro Glu Pro Pro Gly Tyr Phe Val Cys Met Tyr Cys Asp Arg
20          25          30
Lys Phe Phe Ser Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys
35          40          45
Tyr Glu Arg Xaa Trp Pro Ser Ala Ala Gly Arg
50          55
```

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1500372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

```
Met Gly Ser Arg Asp Val Pro Ala Arg Pro Gln Gly Thr Gly Thr Gly
1          5          10          15
Val Val Val Val Glu Asp Glu Ser Ala Thr Arg Met Met Gly Gln Ala
20          25          30
Glu Gly Ser Cys Cys
35
```

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..50
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500373
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:
Met Thr Xaa Ser Arg Asp Arg Val Val Glu Gln His Glu Glu Val Val
1 5 10 15
Gly Val Arg Leu Arg Arg Arg Gly Ala Gly Ser Leu Pro Gln Ala Leu
 20 25 30
Ile Gly Ser Ser Ser Ser Ser Xaa Xaa Xaa Tyr Asn Ser Pro Arg Xaa
 35 40 45
Xaa Arg
50

(2) INFORMATION FOR SEQ ID NO:1465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

```
aaaatagagt tcacacgcac aaccgcgcgc cgcacgccgg gatctcgata gactctggct      60
gccgcggaaa gcggaaagaa ggcagggatc gtggccaaga tgcagatctt cgtgaagacg      120
ctgtcgtcga caaggacgat cacgtggag gttgagcctt cggacacggt ggcggacgtr      180
aaggccaagg tgtacgagtc ggagggcgtc ccgtacacct tggccttcca gaactagagc      240
gcggcagata gctaggtcgc ttctactccc cccatttgc aatgacaaag cgtttttacc      300
tttctagata tgcacttatg tctagatata tagattatct tatacttttd wcgttctktt      360
ttatttatcg tgttttagtt
```

(2) INFORMATION FOR SEQ ID NO:1466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

Asn Arg Val His Thr His Asn Pro Pro Pro His Ala Gly Ile Ser Ile
1 5 10 15
Asp Ser Gly Cys Arg Gly Lys Arg Lys Glu Gly Arg Asp Arg Gly Gln
 20 25 30
Asp Ala Asp Leu Arg Glu Asp Ala Val Val Asp Lys Asp Asp His Ala
 35 40 45
Gly Gly
50

(2) INFORMATION FOR SEQ ID NO:1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

Met Gln Ile Phe Val Lys Thr Leu Ser Ser Thr Arg Thr Ile Thr Leu
1 5 10 15
Glu Val Glu Pro Ser Asp Thr Val Ala Asp Xaa Lys Ala Lys Val Tyr
20 25 30
Glu Ser Glu Gly Val Pro Tyr Thr Leu Ala Phe Gln Asn
35 40 45

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

Met Thr Lys Arg Phe Tyr Leu Ser Arg Tyr Ala Leu Met Ser Arg Tyr
1 5 10 15
Ile Asp Tyr Leu Ile Leu Xaa Xaa Phe Xaa Phe Ile Tyr Arg Val Leu
20 25 30
Val

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

aaaaaaccaa atcgaagatc tttgaaagtt tccttttttc cgaaatctga gcttgggtat	60
tgttggataa gcttctcgga gattgagatt gaggattttg ataggtgagg agattgaaag	120
atttggattt ttgggcggca aaaatggtga tgcagacgga agctagggtt ggtgtgagct	180
caggacatgg cgtagcttcg tcttctcacc gttaaaccga ggaccagaga tcacatatcg	240
aatcggcgctc gcagctctta gccggaggac tcgctgggtgc ttttagcaag acttgactg	300
ctcctctatc tcgtctcacc attctcttcc aggtgcaagg tatgcacaca aatgctgcag	360
ctttaagaaa gccaaacata ttacacgagg cttcacggat attgaatgaa gaaggattga	420
aagctttttg gaaagggaat ctagttacta ttgctcaccg gcttccatat tcttctgtta	480
atttctacgc atatgaacac tacaagaagt tcatgtatat ggttactggg atggaaaatc	540
acaaggagag tataagttca aacctttttg tacattttgt agccggtggt ttggctggaa	600
tcacagctgc ttctgccact tatccacttg atcttgtag aactcgtctt gctgctcaga	660
caaaagtaat ctactactcg ggtatctggc atactctgcg ctctattaca accgatgaag	720
gtatctttggg cctctacaag ggactaggaa caacgcttgt ggggtgtggg cctagtattg	780
ccattagctt ttctgtgtat gaatcattga gatcttattg gaggtcaact aggcccatg	840
attcccctat catggtcagt ctagcttggtg gaagtctttc aggaatagca tcttcaacag	900
ctacgtttcc attggatctg gtgagaagaa cgaagcagct ggaaggaata ggccggcgag	960
cggtagtgta caagacaggt ttgttaggca cattaaagcg tattgttcaa acggaaggag	1020
cgagaggcct gtacagagga attcttccag agtactacaa agtggtacct ggtgtaggga	1080
tttgcttcat gacctacgag aactcaagc tttacttcaa ggaatcttct tcgaatctat	1140
aacggtttaa aaggttggtg gatttgttta ggtctatttt tgggtgagagg aaaaaactg	1200

taaaaaccaa acagcggaaa atgataatgt atacgaaatg tagaattata tatgtagttg 1260
ttggatgtag cttatacgag attaacattt gtattggtac aatccttttc cattgttaca 1320
tggtt

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

Met	Val	Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly
1			5						10					15	
Val	Ala	Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile
		20						25					30		
Glu	Ser	Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser
		35					40					45			
Lys	Thr	Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val
	50					55					60				
Gln	Gly	Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu
65					70					75					80
His	Glu	Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp
				85					90					95	
Lys	Gly	Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val
		100					105						110		
Asn	Phe	Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr
		115					120						125		
Gly	Met	Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His
	130					135					140				
Phe	Val	Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr
145					150					155					160
Pro	Leu	Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile
				165					170					175	
Tyr	Tyr	Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu
		180					185						190		
Gly	Ile	Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val
		195					200					205			
Gly	Pro	Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser
	210					215					220				
Tyr	Trp	Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu
225					230					235					240
Ala	Cys	Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro
			245						250					255	
Leu	Asp	Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg
		260					265						270		
Ala	Val	Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val
		275					280					285			
Gln	Thr	Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr
	290					295						300			
Tyr	Lys	Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr
305					310					315					320
Leu	Lys	Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu				
				325					330						

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..330
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500389
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly	Val	Ala
1				5					10					15	
Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile	Glu	Ser
			20					25					30		
Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser	Lys	Thr
		35				40					45				
Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val	Gln	Gly
	50				55					60					
Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu	His	Glu
65				70					75					80	
Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp	Lys	Gly
			85					90						95	
Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val	Asn	Phe
		100						105					110		
Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr	Gly	Met
		115				120						125			
Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His	Phe	Val
	130					135					140				
Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr	Pro	Leu
145				150					155					160	
Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile	Tyr	Tyr
			165					170						175	
Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu	Gly	Ile
		180						185					190		
Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val	Gly	Pro
		195				200						205			
Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser	Tyr	Trp
	210				215						220				
Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu	Ala	Cys
225				230						235				240	
Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro	Leu	Asp
			245					250						255	
Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg	Ala	Val
		260						265					270		
Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val	Gln	Thr
		275				280						285			
Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr	Tyr	Lys
	290				295						300				
Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr	Leu	Lys
305				310						315				320	
Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu						
				325				330							

- (2) INFORMATION FOR SEQ ID NO:1472:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..266
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

Met His Thr Asn Ala Ala Ala Leu Arg Lys Pro Ser Ile Leu His Glu
1 5 10 15
Ala Ser Arg Ile Leu Asn Glu Gly Leu Lys Ala Phe Trp Lys Gly
20 25 30
Asn Leu Val Thr Ile Ala His Arg Leu Pro Tyr Ser Ser Val Asn Phe
35 40 45
Tyr Ala Tyr Glu His Tyr Lys Lys Phe Met Tyr Met Val Thr Gly Met
50 55 60
Glu Asn His Lys Glu Ser Ile Ser Ser Asn Leu Phe Val His Phe Val
65 70 75 80
Ala Gly Gly Leu Ala Gly Ile Thr Ala Ala Ser Ala Thr Tyr Pro Leu
85 90 95
Asp Leu Val Arg Thr Arg Leu Ala Ala Gln Thr Lys Val Ile Tyr Tyr
100 105 110
Ser Gly Ile Trp His Thr Leu Arg Ser Ile Thr Thr Asp Glu Gly Ile
115 120 125
Leu Gly Leu Tyr Lys Gly Leu Gly Thr Thr Leu Val Gly Val Gly Pro
130 135 140
Ser Ile Ala Ile Ser Phe Ser Val Tyr Glu Ser Leu Arg Ser Tyr Trp
145 150 155 160
Arg Ser Thr Arg Pro His Asp Ser Pro Ile Met Val Ser Leu Ala Cys
165 170 175
Gly Ser Leu Ser Gly Ile Ala Ser Ser Thr Ala Thr Phe Pro Leu Asp
180 185 190
Leu Val Arg Arg Thr Lys Gln Leu Glu Gly Ile Gly Gly Arg Ala Val
195 200 205
Val Tyr Lys Thr Gly Leu Leu Gly Thr Leu Lys Arg Ile Val Gln Thr
210 215 220
Glu Gly Ala Arg Gly Leu Tyr Arg Gly Ile Leu Pro Glu Tyr Tyr Lys
225 230 235 240
Val Val Pro Gly Val Gly Ile Cys Phe Met Thr Tyr Glu Thr Leu Lys
245 250 255
Leu Tyr Phe Lys Asp Leu Ser Ser Asn Leu
260 265

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

tcccaagtga taatgcaagt aatgaaatgg aaaggcgtcc accccggaag cgaaagtttc 60
aggaacttcc agctgattgt aaggttccag aaaaagacaa acagcaatcg gagttagcaa 120
tgacaggtga tgttactcca tcagcaaata gagtgcggtc gccgccttca ccaagatctg 180
taatgcctcc tcctccacca aagaccatcg caccaccgcc ttctaagacc atgtctcctc 240
catcatcaaa aagcatgctt cctccaccac cagtttctaa gaccatgtct cctctaacat 300
caaaaagcat gcttcctcca ccaccgcat ttacactgac aactcaacct tcaagattac 360
aggacaacca catcagtgtg aagaaaccaa atccagttcc agatacgtta ataaagctga 420
tggaatatgg agacgatgaa gacgatgatg acgatcctga tgagccattg acaactagat 480
cgtgacagtg tattagatta cagaaccttc ttatctggca acaaaatgtc aatttgtgtt 540
tgtaacaata gaaagaaatg ttggtctctt actgatttgg aacttcattg cctaaggcta 600
ttagttaaat atttaagaca ttagctactt gttttgcaag gcactgctcg ttttgttgta 660
tttcttatca ttaatacata atggtt

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500392
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

Pro	Ser	Asp	Asn	Ala	Ser	Asn	Glu	Met	Glu	Arg	Arg	Pro	Pro	Arg	Lys	
1			5				10								15	
Arg	Lys	Phe	Gln	Glu	Leu	Pro	Ala	Asp	Cys	Lys	Val	Pro	Glu	Lys	Asp	
			20				25						30			
Lys	Gln	Gln	Ser	Glu	Leu	Ala	Met	Thr	Gly	Asp	Val	Thr	Pro	Ser	Ala	
			35				40					45				
Asn	Arg	Val	Arg	Ser	Pro	Pro	Ser	Pro	Arg	Ser	Val	Met	Pro	Pro	Pro	
			50				55				60					
Pro	Pro	Lys	Thr	Ile	Ala	Pro	Pro	Pro	Ser	Lys	Thr	Met	Ser	Pro	Pro	
65					70					75					80	
Ser	Ser	Lys	Ser	Met	Leu	Pro	Pro	Pro	Pro	Arg	Ser	Lys	Thr	Met	Ser	
				85						90				95		
Pro	Leu	Thr	Ser	Lys	Ser	Met	Leu	Pro	Pro	Pro	Pro	Arg	Phe	Thr	Leu	
				100					105					110		
Thr	Thr	Gln	Pro	Ser	Arg	Leu	Gln	Asp	Asn	His	Ile	Ser	Val	Lys	Lys	
				115				120					125			
Pro	Asn	Pro	Val	Pro	Asp	Thr	Leu	Ile	Lys	Leu	Met	Glu	Tyr	Gly	Asp	
			130				135				140					
Asp	Glu	Asp	Asp	Asp	Asp	Pro	Asp	Glu	Pro	Leu	Thr	Thr	Arg	Ser		
145					150					155				160		

- (2) INFORMATION FOR SEQ ID NO:1475:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500393
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

Met	Glu	Arg	Arg	Pro	Pro	Arg	Lys	Arg	Lys	Phe	Gln	Glu	Leu	Pro	Ala	
1				5					10						15	
Asp	Cys	Lys	Val	Pro	Glu	Lys	Asp	Lys	Gln	Gln	Ser	Glu	Leu	Ala	Met	
			20					25					30			
Thr	Gly	Asp	Val	Thr	Pro	Ser	Ala	Asn	Arg	Val	Arg	Ser	Pro	Pro	Ser	
			35				40					45				
Pro	Arg	Ser	Val	Met	Pro	Pro	Pro	Pro	Lys	Thr	Ile	Ala	Pro	Pro		
			50				55				60					
Pro	Ser	Lys	Thr	Met	Ser	Pro	Pro	Ser	Ser	Lys	Ser	Met	Leu	Pro	Pro	
65				70						75				80		
Pro	Pro	Arg	Ser	Lys	Thr	Met	Ser	Pro	Leu	Thr	Ser	Lys	Ser	Met	Leu	
				85					90					95		
Pro	Pro	Pro	Pro	Arg	Phe	Thr	Leu	Thr	Thr	Gln	Pro	Ser	Arg	Leu	Gln	
				100				105					110			
Asp	Asn	His	Ile	Ser	Val	Lys	Lys	Pro	Asn	Pro	Val	Pro	Asp	Thr	Leu	
			115				120						125			
Ile	Lys	Leu	Met	Glu	Tyr	Gly	Asp	Asp	Glu	Asp	Asp	Asp	Asp	Asp	Pro	

130 135 140
Asp Glu Pro Leu Thr Thr Arg Ser
145 150
(2) INFORMATION FOR SEQ ID NO:1476:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1500394
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:
Met Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro
1 5 10 15
Ser Pro Arg Ser Val Met Pro Pro Pro Pro Pro Lys Thr Ile Ala Pro
20 25 30
Pro Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro
35 40 45
Pro Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met
50 55 60
Leu Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu
65 70 75 80
Gln Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr
85 90 95
Leu Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Asp
100 105 110
Pro Asp Glu Pro Leu Thr Thr Arg Ser
115 120

(2) INFORMATION FOR SEQ ID NO:1477:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..441
(D) OTHER INFORMATION: / Ceres Seq. ID 1500395
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:
ccagacttta ttccccaaaa accaaaataa tcgccaccgc tctccgcacg gaaccgaagc 60
ggcggcgatg gcggcggaga agccggctcc cgtgcgcgtg ctctactgcg gcgtctgcgg 120
cctcccgcc gagtactgcg agttcggccc cgacttcgag cgctgcaagc cctggctgcg 180
cgcgcatgns ccggcgtcta ccccgacgaa cttgtcgccg cmtcctcctc ctcatccggm 240
ggcggcgaca aggacgtcga cagggtcggg gatcgcctcc agggcgctcg gatctccgac 300
ggctccacca gcgccgcagg gatgcttccg cgtctaagcc ccaagaggcg aaacgcctgc 360
mtggtggtaa gctcaagaaa aaggagaagc aagaagtggc cattgagaag attgtccgta 420
acaagcgcaa atgtgttact g

(2) INFORMATION FOR SEQ ID NO:1478:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1500396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

Gln	Thr	Leu	Phe	Pro	Lys	Asn	Gln	Asn	Asn	Arg	His	Arg	Ser	Pro	His
1				5					10					15	
Gly	Thr	Glu	Ala	Ala	Ala	Met	Ala	Ala	Glu	Lys	Pro	Ala	Pro	Val	Arg
			20					25				30			
Val	Leu	Tyr	Cys	Gly	Val	Cys	Gly	Leu	Pro	Ala	Glu	Tyr	Cys	Glu	Phe
		35					40				45				
Gly	Pro	Asp	Phe	Glu	Arg	Cys	Lys	Pro	Trp	Leu	Arg	Ala	His	Xaa	Pro
	50					55					60				
Ala	Ser	Thr	Pro	Thr	Asn	Leu	Ser	Pro	Xaa	Pro	Pro	Pro	His	Pro	Xaa
65					70					75					80
Ala	Ala	Thr	Arg	Thr	Ser	Thr	Gly	Ser	Gly	Ile	Ala	Ser	Arg	Ala	Ser
			85						90					95	
Gly	Ser	Pro	Thr	Ala	Pro	Pro	Ala	Pro	Gln	Gly	Cys	Phe	Arg	Val	
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1500397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

Arg	Leu	Tyr	Ser	Pro	Lys	Thr	Lys	Ile	Ile	Ala	Thr	Ala	Leu	Arg	Thr
1				5					10					15	
Glu	Pro	Lys	Arg	Arg	Arg	Trp	Arg	Arg	Arg	Ser	Arg	Leu	Pro	Cys	Ala
		20					25					30			
Cys	Ser	Thr	Ala	Ala	Ser	Ala	Ala	Ser	Arg	Pro	Ser	Thr	Ala	Ser	Ser
		35				40					45				
Ala	Pro	Thr	Ser	Ser	Ala	Ala	Ser	Pro	Gly	Cys	Ala	Arg	Met	Xaa	Arg
	50					55					60				
Arg	Leu	Pro	Arg	Arg	Thr	Cys	Arg	Arg	Xaa	Leu	Leu	Ile	Arg	Xaa	
65					70				75					80	
Arg	Arg	Gln	Gly	Arg	Arg	Gln	Gly	Arg	Gly	Ser	Pro	Pro	Gly	Arg	Arg
		85					90						95		
Asp	Leu	Arg	Arg	Leu	His	Gln	Arg	Arg	Arg	Asp	Ala	Ser	Ala	Ser	Lys
		100					105					110			
Pro	Gln	Glu	Ala	Lys	Arg	Leu	Xaa	Gly	Gly	Lys	Leu	Lys	Lys	Lys	Glu
	115					120						125			
Lys	Gln	Glu	Val	Val	Ile	Glu	Lys	Ile	Val	Arg	Asn	Lys	Arg	Lys	Cys
	130					135					140				
Val	Thr														
145															

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1500398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

Met Ala Ala Glu Lys Pro Ala Pro Val Arg Val Leu Tyr Cys Gly Val

1	5	10	15
Cys Gly Leu Pro Ala Glu Tyr Cys Glu Phe Gly Pro Asp Phe Glu Arg			
	20	25	30
Cys Lys Pro Trp Leu Arg Ala His Xaa Pro Ala Ser Thr Pro Thr Asn			
	35	40	45
Leu Ser Pro Xaa Pro Pro Pro His Pro Xaa Ala Ala Thr Arg Thr Ser			
	50	55	60
Thr Gly Ser Gly Ile Ala Ser Arg Ala Ser Gly Ser Pro Thr Ala Pro			
65	70	75	80
Pro Ala Pro Gln Gly Cys Phe Arg Val			

(2) INFORMATION FOR SEQ ID NO:1481:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

atccctccct ccctcatcgc gttttattat tccggtcctt cttcattcgg cccttcgccg	60
ctgctatatt tcgcggccgc cttgcctcct aataatagcm gccgcggcag tggataccgc	120
caccgccatg ggagcgctcg aggaggccca cctcgcggcc gccgcgtgcg cgtgcgagga	180
ggaggaggaa agcgactaca tcggcctcct cgcaggggaa gcgcggcgcg gcgacgccgt	240
ggagccggcc gtgcgcgccc tgcgtctggg gctcgggtgag gacgaccgcc gcgarggcct	300
gctccggacg cccaagcgcg tcgccaaaggc cttccgcgac ggcacccgag gctacaggca	360
aaaagtaaaa gacatagtgc aaggtgctct gtttccarag gttggtgtgg ataaaaggac	420
tggtatctgct g	

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

Ile Pro Pro Ser Leu Ile Ala Phe Tyr Tyr Ser Arg Pro Ser Ser Phe			
1	5	10	15
Gly Pro Ser Pro Leu Leu Tyr Phe Ala Ala Ala Leu Pro Pro Asn Asn			
	20	25	30
Ser Xaa Arg Gly Ser Gly Tyr Arg His Arg His Gly Ser Ala Arg Gly			
	35	40	45
Gly Pro Pro Arg Gly Arg Arg Val Arg Val Arg Gly Gly Gly Lys			
	50	55	60
Arg Leu His Arg Pro Pro Arg Arg Gly Ser Gly Gly Gly Arg Arg Arg			
65	70	75	80
Gly Ala Gly Arg Ala Arg Pro Ala Ala Gly Ala Arg			
	85	90	

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1500409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

```
Ser Leu Pro Pro Ser Ser Arg Phe Ile Ile Pro Val Leu Leu His Ser
1          5          10          15
Ala Leu Arg Arg Cys Tyr Ile Ser Arg Pro Pro Cys Leu Leu Ile Ile
20          25          30
Xaa Ala Ala Ala Val Asp Thr Ala Thr Ala Met Gly Ala Leu Glu Glu
35          40          45
Ala His Leu Ala Ala Ala Ala Cys Ala Cys Glu Glu Glu Glu Ser
50          55          60
Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala Ala Ala Gly Asp Ala Val
65          70          75          80
Glu Pro Ala Val Arg Ala Leu Leu Leu Gly Leu Gly Glu Asp Asp Arg
85          90          95
Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg Val Ala Lys Ala Phe Arg
100         105         110
Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val Lys Asp Ile Val Gln Gly
115         120         125
Ala Leu Phe Pro Xaa Val Gly Val Asp Lys Arg Thr Gly Ser Ala
130         135         140
```

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

```
Met Gly Ala Leu Glu Glu Ala His Leu Ala Ala Ala Cys Ala Cys
1          5          10          15
Glu Glu Glu Glu Glu Ser Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala
20          25          30
Ala Ala Gly Asp Ala Val Glu Pro Ala Val Arg Ala Leu Leu Leu Gly
35          40          45
Leu Gly Glu Asp Asp Arg Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg
50          55          60
Val Ala Lys Ala Phe Arg Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val
65          70          75          80
Lys Asp Ile Val Gln Gly Ala Leu Phe Pro Xaa Val Gly Val Asp Lys
85          90          95
Arg Thr Gly Ser Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1500422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

agcaaaccct agcgcannc anccacccac ccactcgctt cagccgcctc cgccgcgcgt	60
acaagcaggt ggagacagga tgccggctgg ccacggcctg cgctcgcgga cgcgcgacct	120
cttcgcgcgc cccttcgcga agaagggcta catcccgctc accacctacc tccgcacct	180
caagatcggc gattacgtcg atgtcaaggt gaacggcgcc gtccacaagg ggatgccgca	240
caagttctac caccggcgca ccggtcgctg ctggaacgtc accaagcgcg ccacgcgcgt	300
cgaggtcaac aagcaggtag acaacgcgga tccctttttc gcagaggcaa ttacgattag	360
tgcgctggcg catcttctga tcgtttcatt ctaggaaatg taacgsttta atatagaatg	420
gsggctatgt gctgacgggt ttgtttgatt tggatttata gaatttgtac	

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

Ala Asn Pro Ser Ala Xaa Xaa Pro Pro Thr His Ser Leu Gln Pro Pro	
1 5 10 15	
Pro Pro Arg Val Gln Ala Gly Gly Asp Arg Met Pro Ala Gly His Gly	
20 25 30	
Leu Arg Ser Arg Thr Arg Asp Leu Phe Ala Arg Pro Phe Arg Lys Lys	
35 40 45	
Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg Thr Tyr Lys Ile Gly Asp	
50 55 60	
Tyr Val Asp Val Lys Val Asn Gly Ala Val His Lys Gly Met Pro His	
65 70 75 80	
Lys Phe Tyr His Gly Arg Thr Gly Arg Val Trp Asn Val Thr Lys Arg	
85 90 95	
Ala Ile Gly Val Glu Val Asn Lys Gln Val Asp Asn Ala Asp Pro Phe	
100 105 110	
Phe Ala Glu Ala Ile Thr Ile Ser Ala Leu Ala His Leu Leu Ile Val	
115 120 125	
Ser Phe	
130	

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1500424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

Gln Thr Leu Ala Xaa Xaa Xaa His Pro Pro Thr Arg Phe Ser Arg Leu	
1 5 10 15	
Arg Arg Ala Tyr Lys Gln Val Glu Thr Gly Cys Arg Leu Ala Thr Ala	
20 25 30	
Cys Ala Arg Gly Arg Ala Thr Ser Ser Arg Ala Pro Ser Ala Arg Arg	
35 40 45	
Ala Thr Ser Arg Ser Pro Pro Thr Ser Ala Pro Thr Arg Ser Ala Ile	
50 55 60	
Thr Ser Met Ser Arg	
65	

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1500425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

```
Met Pro Ala Gly His Gly Leu Arg Ser Arg Thr Arg Asp Leu Phe Ala
1          5          10          15
Arg Pro Phe Arg Lys Lys Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg
20          25          30
Thr Tyr Lys Ile Gly Asp Tyr Val Asp Val Lys Val Asn Gly Ala Val
35          40          45
His Lys Gly Met Pro His Lys Phe Tyr His Gly Arg Thr Gly Arg Val
50          55          60
Trp Asn Val Thr Lys Arg Ala Ile Gly Val Glu Val Asn Lys Gln Val
65          70          75          80
Asp Asn Ala Asp Pro Phe Phe Ala Glu Ala Ile Thr Ile Ser Ala Leu
85          90          95
Ala His Leu Leu Ile Val Ser Phe
100
```

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1500464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

```
aatcggaaca attccgcgtt gcccatccat cccggaataa tccccaagga aaccctcgcc      60
cccctccttc cccgccgccg gtcgccagat ctccggtcat ggacgacgac ggcggggcct      120
cccggtcgcc ctccgcgtcc ccgtcgcgtc ctccgtcccc gctccccgtg gccgacccccg      180
tcacggtcgc ngcggcgccg cccggccacg tcgccgtcgc tatccccctc cgcaagcact      240
cgcttctctc cggcgcgccg ggcgggcgcg gcggccgna gggacgattg ggagcgacgg      300
cgccacctcc acgtcatcgc acgcctgggg ggagcgcttc gtggcgctgg gccggggcag      360
cctccgccac ccgcagtggc aggaggtcgc cgaggtcgtc tcctctcgcg acagytactc      420
caaggcgccc caaatccgac gtcccagtgc aag
```

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1500465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

```
Asn Arg Asn Asn Ser Ala Leu Pro Ile His Pro Gly Asn Ile Pro Lys
1          5          10          15
Glu Thr Leu Ala Pro Leu Leu Pro Arg Arg Arg Ser Pro Asp Leu Arg
```

	20		25		30										
Ser	Trp	Thr	Thr	Thr	Ala	Gly	Pro	Pro	Gly	Arg	Pro	Arg	Arg	Pro	Arg
	35						40					45			
Arg	Ala	Leu	Arg	Pro	Arg	Ser	Pro	Trp	Pro	Thr	Pro	Ser	Arg	Ser	Xaa
	50						55					60			
Arg	Arg	Arg	Pro	Ala	Thr	Ser	Pro	Ser	Leu	Ser	Pro	Ser	Ala	Ser	Thr
65					70					75					80
Arg	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Xaa	Arg	Asp	Asp
				85						90				95	
Trp	Glu	Arg	Arg	Arg	His	Leu	His	Ala	His	Arg	Arg	Leu	Gly	Gly	Ala
			100					105					110		
Leu	Arg	Gly	Ala	Gly	Pro	Gly	Gln	Pro	Pro	Pro	Pro	Ala	Val	Ala	Gly
	115						120						125		
Gly	Arg	Arg	Gly	Arg	Leu	Leu	Ser	Arg	Gln	Xaa	Leu	Gln	Gly	Ala	Pro
	130					135						140			
Asn	Pro	Thr	Ser	Gln	Cys	Lys									
145					150										

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

Ile	Gly	Thr	Ile	Pro	Arg	Cys	Pro	Ser	Ile	Pro	Glu	Ile	Ser	Pro	Arg
1				5					10					15	
Lys	Pro	Ser	Pro	Pro	Ser	Phe	Pro	Ala	Ala	Gly	Arg	Gln	Ile	Ser	Gly
			20					25					30		
His	Gly	Arg	Arg	Arg	Arg	Gly	Leu	Pro	Val	Ala	Leu	Ala	Val	Pro	Val
	35					40					45				
Ala	Leu	Ser	Val	Pro	Ala	Pro	Arg	Gly	Arg	Pro	Arg	His	Gly	Arg	Xaa
	50					55					60				
Gly	Ala	Ala	Arg	Pro	Arg	Arg	Arg	Arg	Tyr	Pro	Pro	Gln	Ala	Leu	
65					70				75					80	
Ala	Phe	Leu	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Pro	Xaa	Gly	Thr	Ile
			85						90					95	
Gly	Ser	Asp	Gly	Ala	Thr	Ser	Thr	Leu	Ile	Asp	Ala	Trp	Gly	Glu	Arg
			100					105					110		
Phe	Val	Ala	Leu	Gly	Arg	Gly	Ser	Leu	Arg	His	Pro	Gln	Trp	Gln	Glu
	115					120						125			
Val	Ala	Glu	Val	Val	Ser	Ser	Arg	Asp	Xaa	Tyr	Ser	Lys	Ala	Pro	Gln
	130					135						140			
Ile	Arg	Arg	Pro	Ser	Ala										
145					150										

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

Ser Glu Gln Phe Arg Val Ala His Pro Ser Arg Lys Tyr Pro Gln Gly
1 5 10 15
Asn Pro Arg Pro Pro Pro Ser Pro Pro Val Ala Arg Ser Pro Val
20 25 30
Met Asp Asp Asp Gly Gly Ala Ser Arg Ser Pro Ser Pro Ser
35 40 45
Arg Ser Pro Ser Pro Leu Pro Val Ala Asp Pro Val Thr Val Xaa Ala
50 55 60
Ala Pro Pro Gly His Val Ala Val Ala Ile Pro Leu Arg Lys His Ser
65 70 75 80
Pro Ser Ser Gly Gly Gly Gly Gly Gly Gly Arg Xaa Gly Arg Leu
85 90 95
Gly Ala Thr Ala Pro Pro Pro Arg Ser Ser Thr Pro Gly Gly Ser Ala
100 105 110
Ser Trp Arg Trp Ala Gly Ala Ala Ser Ala Thr Arg Ser Gly Arg Arg
115 120 125
Ser Pro Arg Ser Ser Pro Leu Ala Thr Xaa Thr Pro Arg Arg Pro Lys
130 135 140
Ser Asp Val Pro Val Gln
145 150

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

ggacctttct atcgcgcgca tttcttttcc gaccagccga vcgcccgcgc cctccggcag	60
gtcttcttcc cgccacgac caccacgccc aggtcttccc ggccccgaac gcgagcaccc	120
agccctcctc caggtcttcc ccggcgacga gcgcgtagaa gaggggatcc ttagcacaat	180
ggaagaagga gcaccagggc cgtcgcaagc catcccggat tctggagaca cgtaccgcaa	240
cagctccacc gcgcccgtgg gcagcagctc accgtctgtc gcgaagctcc ggaagctgct	300
gttccggcgg atgtctatcg gcgtcaacga cggccgctac ttccacggcc tgttccactg	360
catcgacaag cagggaacaa tcatactcca ggacgccgta gactaccgca gcgcccgcga	420
ctgctcgctt ccgacggagc agcgggtgcct ggggctcatc ctgatcccg ccgcctgccg	480
gtcgtcgtgc caggtcgatt gctccgttga agagaagatg tcgctcctgt gttttgagtg	540
aatcgtgctt caaagggaat acactacgca tgtactaagt tactggggct catctctgct	600
atctgaaact gagaggcatg attggtgttt cctatttttg aaggattgtt tatt	

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

Asp Leu Ser Ile Ala Arg Ile Phe Phe Pro Thr Ser Arg Xaa Pro Pro
1 5 10 15
Pro Ser Gly Arg Ser Ser Ser Arg Pro Arg Pro Pro Thr Pro Gly Leu
20 25 30
Pro Gly Pro Glu Arg Glu His Pro Ala Leu Leu Gln Val Phe Pro Gly
35 40 45

Asp Glu Arg Val Glu Glu Gly Ile Leu Ser Thr Met Glu Glu Gly Ala
50 55 60
Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly Asp Thr Tyr Arg Asn
65 70 75 80
Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro Ser Val Ala Lys Leu
85 90 95
Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly Val Asn Asp Gly Arg
100 105 110
Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys Gln Gly Asn Ile Ile
115 120 125
Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg His Cys Ser Pro Pro
130 135 140
Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile Pro Ala Ala Cys Arg
145 150 155 160
Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu Lys Met Ser Leu Leu
165 170 175
Cys Phe Glu

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

Met Glu Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly
1 5 10 15
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro
20 25 30
Ser Val Ala Lys Leu Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly
35 40 45
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys
50 55 60
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg
65 70 75 80
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile
85 90 95
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu
100 105 110
Lys Met Ser Leu Leu Cys Phe Glu
115 120

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

gtgcttcaag aattgatccg ttgcgggtgc gacctccagc tccaggagca gcaccaatcc 60
cccaagccgc catggccgcc gacccacgc tgctgcttct cgtacctttc ctgcgccatcc 120
ccctctactt cttcttggcc accagacgta ggacgccacg cgggggcgcg cggctcccgc 180

cggggccgtg ggcgctgccc gtggtcgggc acctgcatca cctagcccgg ggcctcccgc 240
accgcgtcat gcgcgamctg gcgargcgcc acggcccgt catgatgctc cggttcggcg 300
aggccccgt ggtggtggcc tcctcgccgg cmgcrgcgcg cgaggtagtg cggaccacg 360
acgcggcggt crcgtcgccg cccatcggtc ccgtgtmccg gctctggttc

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

Val Leu Gln Glu Leu Ile Arg Ser Arg Cys Asp Leu Gln Leu Gln Glu
1 5 10 15
Gln His Gln Ser Pro Lys Pro Pro Trp Pro Pro Thr Pro Arg Cys Cys
20 25 30
Phe Ser Tyr Leu Ser Ser Pro Ser Pro Ser Thr Ser Ser Trp Pro Pro
35 40 45
Asp Val Gly Arg His Ala Gly Ala Arg Gly Ser Arg Arg Gly Arg Gly
50 55 60
Arg Cys Pro Trp Ser Gly Thr Cys Ile Thr
65 70

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

Ala Ser Arg Ile Asp Pro Phe Ala Val Arg Pro Pro Gly Ala
1 5 10 15
Ala Pro Ile Pro Gln Ala Ala Met Ala Ala Asp Pro Thr Leu Leu Leu
20 25 30
Leu Val Pro Phe Leu Ala Ile Pro Leu Tyr Phe Phe Leu Ala Thr Arg
35 40 45
Arg Arg Thr Pro Arg Gly Gly Ala Arg Leu Pro Pro Gly Pro Trp Ala
50 55 60
Leu Pro Val Val Gly His Leu His His Leu Ala Arg Gly Leu Pro His
65 70 75 80
Arg Val Met Arg Xaa Leu Ala Xaa Arg His Gly Pro Leu Met Met Leu
85 90 95
Arg Phe Gly Glu Val Pro Val Val Val Ala Ser Ser Pro Xaa Xaa Ala
100 105 110
Arg Glu Val Met Arg Thr His Asp Ala Ala Phe Xaa Ser Arg Pro Ile
115 120 125
Gly Pro Val Xaa Arg Leu Trp Phe
130 135

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..113
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500477
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:
Met Ala Ala Asp Pro Thr Leu Leu Leu Leu Val Pro Phe Leu Ala Ile
1 5 10 15
Pro Leu Tyr Phe Phe Leu Ala Thr Arg Arg Arg Thr Pro Arg Gly Gly
 20 25 30
Ala Arg Leu Pro Pro Gly Pro Trp Ala Leu Pro Val Val Gly His Leu
 35 40 45
His His Leu Ala Arg Gly Leu Pro His Arg Val Met Arg Xaa Leu Ala
 50 55 60
Xaa Arg His Gly Pro Leu Met Met Leu Arg Phe Gly Glu Val Pro Val
65 70 75 80
Val Val Ala Ser Ser Pro Xaa Xaa Ala Arg Glu Val Met Arg Thr His
 85 90 95
Asp Ala Ala Phe Xaa Ser Arg Pro Ile Gly Pro Val Xaa Arg Leu Trp
 100 105 110
Phe

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..328
(D) OTHER INFORMATION: / Ceres Seq. ID 1500478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

cagatcttat	cccttccagt	tccaggcagc	atcccagcc	tgacgaagga	attgaggacg	60
ctcgagctcg	agctacgtca	ggrtccaaca	ccascatggt	tacgggaaca	agaggacggt	120
cgtgctctac	ccgtogctgg	gcgtgggcca	cctgatcccg	atggtggagc	tggccaagca	180
cctctgcgc	cacggccacg	gcgcgtcat	cgccgtggtc	aaccgcccgc	acascgacgc	240
cgtgcggcc	gcmgcggtkg	agcgctckc	ggcggycaac	ccggccatcg	cgttccgcct	300
cctgccggtc	ccggccagcc	cggacgcc				

(2) INFORMATION FOR SEQ ID NO:1501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1500479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

Gln Ile Leu Ser	Pro Val Pro Gly	Ser Ile Pro Ser	Leu Thr Lys
1 5	10	15	
Glu Leu Arg Thr	Leu Glu Leu Glu	Leu Arg Gln Xaa	Pro Thr Pro Xaa
20	25	30	
Trp Leu Arg Glu	Gln Glu Asp Val	Arg Ala Leu Pro	Val Ala Gly Arg
35	40	45	
Gly Pro Pro Asp	Pro Asp Gly Gly	Ala Gly Gln Ala	Pro Leu Ala Pro
50	55	60	

Arg Pro Arg Arg Ala His Arg Arg Gly Gln Pro Ala Arg Xaa Arg Arg
65 70 75 80
Arg Val Gly Arg Xaa Gly Xaa Ala Pro Xaa Gly Xaa Gln Pro Gly His
85 90 95
Arg Val Pro Pro Ala Gly Pro Gly Gln Pro Gly Arg
100 105

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

Met Val Glu Leu Ala Lys His Leu Leu Arg His Gly His Gly Ala Leu
1 5 10 15
Ile Ala Val Val Asn Pro Pro Asp Xaa Asp Ala Val Ser Ala Xaa Ala
20 25 30
Xaa Glu Arg Leu Xaa Ala Xaa Asn Pro Ala Ile Ala Phe Arg Leu Leu
35 40 45
Pro Val Pro Ala Ser Pro Asp Ala
50 55

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..531
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

atcaaaactgc acagcttctc ctgcattgcc cttccaggaa tatccacctg gaataaacact 60
tgtacctatg aagagtagga cactagcgcc attccgtaca actaatcttg tggtagtacg 120
atcaaccaat ggtgctggtg gatctacatg ttctgatttt ttgcttcgg gggaagctct 180
gcttatagat cctggatgca gctctcagg tcatgcagag cttgcagatc tcattgattc 240
ccttccaaaa aggttattag ttcttggtac acatcatcat caggatcaca ttgagggtct 300
ttcagtcggt cagagatgca atcctgatgc tgttctcttg acacacccaa gtacaatgga 360
tcgcattggg aaaggaactt ggcagattga ctacacttca gtaactggtg gtgaaaagat 420
atgcataggt gaccaagaac tacaagttgt ttttgcacct ggtcatacag atggtcatat 480
ggggcttctc catgtaaata ccaatacatt ggttggtgga gatcattgtg t

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

Ser Asn Cys Thr Ala Ser Pro Ala Leu Pro Phe Gln Glu Tyr Pro Pro
1 5 10 15

Gly Ile Thr Leu Val Pro Met Lys Ser Arg Thr Leu Ala Pro Phe Arg
20 25 30
Thr Thr Asn Leu Val Val Val Arg Ser Thr Asn Gly Ala Gly Gly Ser
35 40 45
Thr Cys Ser Asp Phe Phe Ala Ser Gly Glu Ala Leu Leu Ile Asp Pro
50 55 60
Gly Cys Ser Ser Gln Val His Ala Glu Leu Ala Asp Leu Ile Asp Ser
65 70 75 80
Leu Pro Lys Arg Leu Leu Val Leu Val Thr His His His Gln Asp His
85 90 95
Ile Glu Gly Leu Ser Val Val Gln Arg Cys Asn Pro Asp Ala Val Leu
100 105 110
Leu Thr His Gln Ser Thr Met Asp Arg Ile Gly Lys Gly Thr Trp Gln
115 120 125
Ile Asp Tyr Thr Ser Val Thr Gly Gly Glu Lys Ile Cys Ile Gly Asp
130 135 140
Gln Glu Leu Gln Val Val Phe Ala Pro Gly His Thr Asp Gly His Met
145 150 155 160
Gly Leu Leu His Val Asn Thr Asn Thr Leu Val Val Gly Asp His Cys
165 170 175

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

Met Lys Ser Arg Thr Leu Ala Pro Phe Arg Thr Thr Asn Leu Val Val
1 5 10 15
Val Arg Ser Thr Asn Gly Ala Gly Gly Ser Thr Cys Ser Asp Phe Phe
20 25 30
Ala Ser Gly Glu Ala Leu Leu Ile Asp Pro Gly Cys Ser Ser Gln Val
35 40 45
His Ala Glu Leu Ala Asp Leu Ile Asp Ser Leu Pro Lys Arg Leu Leu
50 55 60
Val Leu Val Thr His His His Gln Asp His Ile Glu Gly Leu Ser Val
65 70 75 80
Val Gln Arg Cys Asn Pro Asp Ala Val Leu Thr His Gln Ser Thr
85 90 95
Met Asp Arg Ile Gly Lys Gly Thr Trp Gln Ile Asp Tyr Thr Ser Val
100 105 110
Thr Gly Gly Glu Lys Ile Cys Ile Gly Asp Gln Glu Leu Gln Val Val
115 120 125
Phe Ala Pro Gly His Thr Asp Gly His Met Gly Leu Leu His Val Asn
130 135 140
Thr Asn Thr Leu Val Val Gly Asp His Cys
145 150

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..555

(D) OTHER INFORMATION: / Ceres Seq. ID 1500487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

gactccacgc	cgccagtcac	gaccacgccg	cgcctccgcc	tggaaccctt	tagccgagcg	60
gasaagggaa	gaaatgggga	agggtacggg	cagcttcggc	aagcgccgga	acaagacgca	120
cacgctctgc	atccgctgcg	gcggccggcg	tgagcgggcg	gcgtcaagaa	cccgatctta	180
aatcggggcg	ccagccccga	gagctccgac	gccgagtgac	atgagaagcg	agcgagcagc	240
agcagcagca	gccaccgcaa	aggetcaacg	acgacgacgt	ccgttggtgc	gacggcgccc	300
agcgagcat	gccgctgtcg	tcttcgttcg	tatccacgta	cgtaacgacg	cccagctgac	360
ccgcttgcc	acccgtccgt	tctgtgcgac	tgatgggtcg	gtcggcgggc	gtcggcgggc	420
gggctttcgg	tacgtcgtgg	ataagcacga	ggggagggcg	ggcaggcggg	aacggaggcg	480
gaggcgggcg	cccgaagtgg	cggctcttcc	aatgtcaaaa	aaggacagct	gtaacagtga	540
taagaaaaac	aagtc					

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1500488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

Asp	Ser	Thr	Pro	Pro	Val	Thr	Thr	Thr	Pro	Arg	Leu	Arg	Leu	Pro
1			5					10					15	
Phe	Ser	Arg	Ala	Xaa	Lys	Gly	Arg	Asn	Gly	Glu	Gly	Tyr	Gly	Gln
			20				25					30		Leu
Arg	Gln	Ala	Pro	Glu	Gln	Asp	Ala	His	Ala	Leu	His	Pro	Leu	Arg
		35				40					45			Arg
Pro	Ala	Trp	Ser	Gly	Arg	Val	Lys	Asn	Pro	Asp	Leu	Asn	Arg	Ala
	50				55						60			Pro
Ser	Pro	Glu	Ser	Ser	Asp	Ala	Glu							
65					70									

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

Thr	Pro	Arg	Arg	Gln	Ser	Arg	Pro	Arg	Arg	Ala	Ser	Ala	Trp	Asn
1				5					10				15	Pro
Leu	Ala	Glu	Arg	Xaa	Arg	Glu	Glu	Met	Gly	Lys	Gly	Thr	Gly	Ser
		20					25					30		Phe
Gly	Lys	Arg	Arg	Asn	Lys	Thr	His	Thr	Leu	Cys	Ile	Arg	Cys	Gly
		35				40						45		Gly
Arg	Arg	Gly	Ala	Gly	Ala	Ser	Arg	Thr	Arg	Ile				
	50				55									

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1500490
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:
Met Arg Ser Glu Arg Ala Ala Ala Ala Ala Thr Ala Lys Ala Gln
1 5 10 15
Arg Arg Arg Arg Pro Leu Leu Arg Arg Arg Pro Ala Gln His Ala Ala
20 25 30
Val Val Phe Val Arg Ile His Val Arg Thr Thr Ala Gln Leu Thr Arg
35 40 45
Leu Pro Thr Arg Pro Phe Cys Ala Thr Gly Trp Ser Val Gly Gly Arg
50 55 60
Arg Gly Glu Gly Phe Arg Tyr Val Val Asp Lys His Glu Gly Arg Ala
65 70 75 80
Gly Arg Arg Glu Arg Arg Arg Arg Arg Pro Gln Val Ala Val Phe
85 90 95
Pro Asn Val Lys Lys Asp Ser Cys Asn Ser Asp Lys Lys Asn Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:1510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..825
(D) OTHER INFORMATION: / Ceres Seq. ID 1500491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

```
attaaaaagc taatatggct actaggaag agagagataa gtatagatca gtccttgaag 60
atgcatgaca ggttcaatgg aggtatgata accctccaga cttcaatagt gtgaaccagc 120
tctttgaaga aggccagact aaggtgtggc cagaaggttc gttagaagag acagtgcaaa 180
acgcgatcaa gtcattggag atggagttct cacataagat ccgtttacag gacttcaaga 240
ctataaacc tgaagaagttt aagctctttg tcaatggttt atcagctgaa gagacgctta 300
ggcttgggag ttacaatgct ttgctcaaga actctttgcc tgaagagttt cagtactata 360
agcccaggga agagagcttt gagtcacac atgacgcctt tagatctgct ttaccacgcg 420
ggtttgctg ggaaatactc tctgtgtact cggggccgcc tgttatagcc ttcaaattta 480
gacactgggg atactttgaa ggaactttca aaggtcatgc tcctactggg gaaatgggtc 540
aattcctggg tctaggagtt ctaaagggtt acgaatcact tagagcagag gagattgaga 600
tttactatga tccaggagag ctgttcgggg gactactcaa gggacctcct atatcagaga 660
ccaaaaccac agacagtgga gacaacactg cagagaaaca aagctgcca ttcacacact 720
aagataataa gaaaagcaga agtgattttg accctttaaa gaatatattg taacagtctc 780
ttggttattg atgcatggaa taaattataa gttatgttag gcgcc
```

(2) INFORMATION FOR SEQ ID NO:1511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..173
(D) OTHER INFORMATION: / Ceres Seq. ID 1500492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

Met Glu Phe Ser His Lys Ile Arg Leu Gln Asp Phe Lys Thr Ile Asn

1	5	10	15												
Pro	Glu	Lys	Phe	Lys	Leu	Phe	Val	Asn	Gly	Leu	Ser	Ala	Glu	Glu	Thr
		20						25					30		
Leu	Arg	Leu	Gly	Ser	Tyr	Asn	Ala	Leu	Leu	Lys	Asn	Ser	Leu	Pro	Glu
		35					40					45			
Glu	Phe	Gln	Tyr	Tyr	Lys	Pro	Glu	Glu	Glu	Ser	Phe	Glu	Ser	Ser	His
	50					55					60				
Asp	Ala	Phe	Arg	Ser	Ala	Leu	Pro	Arg	Gly	Phe	Ala	Trp	Glu	Ile	Leu
65					70					75				80	
Ser	Val	Tyr	Ser	Gly	Pro	Pro	Val	Ile	Ala	Phe	Lys	Phe	Arg	His	Trp
			85						90					95	
Gly	Tyr	Phe	Glu	Gly	Thr	Phe	Lys	Gly	His	Ala	Pro	Thr	Gly	Glu	Met
		100						105					110		
Val	Gln	Phe	Leu	Gly	Leu	Gly	Val	Leu	Lys	Val	Asp	Glu	Ser	Leu	Arg
		115					120					125			
Ala	Glu	Glu	Ile	Glu	Ile	Tyr	Tyr	Asp	Pro	Gly	Glu	Leu	Phe	Gly	Gly
	130					135					140				
Leu	Leu	Lys	Gly	Pro	Pro	Ile	Ser	Glu	Thr	Lys	Thr	Thr	Asp	Ser	Gly
145					150					155				160	
Asp	Asn	Thr	Ala	Glu	Lys	Gln	Ser	Cys	Pro	Phe	Thr	His			
				165					170						

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..668

(D) OTHER INFORMATION: / Ceres Seq. ID 1500495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

agtacttact	cactctcccc	ccaccgcgc	caggccagac	agactaactg	agcaccgcgt	60
gcaaggagtc	cgcgcccatg	gcgagcacca	acatggcgtc	ggccacctcg	cggttcatgc	120
tggccgcggg	cgtgcccacc	ggcagcagcg	gcgggcgcgt	caacttcgcc	tcggcgccca	180
accggcttgg	caggaggctc	gtggcccggg	ccgacaacga	ggccgccgca	gctgaggcgg	240
cggaagggga	gggtgccgtg	gccaccaagc	ccaaggccga	gaagccgccg	ccgatcgggc	300
ccaatagggg	cgccaagggtg	aagatcctta	ggagggagtc	ctactggtag	aacgggatcg	360
gcaacgtcgt	caccgtcgat	caggatccca	acaccgcgta	cccggtggtt	gtgcggttca	420
acaaggtgaa	ctacgccggc	gtgtccacca	acaactacgc	cttgacgag	gtcttagagg	480
tgaatgagtg	ggggccggcc	ggctcaagg	tccgcgctag	ctaccgtgtg	attgatttgt	540
agtagttgtg	aaatgaggct	gtgaagctgc	atgctgtgct	ggctagcgtc	acaacatcga	600
tcctatgtgt	aatagcataa	tccacataat	catatcatgt	aattgcttgc	tttattcacc	660
gtgtactc						

(2) INFORMATION FOR SEQ ID NO:1513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1500496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

Met	Ala	Ser	Thr	Asn	Met	Ala	Ser	Ala	Thr	Ser	Arg	Phe	Met	Leu	Ala
1					5				10				15		
Ala	Gly	Val	Pro	Thr	Gly	Ser	Ser	Gly	Gly	Arg	Val	Asn	Phe	Ala	Ser
		20						25					30		

Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu
35 40 45
Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys
50 55 60
Pro Lys Ala Glu Lys Pro Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys
65 70 75 80
Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn
85 90 95
Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Val
100 105 110
Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala
115 120 125
Leu Asp Glu Val Leu Glu Val Lys
130 135

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

Met Ala Ser Ala Thr Ser Arg Phe Met Leu Ala Ala Gly Val Pro Thr
1 5 10 15
Gly Ser Ser Gly Gly Arg Val Asn Phe Ala Ser Ala Pro Asn Arg Leu
20 25 30
Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu Ala Ala Ala Glu
35 40 45
Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys Pro Lys Ala Glu Lys
50 55 60
Pro Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys Val Lys Ile Leu Arg
65 70 75 80
Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn Val Val Thr Val Asp
85 90 95
Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Arg Phe Asn Lys Val
100 105 110
Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala Leu Asp Glu Val Leu
115 120 125
Glu Val Lys
130

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

Met Leu Ala Ala Gly Val Pro Thr Gly Ser Ser Gly Gly Arg Val Asn
1 5 10 15
Phe Ala Ser Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala
20 25 30
Asp Asn Glu Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val


```

      35              40              45
Ala Thr Lys Pro Lys Ala Glu Lys Pro Pro Pro Ile Gly Pro Asn Arg
  50              55              60
Gly Ala Lys Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly
  65              70              75              80
Ile Gly Asn Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro
      85              90              95
Val Val Val Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn
      100              105              110
Asn Tyr Ala Leu Asp Glu Val Leu Glu Val Lys
      115              120
```

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

```

gacaacaccg cgcgcgcaat acacgggaca cacacgcaga tccgagctaa ccaccatcga      60
cgagcgccas cgccagcagc cgagccggac cgaccttttc ttttttcttt tacacagcgg      120
gacggagaaa ggagtcaatc agccaaagcc acccaccgct tttaccacc gatcggcggt      180
gccgccgcta gcattgtcgg cttcagctcc atccaaatcc accgccagca agcaagcaag      240
caagccggcg ccatgggtct gccgatgagg agggagaggg acgcgagggc ggagctgaac      300
ctgccgccgg ggttccgggt ccaccccacc gacgacgagc tgggtggagca ctacctgtrc      360
cgcaaggggc ggggcagcgc ctccccgtgc ccatcatcgc cgaggtggac ctgtacaggt      420
tcgac
```

(2) INFORMATION FOR SEQ ID NO:1517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

```

Asp Asn Thr Ala Arg Ala Ile His Gly Thr His Thr Gln Ile Arg Ala
  1              5              10              15
Asn His His Arg Arg Ala Pro Xaa Pro Ala Ala Glu Pro Asp Arg Pro
      20              25              30
Phe Leu Phe Ser Phe Thr Gln Arg Asp Gly Glu Arg Ser Gln Ser Ala
      35              40              45
Lys Ala Thr His Arg Phe Tyr Pro Pro Ile Gly Val Ala Ala Ala Ser
      50              55              60
Ile Val Gly Phe Ser Ser Ile Gln Ile His Arg Gln Gln Ala Ser Lys
      65              70              75              80
Gln Ala Gly Ala Met Gly Leu Pro Met Arg Arg Glu Arg Asp Ala Glu
      85              90              95
Ala Glu Leu Asn Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Asp
      100              105              110
Glu Leu Val Glu His Tyr Leu Xaa Arg Lys Gly Arg Gly Ser Ala Ser
      115              120              125
Pro Cys Pro Ser Ser Pro Arg Trp Thr Cys Thr Gly Ser
      130              135              140
```

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

Thr	Thr	Pro	Arg	Ala	Gln	Tyr	Thr	Gly	His	Thr	Arg	Arg	Ser	Glu	Leu
1				5					10					15	
Thr	Thr	Ile	Asp	Glu	Arg	Xaa	Arg	Gln	Gln	Pro	Ser	Arg	Thr	Asp	Leu
			20					25					30		
Phe	Phe	Phe	Leu	Leu	His	Ser	Gly	Thr	Glu	Lys	Gly	Val	Asn	Gln	Pro
			35				40					45			
Lys	Pro	Pro	Thr	Ala	Phe	Thr	His	Arg	Ser	Ala	Leu	Pro	Pro	Leu	Ala
			50				55				60				
Leu	Ser	Ala	Ser	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Ser	Lys	Gln	Ala	Ser
65					70					75					80
Lys	Pro	Ala	Pro	Trp	Val	Cys	Arg								
							85								

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

attcttcttg	cctcctccct	ccaccagcat	ccctgagtct	gccatgggca	actgctgggg	60
aaccaagatt	agctctgaca	ccgccgcctc	cccttcacac	tcaccgttcc	ctcgacgcga	120
gggtgagatt	ctccggtgtg	ccaatgtcag	gagcttcacc	ttgacggagc	tgatgacctc	180
cacccggaac	ttccggcccg	acagcgtcct	cggcgaggga	ggcttcggct	ccgtcttcaa	240
ggggtggatc	gacgagacca	ccttcgcccc	ggccaggccc	ggcacaggga	tggtcatcgc	300
tgtcaagaag	ctcaaccagc	agggattgca	ggggcacagg	gagtggctgg	ctgaagtcaa	360
ctacctgggc	cagttgtctc	amcccagctc	cgtaargctc	gtaggggtact	gcctccaaga	420
cgagcagcgc	cttctcgtct	acgagttcat	gccgcgarga	agcttkgaga	accatctttt	480
caggacctca	cgt					

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Phe	Phe	Leu	Pro	Pro	Pro	Ser	Thr	Ser	Ile	Pro	Glu	Ser	Ala	Met	Gly
1				5					10					15	
Asn	Cys	Trp	Gly	Thr	Lys	Ile	Ser	Ser	Asp	Thr	Ala	Ala	Ser	Pro	Ser
			20					25					30		

Thr	Ser	Pro	Phe	Pro	Arg	Ser	Glu	Gly	Glu	Ile	Leu	Arg	Cys	Ala	Asn	
		35					40					45				
Val	Arg	Ser	Phe	Thr	Leu	Thr	Glu	Leu	Met	Thr	Ser	Thr	Arg	Asn	Phe	
	50					55					60					
Arg	Pro	Asp	Ser	Val	Leu	Gly	Glu	Gly	Gly	Phe	Gly	Ser	Val	Phe	Lys	
65					70					75					80	
Gly	Trp	Ile	Asp	Glu	Thr	Thr	Phe	Ala	Pro	Ala	Arg	Pro	Gly	Thr	Gly	
			85						90					95		
Met	Val	Ile	Ala	Val	Lys	Lys	Leu	Asn	Gln	Gln	Gly	Leu	Gln	Gly	His	
			100					105					110			
Arg	Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr	Leu	Gly	Gln	Leu	Ser	Xaa	Pro	
	115					120						125				
Ser	Leu	Val	Xaa	Leu	Val	Gly	Tyr	Cys	Leu	Gln	Asp	Glu	Gln	Arg	Leu	
	130					135					140					
Leu	Val	Tyr	Glu	Phe	Met	Pro	Arg	Xaa	Ser	Xaa	Glu	Asn	His	Leu	Phe	
145					150					155					160	
Arg	Thr	Ser	Arg													

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met	Gly	Asn	Cys	Trp	Gly	Thr	Lys	Ile	Ser	Ser	Asp	Thr	Ala	Ala	Ser	
1				5					10					15		
Pro	Ser	Thr	Ser	Pro	Phe	Pro	Arg	Ser	Glu	Gly	Glu	Ile	Leu	Arg	Cys	
			20				25					30				
Ala	Asn	Val	Arg	Ser	Phe	Thr	Leu	Thr	Glu	Leu	Met	Thr	Ser	Thr	Arg	
		35				40					45					
Asn	Phe	Arg	Pro	Asp	Ser	Val	Leu	Gly	Glu	Gly	Gly	Phe	Gly	Ser	Val	
	50				55					60						
Phe	Lys	Gly	Trp	Ile	Asp	Glu	Thr	Thr	Phe	Ala	Pro	Ala	Arg	Pro	Gly	
65				70					75						80	
Thr	Gly	Met	Val	Ile	Ala	Val	Lys	Lys	Leu	Asn	Gln	Gln	Gly	Leu	Gln	
			85					90						95		
Gly	His	Arg	Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr	Leu	Gly	Gln	Leu	Ser	
		100				105						110				
Xaa	Pro	Ser	Leu	Val	Xaa	Leu	Val	Gly	Tyr	Cys	Leu	Gln	Asp	Glu	Gln	
	115				120						125					
Arg	Leu	Leu	Val	Tyr	Glu	Phe	Met	Pro	Arg	Xaa	Ser	Xaa	Glu	Asn	His	
	130				135						140					
Leu	Phe	Arg	Thr	Ser	Arg											
145					150											

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1500507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

Met Thr Ser Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
1 5 10 15
Gly Phe Gly Ser Val Phe Lys Gly Trp Ile Asp Glu Thr Thr Phe Ala
20 25 30
Pro Ala Arg Pro Gly Thr Gly Met Val Ile Ala Val Lys Lys Leu Asn
35 40 45
Gln Gln Gly Leu Gln Gly His Arg Glu Trp Leu Ala Glu Val Asn Tyr
50 55 60
Leu Gly Gln Leu Ser Xaa Pro Ser Leu Val Xaa Leu Val Gly Tyr Cys
65 70 75 80
Leu Gln Asp Glu Gln Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Xaa
85 90 95
Ser Xaa Glu Asn His Leu Phe Arg Thr Ser Arg
100 105

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

acgaacccaa cccagtcgaa ccacctcgcc agtgagcgcc cccctcccgt cctctttccc 60
tgctggccag aactccgaat gaaatcgctg ctccaccagc tttctttacc ttcagcaagc 120
gagccggtag catcaagcta gatcgcgggg aagctcctcg tttcccccat cggcgctgct 180
ctggcgggga gaagcgtcct ctcacggcgg ccgggaagac caatccgcgc cgccagtccc 240
tgcgggcggt tccgtgaggt ggtcttggct cctggggcgg cgtgttcgtg gcggccggcg 300
agatgagcag ccacgcggtt ggaacaagca acggcggatc cggtgatgcg gccgccgggg 360
gcgcggccag gaggaacacc aggatgcca aatattccaa gttcacacag caggagctgc 420
ccgcttkcaa gccgattctt actccaaaat gggttgtctc tgt

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

Thr Asn Pro Thr Gln Ser Asn His Leu Ala Ser Glu Arg Pro Pro Pro
1 5 10 15
Val Leu Phe Pro Cys Trp Pro Glu Leu Arg Met Lys Ser Leu Leu His
20 25 30
Gln Leu Ser Leu Pro Ser Ala Ser Glu Pro Val Ala Ser Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1500518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:

Met Ser Ser His Ala Val Gly Thr Ser Asn Gly Gly Ser Gly Asp Ala
1 5 10 15
Ala Ala Gly Gly Ala Ala Arg Arg Asn Thr Arg Met Pro Lys Tyr Ser
20 25 30
Lys Phe Thr Gln Gln Glu Leu Pro Ala Xaa Lys Pro Ile Leu Thr Pro
35 40 45
Lys Trp Val Val Ser
50

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: / Ceres Seq. ID 1500519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

Met Arg Pro Pro Gly Ala Arg Pro Gly Gly Thr Pro Gly Cys Pro Asn
1 5 10 15
Ile Pro Ser Ser His Ser Arg Ser Cys Pro Leu Xaa Ser Arg Phe Leu
20 25 30
Leu Gln Asn Gly Leu Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..535
(D) OTHER INFORMATION: / Ceres Seq. ID 1500539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

tgggatgaag ccgtgggttat gttaccgtga ctacgactgt aacttcaact ccgacatatt 60
cggttgagttt gctaccgata tcgcatcgaa aatgggtgat ggtccacgac gccatgccac 120
aggaacttca ccaattctgt tacttgcgat ccaagcaaaa ggcacagctg gaatatgac 180
gccggcaagc agaggccgca aattatgccg acggtcattg gaaaataaga gtaaaggacc 240
cgagattcaa aatttgcata gacaaattat gtaattggaa aagtatgctg cggcattggg 300
gcgaatcaaa ttggactgac tacgagtctt ttgttccac cccaccagcc attaccgtag 360
accggagatc atcacttccc ggccataact tgtgacgcaa taattataca tacttattaa 420
tggatttcat gagttttttg gtttgaattg ttgctgcgag attaggtgaa tatcagttgt 480
gtaactatat ctttttcccta tagtttggtc aaattgaata aaacattttt ttgctg

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1500540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

Gly Met Lys Pro Trp Leu Cys Tyr Arg Asp Tyr Asp Cys Asn Phe Asn
1 5 10 15
Ser Asp Ile Phe Val Glu Phe Ala Thr Asp Ile Ala Ser Lys Met Val
20 25 30
Asp Gly Pro Arg Arg His Ala Thr Gly Thr Ser Pro Ile Leu Leu Leu
35 40 45
Ala Ile Gln Ala Lys Gly Thr Ala Gly Ile
50 55

(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1500541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

Met Val His Asp Ala Met Pro Gln Glu Leu His Gln Phe Cys Tyr Leu
1 5 10 15
Arg Ser Lys Gln Lys Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala Glu
20 25 30
Ala Ala Asn Tyr Ala Asp Gly His Trp Lys Ile Arg Val Lys Asp Pro
35 40 45
Arg Phe Lys Ile Cys Ile Asp Lys Leu Cys Asn Trp Lys Ser Met Leu
50 55 60
Arg His Trp Gly Glu Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val Pro
65 70 75 80
Thr Pro Pro Ala Ile Thr Val Asp Arg Arg Ser Ser Leu Pro Gly His
85 90 95
Asn Leu

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1500542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Met Pro Gln Glu Leu His Gln Phe Cys Tyr Leu Arg Ser Lys Gln Lys
1 5 10 15
Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala Glu Ala Ala Asn Tyr Ala
20 25 30
Asp Gly His Trp Lys Ile Arg Val Lys Asp Pro Arg Phe Lys Ile Cys
35 40 45
Ile Asp Lys Leu Cys Asn Trp Lys Ser Met Leu Arg His Trp Gly Glu
50 55 60
Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val Pro Thr Pro Pro Ala Ile
65 70 75 80
Thr Val Asp Arg Arg Ser Ser Leu Pro Gly His Asn Leu
85 90

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1530
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

```
atcgtcgtct tctatTTTTT cttctttctt cgatttcata ccaaaacaag aactctctgt      60
tttcgacaaa aacgaaacct tgagatctat tttgattgac ttttaagaaa gagagagatc      120
tttcttagaa gattttgtct cgtcggcatt gaagatccag ggtttgtctt tcgaaattca      180
gagagaaaaa gggatgatgag gcagagatca aggaacattt aaagccacaa gcttcatctg      240
aaacaatgga caagaaacat aatgtgaaag ggaagagggt atggcagaaa gtcaagtatc      300
aattggtgga gtttcattca ttgcctgctt atttaagaga caatgagtac atcattgggtc      360
attaccgatc cgaatggccg atcaaacaga ttcttctcag catctttacc attcataatg      420
agactttgaa tgtttgagcg cacttgattg ggtttttcct gtttttggcg ctactatat      480
acactgcaac gaaagtaccg agtgcgtgag atcttcattc gtttcaacac cgtttacccg      540
atttggtgag gaaaacagat ctccacaaac ttcattctga gctcatggct cgccttcctt      600
ctagtccatc tagttggcat gtgatggacc ttctttataa ctgtttgctt gaaagatttt      660
ctcatggcaa ctacactgac atgtgtgttc tgcattctgt gaggggaagat cttgcaaact      720
tgatagctcc tttgatcttc aggccaatta ctcatgggcc gttttatgca tttctaggtg      780
gtgctatgtt ctgtctatta gcaagcagca cgtgccacct cctctcatgt cactcagagc      840
gagtctccta cataatgctt aggctttatt acgccggcat cgcagctcta atagcgactt      900
ccttctaccc tccggtttat tactccttca tgtgtgatcc tttcttctgc aacctctact      960
taggattcat aaccatctta ggaatcgcca ctgtgcttgt ttctctcctc ccggttttcc      1020
aaagcccgga gtttcgggtg gtgagggcgt ctctgttctt tggaatggga ttctctggct      1080
tagctccgat tcttcacaag ctgataatct ttggggacca acctgaagcc cttcacacga      1140
caggttatga gattttgatg ggtttgcttt atgggttagg agctctggtt tatgcaacta      1200
ggatcccaga gagatggatg ccgggtaaat tcgatatagc aggacatagc catcagttgt      1260
ttcatgttct ggttgttctg gtgcgttcac gcactataga gctgggctag tgtatcttaa      1320
gtggagagat atygaaggat gttgaagatg aagattgaag attagatgga atctttgaat      1380
cttgtttgta gtagcttcat ataaaagttg gattatgtaa agtcttatat gtaatcaaac      1440
gtttaattgt ttcctttatt caacaaagga tttatattgt taatccacat atgtattact      1500
ggttaagaaa gctgaaggat tcatatTTTT
```

(2) INFORMATION FOR SEQ ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

```
Met Gly Asp Glu Ala Glu Ile Lys Glu His Leu Lys Pro Gln Ala Ser
1           5           10           15
Ser Glu Thr Met Asp Lys Lys His Asn Val Lys Gly Lys Arg Leu Trp
20           25           30
Gln Lys Val Lys Tyr Gln Leu Val Glu Phe His Ser Leu Pro Ala Tyr
35           40           45
Leu Arg Asp Asn Glu Tyr Ile Ile Gly His Tyr Arg Ser Glu Trp Pro
50           55           60
Ile Lys Gln Ile Leu Leu Ser Ile Phe Thr Ile His Asn Glu Thr Leu
65           70           75           80
Asn Val Trp Thr His Leu Ile Gly Phe Phe Leu Phe Leu Ala Leu Thr
85           90           95
```

```

Ile Tyr Thr Ala Thr Lys Val Pro Ser Val Val Asp Leu His Ser Leu
      100      105      110
Gln His Arg Leu Pro Asp Leu Leu Arg Lys Thr Asp Leu His Lys Leu
      115      120      125
His Ser Glu Leu Met Ala Arg Leu Pro Ser Ser Pro Ser Ser Trp His
      130      135      140
Val Met Asp Leu Leu Tyr Asn Cys Leu Pro Glu Arg Phe Ser His Gly
      145      150      155      160
Asn Tyr Thr Asp Met Cys Val Leu His Ser Val Arg Glu Asp Leu Ala
      165      170      175
Asn Leu Ile Ala Pro Leu Ile Phe Arg Pro Ile Thr Arg Trp Pro Phe
      180      185      190
Tyr Ala Phe Leu Gly Gly Ala Met Phe Cys Leu Leu Ala Ser Ser Thr
      195      200      205
Cys His Leu Leu Ser Cys His Ser Glu Arg Val Ser Tyr Ile Met Leu
      210      215      220
Arg Leu Tyr Tyr Ala Gly Ile Ala Ala Leu Ile Ala Thr Ser Phe Tyr
      225      230      235      240
Pro Pro Val Tyr Tyr Ser Phe Met Cys Asp Pro Phe Phe Cys Asn Leu
      245      250      255
Tyr Leu Gly Phe Ile Thr Ile Leu Gly Ile Ala Thr Val Leu Val Ser
      260      265      270
Leu Leu Pro Val Phe Gln Ser Pro Glu Phe Arg Val Val Arg Ala Ser
      275      280      285
Leu Phe Phe Gly Met Gly Phe Ser Gly Leu Ala Pro Ile Leu His Lys
      290      295      300
Leu Ile Ile Phe Trp Asp Gln Pro Glu Ala Leu His Thr Thr Gly Tyr
      305      310      315      320
Glu Ile Leu Met Gly Leu Leu Tyr Gly Leu Gly Ala Leu Val Tyr Ala
      325      330      335
Thr Arg Ile Pro Glu Arg Trp Met Pro Gly Lys Phe Asp Ile Ala Gly
      340      345      350
His Ser His Gln Leu Phe His Val Leu Val Val Leu Val Arg Ser Arg
      355      360      365
Thr Ile Glu Leu Gly
      370

```

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

```

Met Asp Lys Lys His Asn Val Lys Gly Lys Arg Leu Trp Gln Lys Val
1      5      10      15
Lys Tyr Gln Leu Val Glu Phe His Ser Leu Pro Ala Tyr Leu Arg Asp
      20      25      30
Asn Glu Tyr Ile Ile Gly His Tyr Arg Ser Glu Trp Pro Ile Lys Gln
      35      40      45
Ile Leu Leu Ser Ile Phe Thr Ile His Asn Glu Thr Leu Asn Val Trp
      50      55      60
Thr His Leu Ile Gly Phe Phe Leu Phe Leu Ala Leu Thr Ile Tyr Thr
      65      70      75      80
Ala Thr Lys Val Pro Ser Val Val Asp Leu His Ser Leu Gln His Arg
      85      90      95
Leu Pro Asp Leu Leu Arg Lys Thr Asp Leu His Lys Leu His Ser Glu

```


	(A1)	(A1) Sequence Description																
Met	Ala	Arg	Leu		Pro	Ser	Ser	Pro	Ser		Ser	Trp	His	Val	Met	Asp	Leu	
1					5					10						15		
Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly	Asn	Tyr	Thr	Asp			
			20					25					30					
Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala	Asn	Leu	Ile	Ala			
			35				40					45						
Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe	Tyr	Ala	Phe	Leu			
		50				55					60							
Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr	Cys	His	Leu	Leu			
65					70					75					80			
Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu	Arg	Leu	Tyr	Tyr			
				85					90					95				
Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr	Pro	Pro	Val	Tyr			
			100					105					110					
Tyr	Ser	Phe	Met	Cys	Asp	Pro	Phe	Cys	Asn	Leu	Tyr	Leu	Gly	Phe				
		115					120				125							

Ile Thr Ile Leu Gly Ile Ala Thr Val Leu Val Ser Leu Leu Pro Val
130 135 140
Phe Gln Ser Pro Glu Phe Arg Val Val Arg Ala Ser Leu Phe Phe Gly
145 150 155 160
Met Gly Phe Ser Gly Leu Ala Pro Ile Leu His Lys Leu Ile Ile Phe
165 170 175
Trp Asp Gln Pro Glu Ala Leu His Thr Thr Gly Tyr Glu Ile Leu Met
180 185 190
Gly Leu Leu Tyr Gly Leu Gly Ala Leu Val Tyr Ala Thr Arg Ile Pro
195 200 205
Glu Arg Trp Met Pro Gly Lys Phe Asp Ile Ala Gly His Ser His Gln
210 215 220
Leu Phe His Val Leu Val Val Leu Val Arg Ser Arg Thr Ile Glu Leu
225 230 235 240
Gly

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

atccaatatt tctatggagt catcttcttc actccttcat cactcttacc tctcttacct	60
taatccaaaa tttggaaaaa gacctttggg ttctttatcca ttaatgcaga gttcgcgaaa	120
atgcaaacaa actcgcattht gttctaacaa gatgtatgtt cccggctttg gagaagcttc	180
accggaggct aaggcagcga agcatcttca tgacttcttt acttacgttg cagtggaggat	240
agtgtctgct cagcttgaga gttataatcc tgaggcttat atggagttga gagaattttt	300
agatacaaac tctgtaagtg acggtgataa attctgcgcc actctcatgc gtcgctcttc	360
acgtcacatg aacttagccc ttcgaatttt agaggtagcg tctgcttatt gtaaaaaacga	420
tttcgaatgg gataatatga agcgctcgc cttcaagaac gtagatgatt ccaacacaag	480
actcatgcgc gagtacgtct tggagactag ccatgtcgaa accgattctg ataagtgaag	540
ccgaatatct cttcgaatca cattcatata tatagagtct tgagagtata cacacttgaa	600
accgtttgta catacatata cataccattg tgctatgtta ctcccagggt ttgataacctc	660

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

Ser Asn Ile Ser Met Glu Ser Ser Ser Ser Leu Leu His His Ser Tyr
1 5 10 15
Leu Ser Tyr Leu Asn Pro Lys Phe Gly Lys Arg Pro Leu Val Ser Tyr
20 25 30
Pro Leu Met Gln Ser Ser Arg Lys Cys Lys Gln Thr Arg Ile Cys Ser
35 40 45
Asn Lys Met Tyr Val Pro Gly Phe Gly Glu Ala Ser Pro Glu Ala Lys
50 55 60
Ala Ala Lys His Leu His Asp Phe Phe Thr Tyr Val Ala Val Arg Ile

65					70					75					80
Val	Ser	Ala	Gln	Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu
				85					90					95	
Arg	Glu	Phe	Leu	Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys
			100					105					110		
Ala	Thr	Leu	Met	Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg
		115					120				125				
Ile	Leu	Glu	Val	Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp
	130					135					140				
Asn	Met	Lys	Arg	Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg
145					150					155					160
Leu	Met	Arg	Glu	Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser
			165					170						175	

Asp Lys

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1500560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr	Leu	Ser	Tyr	Leu
1			5						10					15	
Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr	Pro	Leu	Met	Gln
			20					25					30		
Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser	Asn	Lys	Met	Tyr
		35					40					45			
Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys	Ala	Ala	Lys	His
	50					55					60				
Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Ala	Val	Arg	Ile	Val	Ser	Ala	Gln
65					70					75					80
Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu	Arg	Glu	Phe	Leu
				85					90					95	
Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys	Ala	Thr	Leu	Met
			100					105					110		
Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg	Ile	Leu	Glu	Val
		115					120					125			
Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp	Asn	Met	Lys	Arg
	130					135					140				
Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg	Leu	Met	Arg	Glu
145					150					155					160
Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser	Asp	Lys		
			165					170							

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1500561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

Met Gln Ser Ser Arg Lys Cys Lys Gln Thr Arg Ile Cys Ser Asn Lys
1 5 10 15
Met Tyr Val Pro Gly Phe Gly Glu Ala Ser Pro Glu Ala Lys Ala Ala
20 25 30
Lys His Leu His Asp Phe Phe Thr Tyr Val Ala Val Arg Ile Val Ser
35 40 45
Ala Gln Leu Glu Ser Tyr Asn Pro Glu Ala Tyr Met Glu Leu Arg Glu
50 55 60
Phe Leu Asp Thr Asn Ser Val Ser Asp Gly Asp Lys Phe Cys Ala Thr
65 70 75 80
Leu Met Arg Arg Ser Ser Arg His Met Asn Leu Ala Leu Arg Ile Leu
85 90 95
Glu Val Arg Ser Ala Tyr Cys Lys Asn Asp Phe Glu Trp Asp Asn Met
100 105 110
Lys Arg Leu Ala Phe Lys Asn Val Asp Asp Ser Asn Thr Arg Leu Met
115 120 125
Arg Glu Tyr Val Leu Glu Thr Ser His Val Glu Thr Asp Ser Asp Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1616
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

atcgataacc	aaataaaaaa	tggcgatctc	tttcctctgt	gtttttctca	tcaccttcgt	60
ttcgtaaatc	ttttttgcc	agaaaatcaa	acgatcaaaa	tggaatcttc	ctccaagccc	120
tccaagttt	ccggtcacg	ggaacttaca	tcagattgga	gaattgcctc	acaggtcact	180
tcaacatctc	gccgaaagat	acggacctgt	gatgcttctt	cactttgggt	ttgtccctat	240
aactgtggtc	tcacgagag	aagccgctga	agaagtgcct	agaactcatg	acctagactg	300
ttgcagcagg	cctaagcttg	tcgggacaag	gttactctcg	gcgggatttt	aaagatatcg	360
gttttacgcc	atacggtaac	gaggtggaag	gcgcggcgta	aggtttgccc	tgcgtgagac	420
ttttctgttt	gaaaaagggt	cagtccttta	ggcatatccg	agaggaagaa	tgtaactttc	480
tggtaagca	actgtcgga	tccgcggttg	atcgctctcc	ggtcgatttg	agcaaattcc	540
ttttctggct	aaccgctagt	atccttttta	gagttgcctt	aggacagaat	tttcacgaga	600
gcgattttat	cgataaagaa	aagatogaag	agctcgtgtt	cgaagctgag	actgccctag	660
caagtttcac	ttgttctgat	ttcttccttg	ttgcgggact	tggatggctc	gttgattggg	720
tttccggaca	acacaagaga	ctcaacgatg	ttttttacaa	gctcgatgct	ctgtttcaat	780
atgtcataga	tgatcattta	aatcctggaa	gatcaaaaaga	gcacgaagac	atcatcgatt	840
caatgttgga	tgtgattcat	aaacaaggag	aggatagttc	cttagagctc	acaatagatc	900
atatcaagg	gtttctcgcg	aatatatctt	ttgcagggat	agacacagg	gccatcacca	960
tgatatgggc	agtgcaggag	ctcggttaaaa	acccgaaact	gataaagaaa	gttcaaggcg	1020
atatccgaga	acaacttggc	agcaataagg	agagaatcac	cgaggaagat	atcgagaaag	1080
ttccttactt	gaagatggta	atcaaagaaa	cattcagggt	acaccagca	gctcctctta	1140
tacttccaag	ggaacaatg	gctcacatca	aagttcaagg	gtatgatatt	cctcccaaga	1200
ggaggatctt	ggtcaatgtt	tcggcaatat	gaagagatcc	caaactctgg	acaaaccgga	1260
aagagtttga	ccctgagagg	tttatggata	gctttgttga	ttatagggga	caacattacg	1320
agctcttacc	atttgggtcc	ggtcgaagga	tatgtcccgg	gatgccaatg	gggattgctg	1380
ccgtcgaatt	gggactcttg	aacttacttt	acttcttcga	ttggaagttg	cctgatggga	1440
tgacacataa	agatatcgat	actgaagaag	ctggtactct	tacaatagtc	aagaaagtac	1500
ctctcaagct	cgttccagtt	cgagttcagt	gatcagacca	aactccaaac	cttttgaata	1560
aatatatcat	gcaaatcatg	taagcttctc	tgatgatgta	tgaagtatat	ttttcc	

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..229
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

```
Met Leu Asp Val Ile His Lys Gln Gly Glu Asp Ser Ser Leu Glu Leu
1      5      10      15
Thr Ile Asp His Ile Lys Gly Phe Leu Ala Asn Ile Phe Leu Ala Gly
20     25     30
Ile Asp Thr Gly Ala Ile Thr Met Ile Trp Ala Val Thr Glu Leu Val
35     40     45
Lys Asn Pro Lys Leu Ile Lys Lys Val Gln Gly Asp Ile Arg Glu Gln
50     55     60
Leu Gly Ser Asn Lys Glu Arg Ile Thr Glu Glu Asp Ile Glu Lys Val
65     70     75     80
Pro Tyr Leu Lys Met Val Ile Lys Glu Thr Phe Arg Leu His Pro Ala
85     90     95
Ala Pro Leu Ile Leu Pro Arg Glu Thr Met Ala His Ile Lys Val Gln
100    105    110
Gly Tyr Asp Ile Pro Pro Lys Arg Arg Ile Leu Val Asn Val Ser Ala
115    120    125
Ile Gly Arg Asp Pro Lys Leu Trp Thr Asn Pro Lys Glu Phe Asp Pro
130    135    140
Glu Arg Phe Met Asp Ser Phe Val Asp Tyr Arg Gly Gln His Tyr Glu
145    150    155    160
Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Met Pro Met
165    170    175
Gly Ile Ala Ala Val Glu Leu Gly Leu Leu Asn Leu Leu Tyr Phe Phe
180    185    190
Asp Trp Lys Leu Pro Asp Gly Met Thr His Lys Asp Ile Asp Thr Glu
195    200    205
Glu Ala Gly Thr Leu Thr Ile Val Lys Lys Val Pro Leu Lys Leu Val
210    215    220
Pro Val Arg Val Gln
225
```

(2) INFORMATION FOR SEQ ID NO:1541:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..190
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

```
Met Ile Trp Ala Val Thr Glu Leu Val Lys Asn Pro Lys Leu Ile Lys
1      5      10      15
Lys Val Gln Gly Asp Ile Arg Glu Gln Leu Gly Ser Asn Lys Glu Arg
20     25     30
Ile Thr Glu Glu Asp Ile Glu Lys Val Pro Tyr Leu Lys Met Val Ile
35     40     45
Lys Glu Thr Phe Arg Leu His Pro Ala Ala Pro Leu Ile Leu Pro Arg
50     55     60
Glu Thr Met Ala His Ile Lys Val Gln Gly Tyr Asp Ile Pro Pro Lys
```

65	70	75	80
Arg Arg Ile Leu Val Asn Val Ser Ala Ile Gly Arg Asp Pro Lys Leu			
	85	90	95
Trp Thr Asn Pro Lys Glu Phe Asp Pro Glu Arg Phe Met Asp Ser Phe			
	100	105	110
Val Asp Tyr Arg Gly Gln His Tyr Glu Leu Leu Pro Phe Gly Ser Gly			
	115	120	125
Arg Arg Ile Cys Pro Gly Met Pro Met Gly Ile Ala Ala Val Glu Leu			
	130	135	140
Gly Leu Leu Asn Leu Leu Tyr Phe Phe Asp Trp Lys Leu Pro Asp Gly			
	145	150	155
Met Thr His Lys Asp Ile Asp Thr Glu Glu Ala Gly Thr Leu Thr Ile			
	165	170	175
Val Lys Lys Val Pro Leu Lys Leu Val Pro Val Arg Val Gln			
	180	185	190

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met Val Ile Lys Glu Thr Phe Arg Leu His Pro Ala Ala Pro Leu Ile
1 5 10 15
Leu Pro Arg Glu Thr Met Ala His Ile Lys Val Gln Gly Tyr Asp Ile
20 25 30
Pro Pro Lys Arg Arg Ile Leu Val Asn Val Ser Ala Ile Gly Arg Asp
35 40 45
Pro Lys Leu Trp Thr Asn Pro Lys Glu Phe Asp Pro Glu Arg Phe Met
50 55 60
Asp Ser Phe Val Asp Tyr Arg Gly Gln His Tyr Glu Leu Leu Pro Phe
65 70 75 80
Gly Ser Gly Arg Arg Ile Cys Pro Gly Met Pro Met Gly Ile Ala Ala
85 90 95
Val Glu Leu Gly Leu Leu Asn Leu Leu Tyr Phe Phe Asp Trp Lys Leu
100 105 110
Pro Asp Gly Met Thr His Lys Asp Ile Asp Thr Glu Glu Ala Gly Thr
115 120 125
Leu Thr Ile Val Lys Lys Val Pro Leu Lys Leu Val Pro Val Arg Val
130 135 140
Gln
145

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

tttctctcttc ttccatctcc acaaattcca aacatctctc tctctttctc tctcacacac
aaaattgcag aagaagaaga gtcattgaatg gtgaagaaag cttttagtaa gattgctctg

60
120

tttttgttga	gattgatcct	tctggaagat	atggaagata	cgatgaaata	cttggcacaag	180
gagcttcaaa	gacagtatac	agagcatttg	atgagtatga	aggtatagaa	gtagcatgga	240
accaagtaaa	gcttcgaaat	ttcacaagga	atcctgagga	attagagaag	tttttcagag	300
agattcatct	tctcaagact	ttgaatcatc	aaaacattat	gaaattctac	acttcttggg	360
ttgataccaa	caatttatca	atcaattttg	tcactgaact	cttcacctct	ggtactctca	420
gacagtatag	gttgagacat	agaagagtga	atattagagc	agtgaagcaa	tggtgcaagc	480
agattttaaa	agggcttctt	tatttacata	gtcgttctcc	accaattata	catagagatc	540
tcaaatgtga	taacattttc	atcaatggaa	accaaggtga	agtcaagatc	ggtgaccttg	600
gactcgctgc	gattcttcgt	aaatcacatg	ccgttcgttg	cgttggaacc	cctgagttta	660
tggctccaga	agtgtatgat	gaggaatata	atgagttggg	tgatgtatat	gcttttggca	720
tgtgtgtgtt	ggagatgggt	acttttgatt	atccttacag	tgaatgtact	cacccggcac	780
aaatctacaa	gaaagttacc	tcggggaaaa	agcctgaagc	tttttactta	gtgaaggatc	840
ctgaggttcg	tgagtttggt	gagaagtgtt	tagctaactg	gacgtgtagg	ctaacggcat	900
tggagctttt	acaagaccct	tttctacaag	atgataatat	ggatggattt	gttatgagac	960
ctattgatta	ctacaatggg	tatgatgaaa	ctgggtgtgt	ccttagacat	cctttgattg	1020
atgacctctt	ttaccatgat	cagtttgagt	cgtcacagat	atgtgagatc	gatcttttcg	1080
ctaacgatga	tgaagatcat	gtcgacatct	cgattaaagg	gaagagaaac	ggtgatgatg	1140
ggatattctt	gagacttaga	atatctgatg	ctgaaggacg	gataaggaaac	atttacttcc	1200
cgtttgagac	ggctattgat	actgcatgga	gtgtagcggg	tgagatgggt	tcagagctcg	1260
acataacgaa	tcaagatggt	gcgaaaatcg	cggagatgat	cgatgcagag	attgctgcat	1320
tgggtgctga	ttggaaaaat	gatacagaaa	gttcccaaaa	tgtaaaacaac	aacaagaaca	1380
acaacactgc	aggattctgt	ggagagtgtg	cttcaaacgg	gtatatacaa	gagactgtat	1440
catcaggaga	aaaatctcat	cataatcatc	atgagttcga	tagttctgaa	gacaagagct	1500
gttcttcggt	tcacggtagg	tttgccgata	tgtgggggtt	gcgagaatca	tattctgatg	1560
atggagaaaa	acagagctca	aggaagggtt	gaagtggacg	gtggtcggag	aatgagatga	1620
gacgagaact	gagatggctt	aaggcaaggc	acaagattca	acttatgaaa	atgagaggtc	1680
aaacgatctg	cgagacaccg	atagagatct	ctcttacacc	gggaacttca	gtttcggttac	1740
ctcttcttta	cagggtctata	tcacttcctg	tggatgccgt	ggatatgtga	cattattgta	1800
aagtctgatg	atagttatca	cttatatttg	tatgtttcga	catttttaac	ttttgttaag	1860
ttaaaaagtt	atgacatagt	gtactttatt	taaagagaag	aagagtaaac	gaaaaacata	1920

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

Ser	Ser	Ser	Ser	Ile	Ser	Thr	Asn	Ser	Lys	His	Leu	Ser	Leu	Phe	Leu
1				5					10					15	
Ser	His	Thr	Gln	Asn	Cys	Arg	Arg	Arg	Val	Met	Asn	Gly	Glu	Glu	
			20					25				30			
Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu	Ile	Asp	Pro	Ser	Gly
		35					40					45			
Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys	Gly	Ala	Ser	Lys	Thr
	50				55						60				
Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile	Glu	Val	Ala	Trp	Asn
65				70					75					80	
Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro	Glu	Glu	Leu	Glu	Lys
			85					90					95		
Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu	Asn	His	Gln	Asn	Ile
			100					105					110		
Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	Asn	Leu	Ser	Ile	Asn
		115					120					125			
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	Arg	Gln	Tyr	Arg	Leu
		130					135					140			

Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln
145					150					155					160
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile
				165					170					175	
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly
			180					185					190		
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser
		195					200					205			
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val
	210					215					220				
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met
225					230					235					240
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr
				245					250					255	
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu
			260					265						270	
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys
		275					280					285			
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln
	290					295					300				
Asp	Pro	Phe	Leu	Gln	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro	
305					310				315					320	
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His
				325					330					335	
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln
			340					345						350	
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Asp	His	Val	Asp
		355				360						365			
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile	Phe	Leu	Arg
	370					375					380				
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile	Tyr	Phe	Pro
385					390					395					400
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val	Glu	Met	Val
			405						410					415	
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile	Ala	Glu	Met
			420					425					430		
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys	Asn	Asp	Thr
		435				440						445			
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn	Thr	Ala	Gly
	450					455					460				
Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile	Gln	Glu	Thr	Val	Ser
465					470					475					480
Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu	Phe	Asp	Ser	Ser	Glu
				485					490					495	
Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe	Ala	Asp	Met	Trp	Gly
			500					505					510		
Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys	Gln	Ser	Ser	Arg	Lys
		515					520					525			
Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met	Arg	Arg	Glu	Leu	Arg
						535					540				
Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met	Lys	Met	Arg	Gly	Gln
545					550					555					560
Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu	Thr	Pro	Gly	Thr	Ser
				565					570					575	
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser	Leu	Pro	Val	Asp	Ala
			580					585					590		
Val	Asp	Met													
		595													

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 568 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..568
(D) OTHER INFORMATION: / Ceres Seq. ID 1500616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

Met	Asn	Gly	Glu	Glu	Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu	
1			5					10							15	
Ile	Asp	Pro	Ser	Gly	Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys	
			20				25						30			
Gly	Ala	Ser	Lys	Thr	Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile	
		35					40					45				
Glu	Val	Ala	Trp	Asn	Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro	
	50					55				60						
Glu	Glu	Leu	Glu	Lys	Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu	
65				70					75						80	
Asn	His	Gln	Asn	Ile	Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	
			85					90						95		
Asn	Leu	Ser	Ile	Asn	Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	
			100					105					110			
Arg	Gln	Tyr	Arg	Leu	Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	
	115						120					125				
Gln	Trp	Cys	Lys	Gln	Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	
	130					135					140					
Ser	Pro	Pro	Ile	Ile	His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	
145					150					155					160	
Asn	Gly	Asn	Gln	Gly	Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	
			165					170						175		
Ile	Leu	Arg	Lys	Ser	His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	
		180						185					190			
Met	Ala	Pro	Glu	Val	Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	
	195						200					205				
Tyr	Ala	Phe	Gly	Met	Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	
	210					215					220					
Tyr	Ser	Glu	Cys	Thr	His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	
225					230					235					240	
Gly	Lys	Lys	Pro	Glu	Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	
			245						250					255		
Glu	Phe	Val	Glu	Lys	Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	
		260						265					270			
Leu	Glu	Leu	Leu	Gln	Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly	
	275						280					285				
Phe	Val	Met	Arg	Pro	Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	
	290					295					300					
Val	Phe	Leu	Arg	His	Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	
305				310						315					320	
Phe	Glu	Ser	Ser	Gln	Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	
			325						330					335		
Glu	Asp	His	Val	Asp	Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	
		340						345					350			
Gly	Ile	Phe	Leu	Arg	Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	
	355					360						365				
Asn	Ile	Tyr	Phe	Pro	Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	
	370					375					380					
Ala	Val	Glu	Met	Val	Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	
385				390						395					400	
Lys	Ile	Ala	Glu	Met	Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	
			405					410						415		

Trp	Lys	Asn	Asp	Thr	Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn
			420					425					430		
Asn	Asn	Thr	Ala	Gly	Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile
			435				440					445			
Gln	Glu	Thr	Val	Ser	Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu
			450			455						460			
Phe	Asp	Ser	Ser	Glu	Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe
465					470						475				480
Ala	Asp	Met	Trp	Gly	Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys
				485				490						495	
Gln	Ser	Ser	Arg	Lys	Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met
			500					505					510		
Arg	Arg	Glu	Leu	Arg	Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met
			515				520					525			
Lys	Met	Arg	Gly	Gln	Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu
			530				535					540			
Thr	Pro	Gly	Thr	Ser	Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser
545					550					555					560
Leu	Pro	Val	Asp	Ala	Val	Asp	Met								
							565								

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1500617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	Asn	Leu	Ser	Ile	Asn
1				5					10					15	
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	Arg	Gln	Tyr	Arg	Leu
			20					25					30		
Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln
			35				40					45			
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile
			50			55					60				
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly
65				70					75					80	
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser
				85				90						95	
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val
			100					105					110		
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met
			115				120					125			
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr
			130			135					140				
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu
145				150					155					160	
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys
			165					170						175	
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln
			180				185					190			
Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro
			195				200					205			
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His
			210			215					220				
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln

225 230 235 240
Ile Cys Glu Ile Asp Leu Phe Ala Asn Asp Asp Glu Asp His Val Asp
245 250 255
Ile Ser Ile Lys Gly Lys Arg Asn Gly Asp Asp Gly Ile Phe Leu Arg
260 265 270
Leu Arg Ile Ser Asp Ala Glu Gly Arg Ile Arg Asn Ile Tyr Phe Pro
275 280 285
Phe Glu Thr Ala Ile Asp Thr Ala Trp Ser Val Ala Val Glu Met Val
290 295 300
Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala Lys Ile Ala Glu Met
305 310 315 320
Ile Asp Ala Glu Ile Ala Ala Leu Val Pro Asp Trp Lys Asn Asp Thr
325 330 335
Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn Asn Asn Thr Ala Gly
340 345 350
Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile Gln Glu Thr Val Ser
355 360 365
Ser Gly Glu Lys Ser His His Asn His His Glu Phe Asp Ser Ser Glu
370 375 380
Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe Ala Asp Met Trp Gly
385 390 395 400
Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys Gln Ser Ser Arg Lys
405 410 415
Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met Arg Arg Glu Leu Arg
420 425 430
Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met Lys Met Arg Gly Gln
435 440 445
Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu Thr Pro Gly Thr Ser
450 455 460
Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser Leu Pro Val Asp Ala
465 470 475 480
Val Asp Met

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

attctgaata agatcaagaa tttacagggtt ctctcttctc tctctctcaa gttctgtttt	60
gtttatacaa attacaactt tagtttcgta aatagggtact cattagttga tcattgctct	120
ctatgtcttg ctatgcaatt caataggcta gtgtatcacc aatcacagat ccgggatccc	180
ggcttagtaa acattataaa gcttgcatat acactttatt tggatttgga tttagtaaaa	240
aaattcattt tacagtattt gaaaaaatac aaaatggcga aaatctaccg gaagttgaca	300
ggctacggtg gtgaaggagg gcgtgaatgg gacgatgatg tatatgaggg tgtaagaaaa	360
gtgtatgtag gacaagatat caatcgtatc acttacgtca aattcgagta tgtgaaggaa	420
gacggccaag tagtaacaac tgaatatggg aaaatcattc aacaacccaa agagtttgta	480
cttcaatatac cggacgaaca tatcatagcg gtggaaggaa actatcgcg agtggctcta	540
tgtgccacag aggtgatcac aaacctcgct ttcaagacct caaagggtag aaagtcacca	600
ctgtttggtc caaacttgct tgggaattac accggtacaa agttcgttat tgaggatgga	660
ggaaagaaga tcgtagggtt tcatggacgg tcgggtaatg ctctcgacgc gcttggagtt	720
tactttgtac atggctctct aacaacgtct ccgcctgttt acaagctgga tgcccaagggt	780
ggtacagacg ggcgtgtttg ggtgatgggt tcttaacgac gcgttaaata gctgcgtatt	840
ggtcaagata attctcgtat tacttattta gagttcgagt acgagaaagg cggtaaagta	900
gagacatgtc gccatggggt gaaacaagaa agatcactga agtttgagct taaccaggat	960

```
gaatacatca aatcggtgga agcaacctat gataaacggg acattttccg caatgtcgtc 1020
attacatcgc ttmcatttga aacatcggaag gggagmacgt cattctctgg gtataaggga 1080
ggtaagaagt ttaagctaga gcaaaagggg cgtaggcttg tcgggttcca tggaaggaa 1140
ggttcagcta ttgatgccct tggagcatat tttgcaccta ttcctactcc gactcctata 1200
attccagaag aaactaccag caataggcgg cagcggagga gttgcatggg atgatgggtg 1260
ctacgatggt gtaagggaag tacttgtagg acaaggtaac gatggtgtag cctttgtcaa 1320
gtttgaatac aataaaggaa aagatcttgt atctggagat gaccatggga agatgacatt 1380
actcggaact gaagagtttg tgcttgaaga tgggtgaatat ctacaggcca tagatggcta 1440
ttacgataag attttcggag tcgagacacc aatgattatc tgtcttcagt ttaagacgaa 1500
caaaaggag tc
```

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1500619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

```
Ile Leu Asn Lys Ile Lys Asn Leu Gln Val Leu Ser Ser Leu Ser Leu
1           5           10           15
Lys Phe Cys Phe Val Tyr Thr Asn Tyr Asn Phe Ser Phe Val Asn Arg
          20           25           30
Tyr Ser Leu Val Asp His Cys Ser Leu Cys Leu Ala Met Gln Phe Asn
          35           40           45
Arg Leu Val Tyr His Gln Ser Gln Ile Arg Asp Pro Gly Leu Val Asn
          50           55           60
Ile Ile Lys Leu Ala Tyr Thr Leu Tyr Leu Asp Leu Asp Leu Val Lys
65           70           75           80
Lys Phe Ile Leu Gln Tyr Leu Lys Lys Tyr Lys Met Ala Lys Ile Tyr
          85           90           95
Arg Lys Leu Thr Gly Tyr Gly Gly Glu Gly Gly Arg Glu Trp Asp Asp
          100          105          110
Asp Val Tyr Glu Gly Val Arg Lys Val Tyr Val Gly Gln Asp Ile Asn
          115          120          125
Arg Ile Thr Tyr Val Lys Phe Glu Tyr Val Lys Glu Asp Gly Gln Val
130          135          140
Val Thr Thr Glu Tyr Gly Lys Ile Ile Gln Gln Pro Lys Glu Phe Val
145          150          155          160
Leu Gln Tyr Pro Asp Glu His Ile Ile Ala Val Glu Gly Asn Tyr Arg
          165          170          175
Gly Val Ala Leu Cys Ala Thr Glu Val Ile Thr Asn Leu Val Phe Lys
          180          185          190
Thr Ser Lys Gly Arg Lys Ser Pro Leu Phe Gly Pro Asn Leu Leu Gly
          195          200          205
Ile Thr Thr Gly Thr Lys Phe Val Ile Glu Asp Gly Gly Lys Lys Ile
210          215          220
Val Gly Phe His Gly Arg Ser Gly Asn Ala Leu Asp Ala Leu Gly Val
225          230          235          240
Tyr Phe Val His Gly Ser Leu Thr Thr Ser Pro Pro Val Tyr Lys Leu
          245          250          255
Asp Ala Gln Gly Gly Thr Asp Gly Arg Val Trp Asp Asp Gly Ser Tyr
          260          265          270
Asp Gly Val Lys Ser Leu Arg Ile Gly Gln Asp Asn Ser Arg Ile Thr
          275          280          285
Tyr Leu Glu Phe Glu Tyr Glu Lys Gly Gly Lys Leu Glu Thr Cys Arg
290          295          300
His Gly Val Lys Gln Glu Arg Ser Leu Lys Phe Glu Leu Asn Pro Asp
```

305					310					315				320	
Glu	Tyr	Ile	Lys	Ser	Val	Glu	Ala	Thr	Tyr	Asp	Lys	Pro	Asp	Ile	Phe
				325					330					335	
Arg	Asn	Val	Val	Ile	Thr	Ser	Leu	Xaa	Phe	Glu	Thr	Ser	Lys	Gly	Xaa
			340					345					350		
Thr	Ser	Phe	Ser	Gly	Tyr	Lys	Gly	Gly	Lys	Lys	Phe	Lys	Leu	Glu	Gln
		355					360					365			
Lys	Gly	Arg	Arg	Leu	Val	Gly	Phe	His	Gly	Lys	Glu	Gly	Ser	Ala	Ile
		370				375					380				
Asp	Ala	Leu	Gly	Ala	Tyr	Phe	Ala	Pro	Ile	Pro	Thr	Pro	Thr	Pro	Ile
385					390					395					400
Ile	Pro	Glu	Glu	Thr	Ser	Asn	Arg	Arg	Gln	Arg	Arg	Ser	Cys	Met	
			405					410					415		

Gly

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..373

(D) OTHER INFORMATION: / Ceres Seq. ID 1500620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met	Gln	Phe	Asn	Arg	Leu	Val	Tyr	His	Gln	Ser	Gln	Ile	Arg	Asp	Pro
1			5						10					15	
Gly	Leu	Val	Asn	Ile	Ile	Lys	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Asp	Leu
			20					25					30		
Asp	Leu	Val	Lys	Lys	Phe	Ile	Leu	Gln	Tyr	Leu	Lys	Lys	Tyr	Lys	Met
		35					40					45			
Ala	Lys	Ile	Tyr	Arg	Lys	Leu	Thr	Gly	Tyr	Gly	Gly	Glu	Gly	Gly	Arg
		50				55					60				
Glu	Trp	Asp	Asp	Asp	Val	Tyr	Glu	Gly	Val	Arg	Lys	Val	Tyr	Val	Gly
65					70					75					80
Gln	Asp	Ile	Asn	Arg	Ile	Thr	Tyr	Val	Lys	Phe	Glu	Tyr	Val	Lys	Glu
			85						90					95	
Asp	Gly	Gln	Val	Val	Thr	Thr	Glu	Tyr	Gly	Lys	Ile	Ile	Gln	Gln	Pro
			100					105					110		
Lys	Glu	Phe	Val	Leu	Gln	Tyr	Pro	Asp	Glu	His	Ile	Ile	Ala	Val	Glu
		115					120					125			
Gly	Asn	Tyr	Arg	Gly	Val	Ala	Leu	Cys	Ala	Thr	Glu	Val	Ile	Thr	Asn
		130				135					140				
Leu	Val	Phe	Lys	Thr	Ser	Lys	Gly	Arg	Lys	Ser	Pro	Leu	Phe	Gly	Pro
145					150					155					160
Asn	Leu	Leu	Gly	Ile	Thr	Thr	Gly	Thr	Lys	Phe	Val	Ile	Glu	Asp	Gly
			165						170					175	
Gly	Lys	Lys	Ile	Val	Gly	Phe	His	Gly	Arg	Ser	Gly	Asn	Ala	Leu	Asp
			180					185					190		
Ala	Leu	Gly	Val	Tyr	Phe	Val	His	Gly	Ser	Leu	Thr	Thr	Ser	Pro	Pro
		195					200						205		
Val	Tyr	Lys	Leu	Asp	Ala	Gln	Gly	Gly	Thr	Asp	Gly	Arg	Val	Trp	Asp
		210				215					220				
Asp	Gly	Ser	Tyr	Asp	Gly	Val	Lys	Ser	Leu	Arg	Ile	Gly	Gln	Asp	Asn
225					230					235					240
Ser	Arg	Ile	Thr	Tyr	Leu	Glu	Phe	Glu	Tyr	Glu	Lys	Gly	Gly	Lys	Leu
			245						250					255	
Glu	Thr	Cys	Arg	His	Gly	Val	Lys	Gln	Glu	Arg	Ser	Leu	Lys	Phe	Glu
			260					265						270	

Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp Lys
275 280 285
Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu Thr
290 295 300
Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys Phe
305 310 315 320
Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys Glu
325 330 335
Gly Ser Ala Ile Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro Thr
340 345 350
Pro Thr Pro Ile Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln Arg
355 360 365
Arg Ser Cys Met Gly
370

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

Met Ala Lys Ile Tyr Arg Lys Leu Thr Gly Tyr Gly Gly Glu Gly Gly
1 5 10 15
Arg Glu Trp Asp Asp Asp Val Tyr Glu Gly Val Arg Lys Val Tyr Val
20 25 30
Gly Gln Asp Ile Asn Arg Ile Thr Tyr Val Lys Phe Glu Tyr Val Lys
35 40 45
Glu Asp Gly Gln Val Val Thr Thr Glu Tyr Gly Lys Ile Ile Gln Gln
50 55 60
Pro Lys Glu Phe Val Leu Gln Tyr Pro Asp Glu His Ile Ile Ala Val
65 70 75 80
Glu Gly Asn Tyr Arg Gly Val Ala Leu Cys Ala Thr Glu Val Ile Thr
85 90 95
Asn Leu Val Phe Lys Thr Ser Lys Gly Arg Lys Ser Pro Leu Phe Gly
100 105 110
Pro Asn Leu Leu Gly Ile Thr Thr Gly Thr Lys Phe Val Ile Glu Asp
115 120 125
Gly Gly Lys Lys Ile Val Gly Phe His Gly Arg Ser Gly Asn Ala Leu
130 135 140
Asp Ala Leu Gly Val Tyr Phe Val His Gly Ser Leu Thr Thr Ser Pro
145 150 155 160
Pro Val Tyr Lys Leu Asp Ala Gln Gly Gly Thr Asp Gly Arg Val Trp
165 170 175
Asp Asp Gly Ser Tyr Asp Gly Val Lys Ser Leu Arg Ile Gly Gln Asp
180 185 190
Asn Ser Arg Ile Thr Tyr Leu Glu Phe Glu Tyr Glu Lys Gly Gly Lys
195 200 205
Leu Glu Thr Cys Arg His Gly Val Lys Gln Glu Arg Ser Leu Lys Phe
210 215 220
Glu Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp
225 230 235 240
Lys Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu
245 250 255
Thr Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys
260 265 270
Phe Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys

```

      275              280              285
Glu Gly Ser Ala Ile Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro
 290              295              300
Thr Pro Thr Pro Ile Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln
 305              310              315              320
Arg Arg Ser Cys Met Gly
      325
```

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..721
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

```

aacttaaaact ctttttagtaa caatggtttc ttcttcttta accaagcttg tgttcttttg      60
ttgtctcctc ctgctcacat tcacggacaa ccttggtggc ggaaaatctg gcaaagtga      120
gctcaatctt tactacgaat cactttgtcc cggttgctcag gaattcatcg tcgatgacct      180
aggtaaaatc tttgactacg atctctacac aatcactgat ctcaagctgt ttccatttgg      240
taatgccgaa ctctccgata atctgactgt cacttgccag catggtgaag aggaatgcaa      300
actaaacgcc cttgaagctt gcgcattaag aacttgcccc gatcagaaat cacaatactc      360
gttcatacgg tgcgtcgaaa gcgatacgaa aggctgggaa tcatgtgtta aaaactctgg      420
acgtgagaaa gacgcaagtg aagaagactg ataattctga agctatttgg gtaaatacca      480
attctcttca tctttacttg aggttttaaat tcttttgatg ttcttttttt ctttcttagt      540
tcttatgggt attgttggtt ttagtggtgt gttgttggtt ttggtgatgt tggtgttcta      600
atcatctctt gtttctttaa ctctggtcct gattatttga ataaaggata tctagagatt      660
gtgttggtgt tgtttttgta ataattagag tttgataaaa graaatwaaa tatttaaggt      720
g
```

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

```

Met Val Ser Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu
 1              5              10              15
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val
 20              25              30
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Gln Glu Phe
 35              40              45
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile
 50              55              60
Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn
 65              70              75              80
Leu Thr Val Thr Cys Gln His Gly Glu Glu Glu Cys Lys Leu Asn Ala
 85              90              95
Leu Glu Ala Cys Ala Leu Arg Thr Trp Pro Asp Gln Lys Ser Gln Tyr
100              105              110
Ser Phe Ile Arg Cys Val Glu Ser Asp Thr Lys Gly Trp Glu Ser Cys
115              120              125
Val Lys Asn Ser Gly Arg Glu Lys Asp Ala Ser Glu Glu Asp
```

130 135 140

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..605

(D) OTHER INFORMATION: / Ceres Seq. ID 1500633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

gcaccccttt	tattgtagcg	acgcaagaag	aagcagctat	agcgtacgat	atcgagcta	60
tcgagtaccg	tggactcaac	gccgttacta	acttcgacat	cagccgttat	ctgaaactcc	120
cgggtgccga	gaaccctatc	gataccgcga	ataatctcct	cgagagtccg	cattctgac	180
ttagccatt	tataaaacct	aaccacgagt	ctgacttata	acagagtcaa	tcttcgtcag	240
aggacaacga	tgatcgga	acaaagctct	tgaagtcgtc	acctttagt	gcagaggagg	300
taatcgacc	atcgacgcca	cctgagattg	ctccgcctcg	tcggagcttc	ccggaagata	360
tccagacgta	tttcgggtgt	caaaactccg	gcaagttaac	ggcggaggaa	gatgatgta	420
tcttcggtga	tttagattct	ttccttacgc	ctgatttcta	cagcgagtta	aatgattgct	480
aaagtgtgt	tcttctgata	agttttgttt	tttagttgtt	cagaatctcg	gttgtgaaaa	540
tcaacattga	cacatcgatt	attctttctt	gtgacaatct	tatataataa	agtttgaatc	600
ttttt						

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1500634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

Thr	Pro	Phe	Ile	Val	Ala	Thr	Gln	Glu	Glu	Ala	Ala	Ile	Ala	Tyr	Asp	
1				5					10					15		
Ile	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	
			20					25					30			
Ile	Ser	Arg	Tyr	Leu	Lys	Leu	Pro	Val	Pro	Glu	Asn	Pro	Ile	Asp	Thr	
			35					40				45				
Ala	Asn	Asn	Leu	Leu	Glu	Ser	Pro	His	Ser	Asp	Leu	Ser	Pro	Phe	Ile	
			50					55				60				
Lys	Pro	Asn	His	Glu	Ser	Asp	Leu	Ser	Gln	Ser	Gln	Ser	Ser	Ser	Glu	
			65					70				75			80	
Asp	Asn	Asp	Asp	Arg	Lys	Thr	Lys	Leu	Leu	Lys	Ser	Ser	Pro	Leu	Val	
			85					90						95		
Ala	Glu	Glu	Val	Ile	Gly	Pro	Ser	Thr	Pro	Pro	Glu	Ile	Ala	Pro	Pro	
			100					105					110			
Arg	Arg	Ser	Phe	Pro	Glu	Asp	Ile	Gln	Thr	Tyr	Phe	Gly	Cys	Gln	Asn	
			115					120					125			
Ser	Gly	Lys	Leu	Thr	Ala	Glu	Asp	Asp	Val	Ile	Phe	Gly	Asp	Leu		
			130					135					140			
Asp	Ser	Phe	Leu	Thr	Pro	Asp	Phe	Tyr	Ser	Glu	Leu	Asn	Asp	Cys		
			145					150					155			

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1393
(D) OTHER INFORMATION: / Ceres Seq. ID 1500645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

```
aagccataga tattgacgaa atacactttt tgtctttttg ttgctgtgca acgtcataga      60
tctaactccg gaagaagaag aagatgagtg acgaaacgac gtcactctccg tccccagctc     120
cggcggaagaa gaagcagaat ctgggatgga tggagtgatg gaggggatgg agcagtggtt     180
tcggggagat tctcttccag aggatcacag cttctcattt ggagaatcct cttcctcttc     240
cttcctgcaa cgacctcaet tgcgttgta cttggtccac cagcggcatt ggccgtgaaa     300
ccgcgaggca gcttgacgaa gctggtgctc atgttgatg ggccgtaagg aacacaaagg     360
cggtcagga gctgatactg caatggcaga acgaatggtc tggtaaaggc tccccactca     420
atattgagga aatggagatt gatctactct caotggattc tgtcgcgaga tttgctgagg     480
ctttcaacgc tcggttagga cctttgcatg ttctgattaa caatgctggg atgtttgcta     540
tgggagagga gcaaaaattc tcagaggaag gatatgagca gcacatgcaa gtgaatcatt     600
tagctccagc gctgctttca gtacttcttt tgccgtctct gatccgaggc tctcctagcc     660
gaatcattaa tgtgaattcc gttatgcata gtgtcgggtt tgttgacccg gatgacatga     720
atgttgtttc tggtagacgt aagtactcaa gccttatagg atactcaagc agcaagcttg     780
cccagattat gtttagtagc attcttttca aaaagcttcc tctggaaaca ggagtcagcg     840
tcgtatgtct atcccctggg gttgtcctaa caaatgttgc cagggatcta tccaggattc     900
ttcaagctct ttacgcagtg ataccttatt tcatattttc accccaagaa ggttgtagaa     960
gttctctatt ctgggccaca gatcctcaga ttccagagta ctgggaaaca ctaaaaaacg    1020
atgattggcc tgtttgccca ttcactctctc aagattgccg ccctgcaaat ccttccgaag    1080
aagcacacaa cacagaaact gcacagagag tgtggaaaaa gacgttagag ctggtgggtc    1140
ttcctctcga tgcagttgag aagctcatag aaggggaaaa tatccaatgc cggtatggag    1200
cacaacacga atagtctttc aaaattacca cagggttaagt gaccattac agatcaaagg    1260
gtaggtaatt gagaaaatat cttttttttt tgtttccttg tattaatcta cagatacag    1320
tggggaatgg atccccagg catgtagttt gcttgagaat gtttgattgt tggataaaag    1380
tcaagcttta gct
```

(2) INFORMATION FOR SEQ ID NO:1556:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..376
(D) OTHER INFORMATION: / Ceres Seq. ID 1500646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

```
Met Ser Asp Glu Thr Thr Ser Ser Pro Ser Pro Ala Pro Ala Lys Lys
1          5          10          15
Lys Gln Asn Leu Gly Trp Met Glu Trp Met Arg Gly Trp Ser Ser Val
20          25          30
Phe Gly Glu Ile Leu Phe Gln Arg Ile Thr Ala Ser His Leu Glu Asn
35          40          45
Pro Leu Pro Leu Pro Ser Val Asn Asp Leu Thr Cys Val Val Thr Gly
50          55          60
Ser Thr Ser Gly Ile Gly Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala
65          70          75          80
Gly Ala His Val Val Met Ala Val Arg Asn Thr Lys Ala Ala Gln Glu
85          90          95
Leu Ile Leu Gln Trp Gln Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu
100         105         110
Asn Ile Glu Ala Met Glu Ile Asp Leu Leu Ser Leu Asp Ser Val Ala
115         120         125
Arg Phe Ala Glu Ala Phe Asn Ala Arg Leu Gly Pro Leu His Val Leu
130         135         140
```

```

Ile Asn Asn Ala Gly Met Phe Ala Met Gly Glu Ala Gln Lys Phe Ser
145          150          155          160
Glu Glu Gly Tyr Glu Gln His Met Gln Val Asn His Leu Ala Pro Ala
          165          170          175
Leu Leu Ser Val Leu Leu Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser
          180          185          190
Arg Ile Ile Asn Val Asn Ser Val Met His Ser Val Gly Phe Val Asp
          195          200          205
Pro Asp Asp Met Asn Val Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu
          210          215          220
Ile Gly Tyr Ser Ser Ser Lys Leu Ala Gln Ile Met Phe Ser Ser Ile
225          230          235          240
Leu Phe Lys Lys Leu Pro Leu Glu Thr Gly Val Ser Val Val Cys Leu
          245          250          255
Ser Pro Gly Val Val Leu Thr Asn Val Ala Arg Asp Leu Ser Arg Ile
          260          265          270
Leu Gln Ala Leu Tyr Ala Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln
          275          280          285
Glu Gly Cys Arg Ser Ser Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro
          290          295          300
Glu Tyr Trp Glu Thr Leu Lys Asn Asp Asp Trp Pro Val Cys Pro Phe
305          310          315          320
Ile Ser Gln Asp Cys Arg Pro Ala Asn Pro Ser Glu Glu Ala His Asn
          325          330          335
Thr Glu Thr Ala Gln Arg Val Trp Lys Lys Thr Leu Glu Leu Val Gly
          340          345          350
Leu Pro Leu Asp Ala Val Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln
          355          360          365
Cys Arg Tyr Gly Ala Gln His Glu
          370          375

```

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

```

Met Glu Trp Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe
1          5          10          15
Gln Arg Ile Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser
          20          25          30
Val Asn Asp Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly
          35          40          45
Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met
          50          55          60
Ala Val Arg Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln
65          70          75          80
Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu
          85          90          95
Ile Asp Leu Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe
          100          105          110
Asn Ala Arg Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met
          115          120          125
Phe Ala Met Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln
          130          135          140
His Met Gln Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu

```

145		150		155		160									
Leu	Pro	Ser	Leu	Ile	Arg	Gly	Ser	Pro	Ser	Arg	Ile	Ile	Asn	Val	Asn
			165						170					175	
Ser	Val	Met	His	Ser	Val	Gly	Phe	Val	Asp	Pro	Asp	Asp	Met	Asn	Val
			180						185					190	
Val	Ser	Gly	Arg	Arg	Lys	Tyr	Ser	Ser	Leu	Ile	Gly	Tyr	Ser	Ser	Ser
		195					200					205			
Lys	Leu	Ala	Gln	Ile	Met	Phe	Ser	Ser	Ile	Leu	Phe	Lys	Lys	Leu	Pro
	210					215					220				
Leu	Glu	Thr	Gly	Val	Ser	Val	Val	Cys	Leu	Ser	Pro	Gly	Val	Val	Leu
225					230					235				240	
Thr	Asn	Val	Ala	Arg	Asp	Leu	Ser	Arg	Ile	Leu	Gln	Ala	Leu	Tyr	Ala
			245						250					255	
Val	Ile	Pro	Tyr	Phe	Ile	Phe	Ser	Pro	Gln	Glu	Gly	Cys	Arg	Ser	Ser
		260						265					270		
Leu	Phe	Ser	Ala	Thr	Asp	Pro	Gln	Ile	Pro	Glu	Tyr	Trp	Glu	Thr	Leu
	275				280							285			
Lys	Asn	Asp	Asp	Trp	Pro	Val	Cys	Pro	Phe	Ile	Ser	Gln	Asp	Cys	Arg
	290				295						300				
Pro	Ala	Asn	Pro	Ser	Glu	Glu	Ala	His	Asn	Thr	Glu	Thr	Ala	Gln	Arg
305				310						315				320	
Val	Trp	Lys	Lys	Thr	Leu	Glu	Leu	Val	Gly	Leu	Pro	Leu	Asp	Ala	Val
			325						330					335	
Glu	Lys	Leu	Ile	Glu	Gly	Glu	Asn	Ile	Gln	Cys	Arg	Tyr	Gly	Ala	Gln
		340					345						350		
His	Glu														

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..351
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

Met	Arg	Gly	Trp	Ser	Ser	Val	Phe	Gly	Glu	Ile	Leu	Phe	Gln	Arg	Ile
1			5					10					15		
Thr	Ala	Ser	His	Leu	Glu	Asn	Pro	Leu	Pro	Leu	Pro	Ser	Val	Asn	Asp
		20						25					30		
Leu	Thr	Cys	Val	Val	Thr	Gly	Ser	Thr	Ser	Gly	Ile	Gly	Arg	Glu	Thr
		35				40						45			
Ala	Arg	Gln	Leu	Ala	Glu	Ala	Gly	Ala	His	Val	Val	Met	Ala	Val	Arg
	50				55					60					
Asn	Thr	Lys	Ala	Ala	Gln	Glu	Leu	Ile	Leu	Gln	Trp	Gln	Asn	Glu	Trp
65			70					75					80		
Ser	Gly	Lys	Gly	Leu	Pro	Leu	Asn	Ile	Glu	Ala	Met	Glu	Ile	Asp	Leu
		85						90					95		
Leu	Ser	Leu	Asp	Ser	Val	Ala	Arg	Phe	Ala	Glu	Ala	Phe	Asn	Ala	Arg
		100					105						110		
Leu	Gly	Pro	Leu	His	Val	Leu	Ile	Asn	Asn	Ala	Gly	Met	Phe	Ala	Met
		115				120						125			
Gly	Glu	Ala	Gln	Lys	Phe	Ser	Glu	Glu	Gly	Tyr	Glu	Gln	His	Met	Gln
	130				135					140					
Val	Asn	His	Leu	Ala	Pro	Ala	Leu	Leu	Ser	Val	Leu	Leu	Leu	Pro	Ser
145				150					155					160	
Leu	Ile	Arg	Gly	Ser	Pro	Ser	Arg	Ile	Ile	Asn	Val	Asn	Ser	Val	Met
			165						170					175	

His Ser Val Gly Phe Val Asp Pro Asp Asp Met Asn Val Val Ser Gly
180 185 190
Arg Arg Lys Tyr Ser Ser Leu Ile Gly Tyr Ser Ser Ser Lys Leu Ala
195 200 205
Gln Ile Met Phe Ser Ser Ile Leu Phe Lys Lys Leu Pro Leu Glu Thr
210 215 220
Gly Val Ser Val Val Cys Leu Ser Pro Gly Val Val Leu Thr Asn Val
225 230 235 240
Ala Arg Asp Leu Ser Arg Ile Leu Gln Ala Leu Tyr Ala Val Ile Pro
245 250 255
Tyr Phe Ile Phe Ser Pro Gln Glu Gly Cys Arg Ser Ser Leu Phe Ser
260 265 270
Ala Thr Asp Pro Gln Ile Pro Glu Tyr Trp Glu Thr Leu Lys Asn Asp
275 280 285
Asp Trp Pro Val Cys Pro Phe Ile Ser Gln Asp Cys Arg Pro Ala Asn
290 295 300
Pro Ser Glu Glu Ala His Asn Thr Glu Thr Ala Gln Arg Val Trp Lys
305 310 315 320
Lys Thr Leu Glu Leu Val Gly Leu Pro Leu Asp Ala Val Glu Lys Leu
325 330 335
Ile Glu Gly Glu Asn Ile Gln Cys Arg Tyr Gly Ala Gln His Glu
340 345 350

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

atagtaaacc	tattagccct	gtctttgctc	ttgaagcaac	tctctocagg	aggggttgttt	60
jcaaagctgc	tgctggtgtg	tcaggtgact	tacctgagag	tactcctaag	gaacttagtc	120
agtatgagaa	gattattgag	cttttgacaa	ccctttttcc	actttgggtt	attttgggaa	180
cacttgttgg	catcttcaag	ccatccttgg	ttacatgggt	ggaaacagat	ctctttactc	240
taggtcttgg	atttcttatg	ctttccatgg	gtttgactct	tacgtttgaa	gatttcagaa	300
gatgtttacg	taatccatgg	acgggtgggtg	ttggttttct	tgctcaatat	atgatcaagc	360
caattctagg	ttttctcatt	gcaatgactc	ttaagctttc	ggcacctctt	gcgactggcc	420
ttatcctagt	ctcatgctgc	cctggaggac	aggcgtcaaa	cgttgctact	tacatttcca	480
aggggaatgt	agcgtctctt	gtactcatga	caacgtgttc	aaccattggg	gctattataa	540
tgactcctct	tcttactaag	cttcttggctg	gtcagcttgt	tcccgttgac	gctgctggac	600
ttgctcttag	tacgtttcaa	gtagtgttgg	ttcctaccat	aattggagtt	ctggcaaagt	660
agttctttcc	taaattttacg	tctaagatca	taacagtgc	gcctctaate	ggagtcattc	720
tgactactct	gctctgtgcc	agccctattg	gacaagttgc	agatgttttg	aaaacccaag	780
gagctcaact	tatactcccg	gtggcactcc	ttcatgctgc	agcctttgct	attggctatt	840
ggattttcaa	gttttctttc	ggcgagtcca	cttcgcgtac	catttctata	gaatgtggaa	900
tgcaaagtgc	agcgtctggg	ttcttgcttg	cacaaaagca	tttcacaaac	cctctagttg	960
ctgttccttc	tgacgtcagt	gttgtctgta	tggcgcttgg	cgggagcggc	ctggccgtgt	1020
tctggagaaa	cctaccgatt	ccggcagatg	acaaggatga	cttcaaagag	taaatgaagt	1080
aggaaaggct	gtttgcatct	tctccaaacg	atgtgattgt	tttggtgtaa	tgtagtaaaa	1140
cattacaaaa	tttgtgttga	aaaacatgaa	acaaaatgtg	tttaagagag	atagaacaaa	1200
gggcgtgcat	gatgacaact	ttgtgggtcaa	cctttttttt	atttctcaat	taatggacaa	1260
atcttttttg	gc					

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..356
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500650
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

Ser	Lys	Pro	Ile	Ser	Pro	Val	Phe	Ala	Leu	Glu	Ala	Thr	Ser	Ser	Arg
1				5					10					15	
Arg	Val	Val	Cys	Lys	Ala	Ala	Ala	Gly	Val	Ser	Gly	Asp	Leu	Pro	Glu
		20						25					30		
Ser	Thr	Pro	Lys	Glu	Leu	Ser	Gln	Tyr	Glu	Lys	Ile	Ile	Glu	Leu	Leu
		35					40					45			
Thr	Thr	Leu	Phe	Pro	Leu	Trp	Val	Ile	Leu	Gly	Thr	Leu	Val	Gly	Ile
	50					55					60				
Phe	Lys	Pro	Ser	Leu	Val	Thr	Trp	Leu	Glu	Thr	Asp	Leu	Phe	Thr	Leu
65				70					75					80	
Gly	Leu	Gly	Phe	Leu	Met	Leu	Ser	Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu
			85						90					95	
Asp	Phe	Arg	Arg	Cys	Leu	Arg	Asn	Pro	Trp	Thr	Val	Gly	Val	Gly	Phe
		100					105					110			
Leu	Ala	Gln	Tyr	Met	Ile	Lys	Pro	Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met
	115					120						125			
Thr	Leu	Lys	Leu	Ser	Ala	Pro	Leu	Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser
	130					135					140				
Cys	Cys	Pro	Gly	Gly	Gln	Ala	Ser	Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys
145				150					155					160	
Gly	Asn	Val	Ala	Leu	Ser	Val	Leu	Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly
			165						170					175	
Ala	Ile	Ile	Met	Thr	Pro	Leu	Leu	Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu
	180						185						190		
Val	Pro	Val	Asp	Ala	Ala	Gly	Leu	Ala	Leu	Ser	Thr	Phe	Gln	Val	Val
	195					200						205			
Leu	Val	Pro	Thr	Ile	Ile	Gly	Val	Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys
	210					215					220				
Phe	Thr	Ser	Lys	Ile	Ile	Thr	Val	Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu
225			230						235					240	
Thr	Thr	Leu	Leu	Cys	Ala	Ser	Pro	Ile	Gly	Gln	Val	Ala	Asp	Val	Leu
			245						250					255	
Lys	Thr	Gln	Gly	Ala	Gln	Leu	Ile	Leu	Pro	Val	Ala	Leu	Leu	His	Ala
		260					265							270	
Ala	Ala	Phe	Ala	Ile	Gly	Tyr	Trp	Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu
	275					280						285			
Ser	Thr	Ser	Arg	Thr	Ile	Ser	Ile	Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala
	290					295					300				
Leu	Gly	Phe	Leu	Leu	Ala	Gln	Lys	His	Phe	Thr	Asn	Pro	Leu	Val	Ala
305				310					315					320	
Val	Pro	Ser	Ala	Val	Ser	Val	Val	Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly
			325					330						335	
Leu	Ala	Val	Phe	Trp	Arg	Asn	Leu	Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp
		340					345						350		
Asp	Phe	Lys	Glu												
		355													

- (2) INFORMATION FOR SEQ ID NO:1561:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1500651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

```
Met Leu Ser Met Gly Leu Thr Leu Thr Phe Glu Asp Phe Arg Arg Cys
1      5      10      15
Leu Arg Asn Pro Trp Thr Val Gly Val Gly Phe Leu Ala Gln Tyr Met
20     25     30
Ile Lys Pro Ile Leu Gly Phe Leu Ile Ala Met Thr Leu Lys Leu Ser
35     40     45
Ala Pro Leu Ala Thr Gly Leu Ile Leu Val Ser Cys Cys Pro Gly Gly
50     55     60
Gln Ala Ser Asn Val Ala Thr Tyr Ile Ser Lys Gly Asn Val Ala Leu
65     70     75     80
Ser Val Leu Met Thr Thr Cys Ser Thr Ile Gly Ala Ile Ile Met Thr
85     90     95
Pro Leu Leu Thr Lys Leu Leu Ala Gly Gln Leu Val Pro Val Asp Ala
100    105    110
Ala Gly Leu Ala Leu Ser Thr Phe Gln Val Val Leu Val Pro Thr Ile
115    120    125
Ile Gly Val Leu Ala Asn Glu Phe Phe Pro Lys Phe Thr Ser Lys Ile
130    135    140
Ile Thr Val Thr Pro Leu Ile Gly Val Ile Leu Thr Thr Leu Leu Cys
145    150    155    160
Ala Ser Pro Ile Gly Gln Val Ala Asp Val Leu Lys Thr Gln Gly Ala
165    170    175
Gln Leu Ile Leu Pro Val Ala Leu Leu His Ala Ala Ala Phe Ala Ile
180    185    190
Gly Tyr Trp Ile Ser Lys Phe Ser Phe Gly Glu Ser Thr Ser Arg Thr
195    200    205
Ile Ser Ile Glu Cys Gly Met Gln Ser Ser Ala Leu Gly Phe Leu Leu
210    215    220
Ala Gln Lys His Phe Thr Asn Pro Leu Val Ala Val Pro Ser Ala Val
225    230    235    240
Ser Val Val Cys Met Ala Leu Gly Gly Ser Gly Leu Ala Val Phe Trp
245    250    255
Arg Asn Leu Pro Ile Pro Ala Asp Asp Lys Asp Asp Phe Lys Glu
260    265    270
```

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1500652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

```
Met Gly Leu Thr Leu Thr Phe Glu Asp Phe Arg Arg Cys Leu Arg Asn
1      5      10      15
Pro Trp Thr Val Gly Val Gly Phe Leu Ala Gln Tyr Met Ile Lys Pro
20     25     30
Ile Leu Gly Phe Leu Ile Ala Met Thr Leu Lys Leu Ser Ala Pro Leu
35     40     45
Ala Thr Gly Leu Ile Leu Val Ser Cys Cys Pro Gly Gly Gln Ala Ser
50     55     60
Asn Val Ala Thr Tyr Ile Ser Lys Gly Asn Val Ala Leu Ser Val Leu
65     70     75     80
Met Thr Thr Cys Ser Thr Ile Gly Ala Ile Ile Met Thr Pro Leu Leu
```

85 90 95
Thr Lys Leu Leu Ala Gly Gln Leu Val Pro Val Asp Ala Ala Gly Leu
100 105 110
Ala Leu Ser Thr Phe Gln Val Val Leu Val Pro Thr Ile Ile Gly Val
115 120 125
Leu Ala Asn Glu Phe Phe Pro Lys Phe Thr Ser Lys Ile Ile Thr Val
130 135 140
Thr Pro Leu Ile Gly Val Ile Leu Thr Thr Leu Leu Cys Ala Ser Pro
145 150 155 160
Ile Gly Gln Val Ala Asp Val Leu Lys Thr Gln Gly Ala Gln Leu Ile
165 170 175
Leu Pro Val Ala Leu Leu His Ala Ala Phe Ala Ile Gly Tyr Trp
180 185 190
Ile Ser Lys Phe Ser Phe Gly Glu Ser Thr Ser Arg Thr Ile Ser Ile
195 200 205
Glu Cys Gly Met Gln Ser Ser Ala Leu Gly Phe Leu Leu Ala Gln Lys
210 215 220
His Phe Thr Asn Pro Leu Val Ala Val Pro Ser Ala Val Ser Val Val
225 230 235 240
Cys Met Ala Leu Gly Ser Gly Leu Ala Val Phe Trp Arg Asn Leu
245 250 255
Pro Ile Pro Ala Asp Asp Lys Asp Asp Phe Lys Glu
260 265

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

gagactgaag atattttaac tttttgattt ttgaagcaca gagtgtgat gatcggtgaa 60
gcctaaggaa ggattttaga aagcaactga gaacaaacct tatccgttac agtggcaatg 120
gaggacaaat cgccgacgtt accgatttct gaagatttat cccggaaaat aatctctctt 180
gccgcccgtg aagctcatat gatcgctctg accggcgatg gatgtgtgta ctcatgggga 240
agaggaatgt ttgggcgtct tggtagcggg aaggaatcgg acgagcttgt tccagttcga 300
gtcagagttcg agttcccaaa tcaagcggaa ggagaacgga ttcgaatcat tgggtgttgct 360
gctgggtgctt atcacagtct cgctgtctca gatgatggct cggtttggtg ttgggggttat 420
aacatttatg gtcaacttgg tttgatggg gaaaactcct tggcaccatg tttggtcaaa 480
aatttgtttg aacaagaagc atctagtctt tctct

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

Met Glu Asp Lys Ser Pro Thr Leu Pro Ile Ser Glu Asp Leu Ser Arg
1 5 10 15
Lys Ile Ile Ser Leu Ala Ala Gly Glu Ala His Thr Ile Ala Leu Thr
20 25 30
Gly Asp Gly Cys Val Tyr Ser Trp Gly Arg Gly Met Phe Gly Arg Leu

35	40	45
Gly Thr Gly Lys Glu Ser Asp Glu Leu Val Pro Val Arg Val Glu Phe		
50	55	60
Glu Phe Pro Asn Gln Ala Glu Gly Glu Arg Ile Arg Ile Ile Gly Val		
65	70	75
Ala Ala Gly Ala Tyr His Ser Leu Ala Val Ser Asp Asp Gly Ser Val		80
	85	90
Trp Cys Trp Gly Tyr Asn Ile Tyr Gly Gln Leu Gly Phe Asp Gly Glu		95
	100	105
Asn Ser Leu Ala Pro Cys Leu Val Lys Asn Leu Phe Glu Gln Glu Ala		110
	115	120
Ser Ser Ser Ser		125
130		

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

Met Asp Val Cys Thr His Gly Glu Glu Glu Cys Leu Gly Val Leu Val		
1	5	10
Arg Val Arg Asn Arg Thr Ser Leu Phe Gln Phe Glu Ser Ser Ser Ser		15
	20	25
Ser Gln Ile Lys Arg Lys Glu Asn Gly Phe Glu Ser Leu Val Leu Leu		30
	35	40
Leu Val Leu Ile Thr Val Ser Leu Ser Gln Met Met Ala Arg Phe Gly		45
	50	55
Val Gly Val Ile Thr Phe Met Val Asn Leu Val Leu Met Gly Lys Thr		60
	65	70
Pro Trp His His Val Trp Ser Lys Ile Cys Leu Asn Lys Lys His Leu		75
	85	90
Val Leu Leu		95

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

Met Phe Gly Arg Leu Gly Thr Gly Lys Glu Ser Asp Glu Leu Val Pro		
1	5	10
Val Arg Val Glu Phe Glu Phe Pro Asn Gln Ala Glu Gly Glu Arg Ile		15
	20	25
Arg Ile Ile Gly Val Ala Ala Gly Ala Tyr His Ser Leu Ala Val Ser		30
	35	40
Asp Asp Gly Ser Val Trp Cys Trp Gly Tyr Asn Ile Tyr Gly Gln Leu		45
	50	55
Gly Phe Asp Gly Glu Asn Ser Leu Ala Pro Cys Leu Val Lys Asn Leu		60
	65	70
		75
		80

Phe Glu Gln Glu Ala Ser Ser Ser Ser
85

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

```
aaaaacccta gaaaacctct ggagctatgg agatgatgca ggattcgttc caagtccata      60
ggattccaca atcgaagtat gtcgatggag ttagatggct tccacaagct tctgctttga      120
atcgtttctt cgcaacagcg tcctatgacg cggattgtga ttcttcatca atcgagatcc      180
aatcgctcga cccaaaccct agagggaatc acaacacgaa cccgttaatc gagtcgttat      240
cttcattggac ttcaccttct cgcgtttcgt ctctagaagt cgcgggaaac ggcgggtggtg      300
gcggttcatt caaaccaatg gtttcagcag ctacgtcttc tggttctctt cacgttctga      360
tgattgattt ggtggaagga gctgcgattg aagaggttta cgcggcggaa gggggagagg      420
tttcatrgtg ggacgcgtgg aaggtgtgga ttggagagag ggaggagaat gtgttactgt      480
tggatgaagt gggagagtga atgtagtga gattgtgaat ggtgaagggt taaggatatg      540
aaaggtcttt gatgggaatg gattggtggc ttatagagct gtgaaatggg cttctccgac      600
tgagtttggt actggaggat atggttttgg ttgcaattg tgggatcaga ggaagtctgg      660
tgaagctgtt tcacaactca aagggaactg gtttcaaggc aaaacttctg caattgtcca      720
ctccattgac attcatccat ctcggaagca cacttgcat gcgggagggt cttcagggtac      780
tgtatttgct tgggatcttc ggtggccaca gcaaccatt gttctttctg gggttggagc      840
aagtgagaat ataaacaatc ctctgtctga aagtgaagta tgggaagttc agtatgactc      900
atacacaaaa tccaacgtct catcctcaag gattctccct gttatgacct gctctgaaga      960
tggaatcctt ggtatcatag aacaagggga agaaccaatc gagcttctgg ctgaaccttg      1020
tgccattaac agttttgaca tcgacaggca aaatccacag gatgtgatat gtagcttgga      1080
gtgggaatca atagcagttt tctcaaggcc ttagtataat atggaactgt gcacgggtatg      1140
ctatgttttc ttctgcgagc tacaacgaag aaattgagga aggtagtgat agatgatgag      1200
agacaagttt aaggaagagg gtgtggaatg tgtttataag tttcattata acaagatctt      1260
aaaatacatt ctgcacaaac agagttttgt attcatctta aagttagtgt gatcttgaag      1320
atttgc
```

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

```
Met Glu Met Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser
1          5          10          15
Lys Tyr Val Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn
20        25        30
Arg Phe Phe Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ser
35        40        45
Ile Glu Ile Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr
50        55        60
Asn Pro Leu Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val
65        70        75        80
Ser Ser Leu Glu Val Ala Gly Asn Gly Gly Gly Gly Ser Phe Lys
85        90        95
```

Pro Met Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met
100 105 110
Ile Asp Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu
115 120 125
Gly Gly Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu
130 135 140
Arg Glu Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

Met Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr
1 5 10 15
Val Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe
20 25 30
Phe Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ser Ile Glu
35 40 45
Ile Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro
50 55 60
Leu Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser
65 70 75 80
Leu Glu Val Ala Gly Asn Gly Gly Gly Gly Ser Phe Lys Pro Met
85 90 95
Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met Ile Asp
100 105 110
Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu Gly Gly
115 120 125
Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu Arg Glu
130 135 140
Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr Val
1 5 10 15
Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe Phe
20 25 30
Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ser Ile Glu Ile
35 40 45
Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro Leu
50 55 60
Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser Leu

(i) SEQUENCE CHARACTERISTICS:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1500669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

```
Met Ala Ser Lys Ile Lys Arg Gln Gly Phe Ile Arg Asn Val Ser Thr
1           5           10           15
Pro Leu Arg Asn Met Ala Ser Val Ala Glu Met Gly Ser Ala Glu Lys
20           25           30
Arg Thr Arg Arg Gly Asp Ala Gly Glu Glu Asp Val Asp Ile Gly Glu
35           40           45
Asp Ile Pro Ile Glu Asp Tyr Pro Ser Xaa Glu Ile Glu Arg Asp Gly
50           55           60
Tyr Cys Ser Cys Ser Cys Cys
65           70
```

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

```
Met Gly Thr Ala Val Ala Ala Ala Ala Ser Ser Gly Ser Ser Ser Ser
1           5           10           15
Gly Ser Ser Ser Ser Ser Gly Gly Ser Ser Ser Ser Ser Asp Ser Gly
20           25           30
Ser Gly Gly Ser Ser Ser Gly Ser Asp Ser Asp Ala Asp Ser Val Gln
35           40           45
Ser Pro Phe Val Glu Ala Lys Glu Ala Gln Cys
50           55
```

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1506

(D) OTHER INFORMATION: / Ceres Seq. ID 1500675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

```
accgagaaat gggatcgta ggaatacag aaaccaacgg caacgcaccg ccaccgtcgt      60
cgaatcaaaa gcctccggct acgaacggcg ttgatgggtc tcatcctcct cctcctcctt      120
taactcctga tcaagctatt atagagtcgg atccgtcgaa gaagaggaaa atgggggatgc      180
ttcctctaga agtgggtact cgtgtgatgt gtcggtggag agacgggaaa caccatccgg      240
tgaaagtaat tgagcgcccg cggataycat aacggcggtc aaaatgatta cgagtattac      300
gttcattaca ctgagtttaa taggaggctg gatgaatgga ctgagctgga ccaactggac      360
cttgattcag tagagtgcgc tgtagatgaa aaattggaag acaaggtaac aagcttgaag      420
gatgacacgt caccagaaga ggaagatcga tgaggacaca tatagagggt catgaagagc      480
tggatgcagc aagtttgctg gaacatgaag agttcacgaa agtgaagaac atatcaacaa      540
ttgagcttg gaaaatagag attgagactt ggtacttctc cccttttccg ccagaataca      600
atgactgtgt gaagctcttt tttgtgagt ttgcctgaa cttcatgaaa cgcaaagagc      660
agcttcaaag gcatatgagr aagtgtgacc tgaagcacc acctggtgat gaaatttacc      720
gaagtggtag cttgtcaatg tttgaggtag atggcaaaaa gaacaagggt tatgcacaga      780
atctctgcta cctggcaaaag ttatttcttg accacaaaac tctttactac gatgttgatt      840
tgtttctatt ctacgttctt tgcgaatgtg atgaccgagg atgccacatg gttgggtact      900
tttcaaagga gaagcattcg gaagaagcat acaacttagc ttgcattcta accctgcctt      960
```

```
catatcaaag aaaaggctat ggaaagttct taatagcctt ttcctatgaa ctgtcaaaga 1020
aagagggaaa agttgggaca ccggraaaga cccttgtcgg atctaggctt actaagctac 1080
agaggttatt ggactcgtgt tctattagaa atcttgaaaa aacataaggg aaacatttct 1140
atcaaggagc tgagcgacgt gacagcaatc aaagcggaag atatatgaag cacacttcag 1200
agcctagaac tgatacagta caggaaagga cagcatgtga tctgtgcgga tccaaagggt 1260
ctggaccgac atctgaaagc tgcaggccga ggtggtcttg atgtagatgc tagcaactg 1320
atttgacac cttacaagga ccagagttaa gagtaagtac actcctcttg tgccattgga 1380
tttgatttga gtgtgtaaagt aaggggctgt cttattctcc tgaaatgtaa gtgtacttta 1440
cttgtaaagt ttgaaatcgt acttggaatg gtgtttgttt acaactnctt ataatgagga 1500
aatttg
```

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1500676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

```
Met Arg Thr His Ile Glu Gly His Glu Leu Asp Ala Ala Ser Leu
1          5          10          15
Arg Glu His Glu Glu Phe Thr Lys Val Lys Asn Ile Ser Thr Ile Glu
20          25          30
Leu Gly Lys Tyr Glu Ile Glu Thr Trp Tyr Phe Ser Pro Phe Pro Pro
35          40          45
Glu Tyr Asn Asp Cys Val Lys Leu Phe Phe Cys Glu Phe Cys Leu Asn
50          55          60
Phe Met Lys Arg Lys Glu Gln Leu Gln Arg His Met Xaa Lys Cys Asp
65          70          75          80
Leu Lys His Pro Pro Gly Asp Glu Ile Tyr Arg Ser Gly Thr Leu Ser
85          90          95
Met Phe Glu Val Asp Gly Lys Lys Asn Lys Val Tyr Ala Gln Asn Leu
100          105          110
Cys Tyr Leu Ala Lys Leu Phe Leu Asp His Lys Thr Leu Tyr Tyr Asp
115          120          125
Val Asp Leu Phe Leu Phe Tyr Val Leu Cys Glu Cys Asp Asp Arg Gly
130          135          140
Cys His Met Val Gly Tyr Phe Ser Lys Glu Lys His Ser Glu Glu Ala
145          150          155          160
Tyr Asn Leu Ala Cys Ile Leu Thr Leu Pro Ser Tyr Gln Arg Lys Gly
165          170          175
Tyr Gly Lys Phe Leu Ile Ala Phe Ser Tyr Glu Leu Ser Lys Lys Glu
180          185          190
Gly Lys Val Gly Thr Pro Xaa Lys Thr Leu Val Gly Ser Arg Leu Thr
195          200          205
Lys Leu Gln Arg Leu Leu Asp Ser Cys Ser Ile Arg Asn Leu Glu Lys
210          215          220
Thr
225
```

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys	Asp	Leu
1			5					10						15	
Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu	Ser	Met
		20					25						30		
Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn	Leu	Cys
		35					40					45			
Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val
	50					55					60				
Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Asp	Arg	Gly	Cys
65					70					75					80
His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu	Ala	Tyr
			85						90					95	
Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys	Gly	Tyr
		100						105					110		
Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Lys	Glu	Gly
	115						120					125			
Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu	Thr	Lys
	130					135					140				
Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu	Lys	Thr
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

Met	Xaa	Lys	Cys	Asp	Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg
1			5						10					15	
Ser	Gly	Thr	Leu	Ser	Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val
		20						25					30		
Tyr	Ala	Gln	Asn	Leu	Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys
	35						40					45			
Thr	Leu	Tyr	Tyr	Asp	Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu
	50					55					60				
Cys	Asp	Asp	Arg	Gly	Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys
65					70					75					80
His	Ser	Glu	Glu	Ala	Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser
			85						90					95	
Tyr	Gln	Arg	Lys	Gly	Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu
	100						105					110			
Leu	Ser	Lys	Lys	Glu	Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val
	115					120						125			
Gly	Ser	Arg	Leu	Thr	Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile
	130					135					140				
Arg	Asn	Leu	Glu	Lys	Thr										
145					150										

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 889 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..889
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500679
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

```
aaaacgaact agagacagtt tgattcgaaa atcttgctcg aaaaatggagg atatcgctcga      60
ccaagaatta agcaattact gggaacctag ctcccttgctc caaaacgaat acttcgaata      120
cgacagctgg cctttggaag aagccatttc tgggtcgtat gattcgagtt cgccggatgg      180
agctgcttcg tcgccggctt ctaagaatat tgtgtcggag agaaacagaa gacagaaact      240
taaccagaga ctcttcgctc ttcgatcagt tgttcccaat atcactaaga tggataaagc      300
ctcaataatc aaagatgcta ttagttacat agaaggatta caatatgaag aaaagaagct      360
cgaagctgag atcagagaac ttgaatctac accaaagagt agccttagtt tcagcaaagg      420
attttgatcg tgatttactt gttcctgtca catccaagaa gatgaagcag cttgattctg      480
gttcttccac ttctctcatc gaagttctcg aattgaaggt aacattcatg ggagagagga      540
caatggtggt gagtgtaaaca tgtaataaga ggacagatac aatggtgaaa ctgtgtgaag      600
tctttgagtc attgaatctc aaaatcctca cttccaatct cacctctttc tctggcatga      660
tcttccacac tgtctttatt gaggcggatg aagaagaaca agaggtgttg cggttaaaaa      720
tagaaacagg aataggagct tataatgaaa ctcaaagccc tactttgagc atcgactctc      780
tttactaata atactttttt tcttctttt ttggttcatt ttggcttctc tctttacaat      840
aatgtatgtc tctcttttca tttttatgat ctccacgtt tgtttgtcc
```

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..141
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500680
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

```
Lys Arg Thr Arg Asp Ser Leu Ile Arg Lys Ser Cys Arg Lys Met Glu
1          5          10          15
Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser Ser Leu
20          25          30
Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu Glu Ala
35          40          45
Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala Ser Ser
50          55          60
Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln Lys Leu
65          70          75          80
Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile Thr Lys
85          90          95
Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile Glu Gly
100         105         110
Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu Leu Glu
115         120         125
Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe
130         135         140
```

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1500681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

Met	Glu	Asp	Ile	Val	Asp	Gln	Glu	Leu	Ser	Asn	Tyr	Trp	Glu	Pro	Ser
1				5						10				15	
Ser	Leu	Leu	Gln	Asn	Glu	Tyr	Phe	Glu	Tyr	Asp	Ser	Trp	Pro	Leu	Glu
			20					25					30		
Glu	Ala	Ile	Ser	Gly	Ser	Tyr	Asp	Ser	Ser	Ser	Pro	Asp	Gly	Ala	Ala
		35					40					45			
Ser	Ser	Pro	Ala	Ser	Lys	Asn	Ile	Val	Ser	Glu	Arg	Asn	Arg	Arg	Gln
	50				55					60					
Lys	Leu	Asn	Gln	Arg	Leu	Phe	Ala	Leu	Arg	Ser	Val	Val	Pro	Asn	Ile
65				70						75				80	
Thr	Lys	Met	Asp	Lys	Ala	Ser	Ile	Ile	Lys	Asp	Ala	Ile	Ser	Tyr	Ile
			85						90				95		
Glu	Gly	Leu	Gln	Tyr	Glu	Glu	Lys	Lys	Leu	Glu	Ala	Glu	Ile	Arg	Glu
			100					105					110		
Leu	Glu	Ser	Thr	Pro	Lys	Ser	Ser	Leu	Ser	Phe	Ser	Lys	Gly	Phe	
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1500682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

Met	Lys	Lys	Arg	Ser	Ser	Lys	Leu	Arg	Ser	Glu	Asn	Leu	Asn	Leu	His
1					5					10				15	
Gln	Arg	Val	Ala	Leu	Val	Ser	Ala	Lys	Asp	Phe	Asp	Arg	Asp	Leu	Leu
			20					25					30		
Val	Pro	Val	Thr	Ser	Lys	Lys	Met	Lys	Gln	Leu	Asp	Ser	Gly	Ser	Ser
		35					40					45			
Thr	Ser	Leu	Ile	Glu	Val	Leu	Glu	Leu	Lys	Val	Thr	Phe	Met	Gly	Glu
	50				55						60				
Arg	Thr	Met	Val	Val	Ser	Val	Thr	Cys	Asn	Lys	Arg	Thr	Asp	Thr	Met
65				70						75				80	
Val	Lys	Leu	Cys	Glu	Val	Phe	Glu	Ser	Leu	Asn	Leu	Lys	Ile	Leu	Thr
			85					90					95		
Ser	Asn	Leu	Thr	Ser	Phe	Ser	Gly	Met	Ile	Phe	His	Thr	Val	Phe	Ile
		100					105						110		
Glu	Ala	Asp	Glu	Glu	Glu	Gln	Glu	Val	Leu	Arg	Leu	Lys	Ile	Glu	Thr
		115					120					125			
Gly	Ile	Gly	Ala	Tyr	Asn	Glu	Thr	Gln	Ser	Pro	Thr	Leu	Ser	Ile	Asp
	130					135						140			
Ser	Leu	Tyr													
145															

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..672

(D) OTHER INFORMATION: / Ceres Seq. ID 1500683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1585:

acaaaaaaaa	acaaaacaaa	aaattatatt	caagagaaaa	aggaaaaaat	gaatttcac	60
tccgatcagg	taaagaaact	ctcaagctca	acaccagagg	agccagacca	caacaagcca	120
gtcgaaggaa	ccgaaacagc	tacaagacca	gctaccaacg	ccgagctcat	ggcaagtgcc	180
aaggttgtag	ctgaagctgc	tcaagccgca	gctcgtaacg	aatcagacaa	actcgacaag	240
ggtaaagtcg	ccggagcctc	tgctgatatc	ttagacgctg	ccgagaaata	cggtaagttc	300
gatgaaaaga	gtagcactgg	tcagtacctc	gacaaggctg	agaagtatct	caacgactac	360
gagtcgtcac	actccaccgg	tgctgggtgg	cctcctcctc	cgacgagtc	ggctgagcca	420
gcaagtcagc	ctgagccggc	ggctaagaaa	gacgatgaag	agtcctggtg	tgggcttgga	480
ggttatgcc	agatggctca	aggtttcttg	aagtgatttg	atctttaatt	gttggttcac	540
attttcgtaa	taataaatta	aataactagt	atcgtttggt	actagtttat	gttgcttcgt	600
ttatgtttat	ggggagtgc	gagtgagtg	aataacttct	ggtgatcatg	aatctaattc	660
atctttgttg	tg					

(2) INFORMATION FOR SEQ ID NO:1586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1500684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

Thr	Lys	Lys	Asn	Lys	Thr	Lys	Asn	Tyr	Ile	Gln	Glu	Lys	Lys	Glu	Lys
1			5					10						15	
Met	Asn	Phe	Ile	Ser	Asp	Gln	Val	Lys	Lys	Leu	Ser	Ser	Ser	Thr	Pro
			20					25					30		
Glu	Glu	Pro	Asp	His	Asn	Lys	Pro	Val	Glu	Gly	Thr	Glu	Thr	Ala	Thr
			35				40					45			
Arg	Pro	Ala	Thr	Asn	Ala	Glu	Leu	Met	Ala	Ser	Ala	Lys	Val	Val	Ala
			50			55				60					
Glu	Ala	Ala	Gln	Ala	Ala	Arg	Asn	Glu	Ser	Asp	Lys	Leu	Asp	Lys	
65				70				75					80		
Gly	Lys	Val	Ala	Gly	Ala	Ser	Ala	Asp	Ile	Leu	Asp	Ala	Ala	Glu	Lys
			85					90					95		
Tyr	Gly	Lys	Phe	Asp	Glu	Lys	Ser	Ser	Thr	Gly	Gln	Tyr	Leu	Asp	Lys
			100				105					110			
Ala	Glu	Lys	Tyr	Leu	Asn	Asp	Tyr	Glu	Ser	Ser	His	Ser	Thr	Gly	Ala
			115			120					125				
Gly	Gly	Pro	Pro	Pro	Pro	Thr	Ser	Gln	Ala	Glu	Pro	Ala	Ser	Gln	Pro
			130			135					140				
Glu	Pro	Ala	Ala	Lys	Lys	Asp	Asp	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Gly
145				150				155						160	
Gly	Tyr	Ala	Lys	Met	Ala	Gln	Gly	Phe	Leu	Lys					
			165					170							

(2) INFORMATION FOR SEQ ID NO:1587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
1 5 10 15
Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
20 25 30
Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
35 40 45
Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
50 55 60
Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys
65 70 75 80
Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys
85 90 95
Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
100 105 110
Gly Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
115 120 125
Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly
130 135 140
Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1500686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
1 5 10 15
Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
20 25 30
Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
35 40 45
Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
50 55 60
Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Pro Thr Ser
65 70 75 80
Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
85 90 95
Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
100 105 110
Phe Leu Lys
115

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1057

(D) OTHER INFORMATION: / Ceres Seq. ID 1500687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

aagctttctt cttgttccta cataccacat ttcctcacc tacatcaaac ctagggtttc

```

ttaactatat caacaacata tataaattta tatataggtt gtgaittatt gaagatcata      120
aagatcaaaa ggagagaggt attaaaaaat gatgtgtagt cgaaggccatt ggagacctgc      180
agaagacgag aagctaagag aactcgtcga acaattttggt cctcataatt ggaacgccat      240
agctcagaag ctctctggtc gatctggttaa gagttgtaga ttgagatggt ttaatcaatt      300
ggatcctagg attaacggaa accctttcac ggaggaagaa gaagaaaggc ttttagcgtc      360
tcatcggatc catgggaaca gatggtctgt gatcgctaga ttttttcccg gtcgaactga      420
taacgctggt aaaaaccatt ggcacgtcat catggctcgt cgtggccgag aacggtccaa      480
gctccgtcca cgaggccttg gccatgatgg cacgggtggc gcgactggga tgattggtaa      540
ttataaagac tgcgataagg agagaagatt ggcaaccaca accgctatca attttcctta      600
tcaattctct catattaatc attttcaagt cctcaaagag ttcttgaccg taaagatcgg      660
gttcagaaat agtactactc caatacaaga aggagcaata gaccaaacta aacgaccgat      720
ggagttctac aattttcttc aagtaaacac ggattcgaag atacacgaat tgatagataa      780
ttcaagaaaa gacgaagaag aagatgtcga tcaaaacaac cgaattccta acgagaattg      840
tgttccattt ttcgactttt tgtctgttgg aaactctgcc tctcagggtt tatgttaatt      900
tgtccgtacc acatgtacta taaggtggac catatgttaa ttaaagataa tgtagaaagt      960
actaatcaat tagagctctt gtttgagcca aatgtgaaaa ttagttaagc catcccaaac     1020
atgttcttgt ataacaata taaggttgta cttttcc

```

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

```

Met Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu Asp Glu Lys Leu
1          5          10          15
Arg Glu Leu Val Glu Gln Phe Gly Pro His Asn Trp Asn Ala Ile Ala
20          25          30
Gln Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe
35          40          45
Asn Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu
50          55          60
Glu Glu Arg Leu Leu Ala Ser His Arg Ile His Gly Asn Arg Trp Ser
65          70          75          80
Val Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn
85          90          95
His Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu
100         105         110
Arg Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met
115         120         125
Ile Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr
130         135         140
Thr Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln
145         150         155         160
Val Leu Lys Glu Phe Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr
165         170         175
Thr Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu
180         185         190
Phe Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu
195         200         205
Ile Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn
210         215         220
Arg Ile Pro Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val
225         230         235         240
Gly Asn Ser Ala Ser Gln Gly Leu Cys
245

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

(2) INFORMATION FOR SEQ ID NO:1592:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1500690

Met	Ala	Arg	Arg	Gly	Arg	Glu	Arg	Ser	Lys	Leu	Arg	Pro	Arg	Gly	Leu
1				5					10					15	
Gly	His	Asp	Gly	Thr	Val	Ala	Ala	Thr	Gly	Met	Ile	Gly	Asn	Tyr	Lys
			20					25					30		
Asp	Cys	Asp	Lys	Glu	Arg	Arg	Leu	Ala	Thr	Thr	Thr	Ala	Ile	Asn	Phe

35 40 45
Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln Val Leu Lys Glu Phe
50 55 60
Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr Thr Pro Ile Gln Glu
65 70 75 80
Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe Tyr Asn Phe Leu
85 90 95
Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile Asp Asn Ser Arg
100 105 110
Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg Ile Pro Asn Glu
115 120 125
Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn Ser Ala Ser
130 135 140
Gln Gly Leu Cys
145

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..546
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

agtaattttc agtcggcgctc cttcttttgt ctgaaccacc ggaggagctc gatccattga	60
ttagaagatg acaactccac aagtgaagac cggtttgttc gttgggttga acaagggaca	120
tggtgttacc agacgtgaat tagctcctcg tcctcgttct cgcaaaggaa aaacgagcaa	180
gaggacaatc tttatcagaa acttgataaa ggaagttgct ggtcaagctc cctatgagaa	240
gagaatcact gagcttttga aggttgctaa gaggaagttg ggaaccaca agagagccaa	300
gcgaaagaga gaggagatgt ccagtgttct ccgcaagatg aggtctggcg gtggtggtgc	360
aactgagaag aagaagtga cgtcacttta agtttgtaa tcgctcgtaa agagttatgg	420
tttcttggtg caaaatcggtt attatgattc ctaagcttct cgtattatgt tttgtagaa	480
tatcggaactt aaagagagtt ttgtctgaga ccagtgaactc tgsctttaaa ctatttgctt	540
cttttg	

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

Met Thr Thr Pro Gln Val Lys Thr Gly Leu Phe Val Gly Leu Asn Lys	
1 5 10 15	
Gly His Val Val Thr Arg Arg Glu Leu Ala Pro Arg Pro Arg Ser Arg	
20 25 30	
Lys Gly Lys Thr Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys	
35 40 45	
Glu Val Ala Gly Gln Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu	
50 55 60	
Lys Val Ala Lys Arg Lys Leu Gly Thr His Lys Arg Ala Lys Arg Lys	
65 70 75 80	
Arg Glu Glu Met Ser Ser Val Leu Arg Lys Met Arg Ser Gly Gly Gly	
85 90 95	

Gly Ala Thr Glu Lys Lys Lys
100

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

tcttttgcgt	gactgtcaaa	tctcattctt	ctctttcttc	tctctctcca	agagaaagaa	60
aatctgagtt	tccgagaaaa	taaaatctca	agagttaaaa	agaaagaaac	ttttgtcgaa	120
gagattccaa	tcggtgatct	ttgtctttct	tttctctaga	aaatctctgt	tgctctatat	180
atatccatat	agatgctcta	agactatagt	tggtgttgca	gataataatg	gagggagaca	240
caatatctag	gatgatggga	agtgagggtc	aaatggatgg	gaagattctt	caaacgtttg	300
agaaaagttt	tggtcaagtg	caaaacatat	tggaccacaa	cagattgctt	ataaacgaga	360
taaacaaaaa	ccatgagtcc	aaaatcccgg	acaacctcgg	acgaaacgtc	ggtttgatcc	420
gagaattgaa	caataacgtg	agaagggttg	ctcatcttta	tgctgatctt	tccaacaact	480
tctccaaatc	catggaagct	tcttctgaag	gagactcatc	agaaggacga	ggtaacagaa	540
gaatcaggcc	tgcttaatta	agaatcaggg	ttgtttcttc	aaaattagct	tcgaaattag	600
cttttaatgt	gggctaattc	cttttctcaa	gtgattggcg	ataaatgttt	taaagcagaa	660
atggtgattg	taattgaaaa	atatgttcaa	tactattatt	tg		

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

Met	Glu	Gly	Asp	Thr	Ile	Ser	Arg	Met	Gly	Ser	Gly	Val	Gln	Met
1				5				10					15	
Asp	Gly	Lys	Ile	Leu	Gln	Thr	Phe	Glu	Lys	Ser	Phe	Val	Gln	Val
			20					25				30		
Asn	Ile	Leu	Asp	His	Asn	Arg	Leu	Leu	Ile	Asn	Glu	Ile	Asn	Gln
			35				40				45			
His	Glu	Ser	Lys	Ile	Pro	Asp	Asn	Leu	Gly	Arg	Asn	Val	Gly	Leu
	50					55				60				
Arg	Glu	Leu	Asn	Asn	Asn	Val	Arg	Arg	Val	Ala	His	Leu	Tyr	Val
65				70					75				80	
Leu	Ser	Asn	Asn	Phe	Ser	Lys	Ser	Met	Glu	Ala	Ser	Ser	Glu	Gly
			85					90					95	
Ser	Ser	Glu	Gly	Arg	Gly	Asn	Arg	Arg	Ile	Arg	Pro	Ala		
			100					105						

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

```
Met Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe
1          5          10          15
Glu Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu
20          25          30
Leu Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn
35          40          45
Leu Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Val Arg
50          55          60
Arg Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser
65          70          75          80
Met Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg
85          90          95
Arg Ile Arg Pro Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1500698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

```
Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe Glu
1          5          10          15
Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu Leu
20          25          30
Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn Leu
35          40          45
Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Val Arg Arg
50          55          60
Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser Met
65          70          75          80
Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg Arg
85          90          95
Ile Arg Pro Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1422

(D) OTHER INFORMATION: / Ceres Seq. ID 1500703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

```
ammaacaaag tctctctccc tctctattc aactttttca gttactttac tccgttcac 60
ttttattttt cttttcgctg attctcatca atactacaaa aatatatact tctatatatc 120
gtgcagaggt tacatgcatt gtrcaatttt gttgtscbga gaaacaagcg gatcagagac 180
aaaatcagag tcggtttcct gctttttgat tcctctttat taatcagcaa agatcgattc 240
cacttctcct ctctctctct ctctctctct gttctttaat ttagagagaa aaaataagca 300
ttcttccttc tctgttttcg agcgggaaat tctggagatg gctatacaag cgcagttgaa 360
```



```
ttacaacgct ccgaatgcga atcaaatcgg ttttggtggg tccgagtttt ctttgatcaa 420
caacaatggc gttattggaa tcggtaacga tcagtcttat cttgtcaata atctccagtt 480
gcagaaagat ttcaaccaac atgctctgtt tcatcatcag catcatcaac aacaacagtc 540
tcctttctca agcttttttag ctgctcagat ggagaaacag aagcaagaga tcgatcagtt 600
catcaaaaata cagaacgaga ggttgagata tgtgttgcaa gaacagagga agcgagaaat 660
ggagatgatt ttaaggaaaa tggagagtaa agctttgctt ttgatgagtc agaaggaaga 720
agaaatgtcg aaagcattga acaagaacat ggaactcgaa gatctggtga gaaaaatgga 780
aatggagaat cagacgtggc agagaatggc tcgtgagAAC gaagcaattg tgcaaacgct 840
aaacacaacg ctcgaacagg ttcgcgagag agccgccacg tgttacgacg ctggtgagggc 900
agaggtggag gacgaagggt cgttttgagg cgkagaagga gacgggaata gtttgccggc 960
gaagaagatg aagatgagta gttgttgctg caattgtggg tctaacggag taacgagrgt 1020
tctgttttcys ccgttttaggc atctctgttg ctgcatggat tscgagraag ggcttmttct 1080
ttgtccgata tgtaataacc ccaagaaaaag cagaatcgag gccctcatit tbtagggaaa 1140
atcctttctt ttctctcmcc ggaaaaatgc ttgcctttgt gttccggtga acgraragtt 1200
tttactccgg gtaratgacg tggcagggtta atttggtaaa aataggggag gaaaggaaaag 1260
tgagattagg gaaagggttag aaatagtaaa aggttatctc aaraagtaaa ttctgattag 1320
ggttttcatt ttcccttttt gttttttggt tctttttcca ttcaatggag gaaaaaaaaga 1380
aaccagctg gatttgatga acataattca ttttttctt ct
```

(2) INFORMATION FOR SEQ ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1500704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

```
Met Ala Ile Gln Ala Gln Leu Asn Tyr Asn Ala Pro Asn Ala Asn Gln
1      5      10      15
Ile Gly Phe Gly Gly Ser Glu Phe Ser Leu Ile Asn Asn Asn Gly Val
      20      25      30
Ile Gly Ile Gly Asn Asp Gln Ser Tyr Leu Val Asn Asn Leu Gln Leu
      35      40      45
Gln Lys Asp Phe Asn Gln His Ala Leu Phe His His Gln His Gln
      50      55      60
Gln Gln Gln Ser Pro Ser Gln Ser Phe Leu Ala Ala Gln Met Glu Lys
      65      70      75      80
Gln Lys Gln Glu Ile Asp Gln Phe Ile Lys Ile Gln Asn Glu Arg Leu
      85      90      95
Arg Tyr Val Leu Gln Glu Gln Arg Lys Arg Glu Met Glu Met Ile Leu
      100     105     110
Arg Lys Met Glu Ser Lys Ala Leu Leu Met Ser Gln Lys Glu Glu
      115     120     125
Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu Leu Glu Asp Leu Leu
      130     135     140
Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln Arg Met Ala Arg Glu
      145     150     155     160
Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr Leu Glu Gln Val Arg
      165     170     175
Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu Ala Glu Val Glu Asp
      180     185     190
Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly Asn Ser Leu Pro Ala
      195     200     205
Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn Cys Gly Ser Asn Gly
      210     215     220
Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His Leu Cys Cys Cys Met
      225     230     235     240
Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile Cys Asn Thr Pro Lys
```

245 250 255
Lys Ser Arg Ile Glu Ala Leu Ile Xaa
260 265
(2) INFORMATION FOR SEQ ID NO:1601:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..188
(D) OTHER INFORMATION: / Ceres Seq. ID 1500705
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:
Met Glu Lys Gln Lys Gln Glu Ile Asp Gln Phe Ile Lys Ile Gln Asn
1 5 10 15
Glu Arg Leu Arg Tyr Val Leu Gln Glu Gln Arg Lys Arg Glu Met Glu
20 25 30
Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met Ser Gln
35 40 45
Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu Leu Glu
50 55 60
Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln Arg Met
65 70 75 80
Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr Leu Glu
85 90 95
Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu Ala Glu
100 105 110
Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly Asn Ser
115 120 125
Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn Cys Gly
130 135 140
Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His Leu Cys
145 150 155 160
Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile Cys Asn
165 170 175
Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa
180 185
(2) INFORMATION FOR SEQ ID NO:1602:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1500706
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:
Met Glu Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met
1 5 10 15
Ser Gln Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu
20 25 30
Leu Glu Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln
35 40 45
Arg Met Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr
50 55 60
Leu Glu Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu
65 70 75 80

Ala Glu Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly
85 90 95
Asn Ser Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn
100 105 110
Cys Gly Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His
115 120 125
Leu Cys Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile
130 135 140
Cys Asn Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa
145 150 155

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1188 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1500707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

```
atcattctcg gtttaactga aacacataat aaaacaaaga gaaagagata taatatgggt      60
gggtgggcaa tcgcagtaca cgggtgtgcc ggtatcgacc ctaatcttcc ggcagagaga      120
caagaagagg cgaaacagct tttaactcgt tgtctcaacc tcggcataat agctttgcgt      180
tccaatgttt ccgccattga cgtcgttgag ctctgcatta gagaattgga gacggatcct      240
ctgtttaatt caggccgtgg atcttctttg acggagaaaag gaacggttga gatggaagct      300
agcattatgg acggtacgaa gagacgatgc ggtgccgttt cggggataac caccgtgaaa      360
aatcctatat ctcttgctcg tctcgtcatg gacaaatctc cccactctta ccttgctttc      420
tcaggtgcag aggatttcgc ccgcaaacag ggagttgaaa ttgtggacaa cgagtacttt      480
gtcacggacg acaacgtagg aatgctcaag ttggccaagg aagctaactc catcttgttt      540
gattaccgga ttccgccgat gggatgtgcc ggcgcagctg cgaccgacag tccaatccaa      600
atgaacggtc ttccgatcag catttacgca ccgggagaca gtcgggtgcg ttgtgggtga      660
cgggaaagga cattgtgccg ccgggacatc cacgggtggt ttaatgaaca agatgatggg      720
aaggattggt gactcgccgc tgataggagc cgggacgtat gcgtcggagt tttgtggtgt      780
gtcgtgtacc ggagaaggag aagccattat aagagcaacc cttagctcgtg atgtgtcagc      840
tgttatggag tataaaggac ttaacctcca agaagcgggt gattacgtca tcaagcatcg      900
acttgacgaa gggttcgcgt gactcattgc tgtctcgaat aaaggagagg tggtttgtgg      960
ttttaactct aatgggatgt tcaggggatg tgcaactgag gatggattca tggacgttgc      1020
tatttgggag tgagaaatat tttagattaa gaaaatgtct tactagtatt taatcagtca      1080
tcgctctatt aatttggtta ttcattatca taaagctgga gtagtaaatt tagttctgtc      1140
gttatcacca gtctatatt gatttgtggt taatgcggtt tcaaattg
```

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1500708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

Ile Ile Leu Gly Leu Thr Glu Thr His Asn Lys Thr Lys Arg Lys Arg
1 5 10 15
Tyr Asn Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile
20 25 30
Asp Pro Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu
35 40 45
Thr Arg Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser

50	55	60
Ala Ile Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro		
65	70	75
Leu Phe Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val		80
	85	90
Glu Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala		95
	100	105
Val Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu		110
	115	120
Val Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu		125
	130	135
Asp Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe		140
145	150	155
Val Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn		160
	165	170
Ser Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala		175
	180	185
Ala Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile		190
	195	200
Tyr Ala Pro Gly Asp Ser Arg Val Arg Cys Gly		205
210	215	

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1500709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile Asp Pro		
1	5	10
Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu Thr Arg		15
	20	25
Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser Ala Ile		30
	35	40
Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro Leu Phe		45
	50	55
Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val Glu Met		60
65	70	75
Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val Ser		80
	85	90
Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val Met		95
	100	105
Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp Phe		110
	115	120
Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val Thr		125
	130	135
Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser Ile		140
145	150	155
Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala		160
	165	170
Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr Ala		175
	180	185
Pro Gly Asp Ser Arg Val Arg Cys Gly		190
	195	200

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1500710
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:
Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val
1 5 10 15
Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val
20 25 30
Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp
35 40 45
Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val
50 55 60
Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser
65 70 75 80
Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala
85 90 95
Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr
100 105 110
Ala Pro Gly Asp Ser Arg Val Arg Cys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..868

(D) OTHER INFORMATION: / Ceres Seq. ID 1500719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

aatcacttgt taattctaag cttcttctct ttccaaaaat ggcgtcatca tcggcttttag	60
ctctcaggag acttctctct tcttccaccg tcgccgtccc tcgcgcccta agagccgttc	120
gtccggtgtc tgcttcttct cgccctcttca ataccaacgc cgccagaaac tatgaagacg	180
gtgtcgatag gaaccatcac tcaaacgcgac atgtttctcg ccacggcggc gatttcttct	240
cagatatact cgatccggtt actccaacga gaagcttgag ccagatgctg aatttcatgg	300
accaggtaag cgaaatccct ttggtatcag ctactcgtgg aatgggagct tctggagtta	360
gacgtggttg gaacgtgaaa gagaaagacg acgcgttgca tctaaggata gatatgccgg	420
gactaagcag agaggatgtg aaattggcct tggaacagaa cacattggtg attagaggag	480
aaggggaaac agaggaggga gaagatgttt ctggagatgg acggaggttt acgagtagga	540
ttgagttacc ggagaaagta tacaagactg atgagattaa ggcggaatat aagaatggtg	600
tggtgaaagt ggtgattcca aagattaaag aggatgagcg taacaatatt cgtcacataa	660
acgttgacta gagtgtttta ttttgatttg tttgagatgg aatggaagta agtgagtga	720
tttgtgaact ttaaggtgtc ctttggtgaa tcaaggagaa tgacatttcc cacggtccta	780
tgtgttcggg attttgactt ttttcgttac atcaatgatc tatgtacgtt tgactacttt	840
catatcatag gttcggattt tgtttccc	

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1500720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

```
Ser Leu Val Asn Ser Lys Leu Leu Leu Phe Pro Lys Met Ala Ser Ser
1      5      10      15
Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser Thr Val Ala Val
      20      25      30
Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala Ser Ser Arg Leu
      35      40      45
Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly Val Asp Arg Asn
      50      55      60
His His Ser Asn Arg His Val Ser Arg His Gly Gly Asp Phe Phe Ser
      65      70      75      80
Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu Ser Gln Met Leu
      85      90      95
Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala Thr Arg
      100     105     110
Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys Glu Lys
      115     120     125
Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser Arg Glu
      130     135     140
Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg Gly Glu
      145     150     155     160
Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg Arg Phe
      165     170     175
Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp Glu Ile
      180     185     190
Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro Lys Ile
      195     200     205
Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn Val Asp
      210     215     220
```

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..210
(D) OTHER INFORMATION: / Ceres Seq. ID 1500721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

```
Met Ala Ser Ser Ser Ala Leu Ala Leu Arg Arg Leu Leu Ser Ser Ser
1      5      10      15
Thr Val Ala Val Pro Arg Ala Leu Arg Ala Val Arg Pro Val Ser Ala
      20      25      30
Ser Ser Arg Leu Phe Asn Thr Asn Ala Ala Arg Asn Tyr Glu Asp Gly
      35      40      45
Val Asp Arg Asn His His Ser Asn Arg His Val Ser Arg His Gly Gly
      50      55      60
Asp Phe Phe Ser Asp Ile Leu Asp Pro Phe Thr Pro Thr Arg Ser Leu
      65      70      75      80
Ser Gln Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val
      85      90      95
Ser Ala Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn
      100     105     110
Val Lys Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly
      115     120     125
Leu Ser Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val
```

130 135 140
Ile Arg Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp
145 150 155 160
Gly Arg Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys
165 170 175
Thr Asp Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val
180 185 190
Ile Pro Lys Ile Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn
195 200 205
Val Asp
210

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala
1 5 10 15
Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys
20 25 30
Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser
35 40 45
Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg
50 55 60
Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg
65 70 75 80
Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp
85 90 95
Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro
100 105 110
Lys Ile Lys Glu Asp Glu Arg Asn Ile Arg His Ile Asn Val Asp
115 120 125

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..763
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

ctgttttttg tctctcgac tcacaagtct cacataatcg aaagctcgca gaagtcaaga 60
ggaagaagat gagtgttaca gtgacaatgc acagtgtctt cgtctacggc agtctcatgg 120
cggacgacgt cgttcgtctc ctccctcaacc gtatccctca aaccgcttcc gcaaccctcc 180
ctgaktkatt cagcatcaaa ggtcgtgttt atccggcgat tataccagct aagtcttgat 240
aaagtctctg gaaaggtgtt atttggatc acagatgatg aacttaatgt tttagatgag 300
tttgaggatg ttgagtatga aagagagaat gttcaagttt tgtaaacaga tagttcagac 360
gagaaactgc aaacaaaaac ctacgtttgg gccaaagaa atgacacctga cctatacggg 420
acatgggatt tcgaggaatg gaagcaactt cacatggaag gtttcttgaa gatgactaaa 480

gaatttgctg aagagttgaa tttaccgaaa tccgagatat gactcgccgc tacattcggg 540
tcagtaaattg aaatctggta tagtttcctc aatgaattgg tcaatatatt cttgggtgttc 600
tctctaggaa gggtttagatt cttcttcattg aatacacata catgagggggg atttgggggtt 660
ttgtgggtatt acttaattca actgataagg aataagaaaa cagctacata ttcttgtgcg 720
gtatgttatt atacaatata catatagaca tgtgttttagc ttc

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

Val	Phe	Gly	Leu	Ser	His	Ser	Gln	Val	Ser	His	Asn	Arg	Lys	Leu	Ala
1			5					10					15		
Glu	Val	Lys	Arg	Lys	Lys	Met	Ser	Gly	Thr	Val	Thr	Met	His	Ser	Val
			20					25					30		
Phe	Val	Tyr	Gly	Ser	Leu	Met	Ala	Asp	Asp	Val	Val	Arg	Leu	Leu	Leu
			35				40					45			
Asn	Arg	Ile	Pro	Gln	Thr	Ala	Ser	Ala	Thr	Leu	Pro	Xaa	Xaa	Phe	Ser
			50				55					60			
Ile	Lys	Gly	Arg	Val	Tyr	Pro	Ala	Ile	Ile	Pro	Ala	Lys	Ser		
			65				70					75			

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

Met	Ser	Gly	Thr	Val	Thr	Met	His	Ser	Val	Phe	Val	Tyr	Gly	Ser	Leu
1			5						10					15	
Met	Ala	Asp	Asp	Val	Val	Arg	Leu	Leu	Leu	Asn	Arg	Ile	Pro	Gln	Thr
			20					25					30		
Ala	Ser	Ala	Thr	Leu	Pro	Xaa	Xaa	Phe	Ser	Ile	Lys	Gly	Arg	Val	Tyr
			35				40					45			
Pro	Ala	Ile	Ile	Pro	Ala	Lys	Ser								
			50				55								

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

Met	His	Ser	Val	Phe	Val	Tyr	Gly	Ser	Leu	Met	Ala	Asp	Val	Val
1			5						10				15	

Arg Leu Leu Leu Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro
20 25 30
Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala
35 40 45

Lys Ser
50

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..846
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

atcctgatcg ggaaacccaa aacgagtggt cgaatagttt ccgactgatt cttccgaggc	60
ttgaagctca atagctatgg cttctctttc agtctcttcc tcttcaacca tcatcgattc	120
aagagctcct ccttctcgac tagcctccgc ctccgctctt tctccgtcgt gcatttcaact	180
tcccacactt ccgattcagt ctcatacccg tgccgctaaa gccactgctt actgtcggaa	240
gattgtgagg aacggttgtga cgagagctac tactgaagtt ggtgaagctc ctgccactac	300
taccgaagct gagactactg agttacctga aatcgtcaag actgctcaag aagcttggga	360
gaaagtggat gacaagtacg ctattggttc tcttgccctt gctagtgtag tggctctttg	420
gggttctgct ggaatgawtt csgcaatcga taggcttcca ttgggttcctg gtgttcttga	480
acttgtaggc atcggttaca caggatgggt cacttacaag aacctgggtc tcaaaccaga	540
cagggagggt ttgtttgaga aggtcaagag cacatacaaa gacatattag ggagcagctg	600
aatcaaagga ggaagaagaa gaagaagagc ctttttgagg ccattcatga attggaatga	660
aggatatcaa aagaatctaa cacaaaggcc acgtccttcc ttcaatcttt ctttcttgta	720
actaaataat ttcatcctt tctctctctc tgtctctggt ctttttttagc tcaaagtatc	780
atccatttat gtcaaagtgt tgtaaattcc tcaagactat atatgagatg ttttgtttca	840
ttttcc	

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

Met Ala Ser Leu Ser Val Ser Ser Ser Thr Ile Ile Asp Ser Arg	
1 5 10 15	
Ala Pro Pro Ser Arg Leu Ala Ser Ala Ser Ala Ser Ser Pro Ser Cys	
20 25 30	
Ile Ser Leu Pro Thr Leu Pro Ile Gln Ser His Thr Arg Ala Ala Lys	
35 40 45	
Ala Thr Ala Tyr Cys Arg Lys Ile Val Arg Asn Val Val Thr Arg Ala	
50 55 60	
Thr Thr Glu Val Gly Glu Ala Pro Ala Thr Thr Glu Ala Glu Thr	
65 70 75 80	
Thr Glu Leu Pro Glu Ile Val Lys Thr Ala Gln Glu Ala Trp Glu Lys	
85 90 95	
Val Asp Asp Lys Tyr Ala Ile Gly Ser Leu Ala Phe Ala Ser Val Val	
100 105 110	
Ala Leu Trp Gly Ser Ala Gly Met Xaa Xaa Ala Ile Asp Arg Leu Pro	
115 120 125	

Leu Val Pro Gly Val Leu Glu Leu Val Gly Ile Gly Tyr Thr Gly Trp
130 135 140
Phe Thr Tyr Lys Asn Leu Val Phe Lys Pro Asp Arg Glu Ala Leu Phe
145 150 155 160
Glu Lys Val Lys Ser Thr Tyr Lys Asp Ile Leu Gly Ser Ser
165 170

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

aaatcaaaac acaacattaa aagctttggc gatttttctc tctgattcaa tcttttcata	60
gtttctaagc tctcagattc ttgaagaagc catggctcgt acgaagcaaa ccgcgagaaa	120
atcacacgga ggaaaagctc cgacgaagca gctcgtacc aaggcgcaa ggaaatctgc	180
accgactacc ggaggagtca agaaacctca ccgtttccgt cctggaaccg tcgctcttcg	240
tgagattcgt aaataccaaa agagcacaga gttgttgaac cgtaaaacttc cattccaacg	300
tcttgttcgt gaaatcgctc aagatttcaa gacggatctg agattccaaa gccatgcagt	360
gtagctctt caagaagctg cggaggcata tttggttggt ttgtttgaag acacaaatct	420
ctgtgccatt catgcaaaga gggttacat tatgcctaaa gatgttcaat tggcaagaag	480
gattcgtgca gagcgtgctt agaaattaga atttaatcca ttcataatgaa ctagtatttt	540
tttttttcta ttagggtttt cgattgtttt tgctttgttg ctttttaaca aaaatacatt	600
atgtcacatt ctctttgaga g	

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser His Gly Gly Lys Ala	
1 5 10 15	
Pro Thr Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Thr	
20 25 30	
Thr Gly Gly Val Lys Lys Pro His Arg Phe Arg Pro Gly Thr Val Ala	
35 40 45	
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Asn Arg	
50 55 60	
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Lys	
65 70 75 80	
Thr Asp Leu Arg Phe Gln Ser His Ala Val Leu Ala Leu Gln Glu Ala	
85 90 95	
Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala	
100 105 110	
Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Val Gln Leu Ala	
115 120 125	
Arg Arg Ile Arg Ala Glu Arg Ala	
130 135	

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1795
(D) OTHER INFORMATION: / Ceres Seq. ID 1500758
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

```
agagatcaag agagagatat ggagagaact ttgcttcaat ggagactatt gcctcttctc      60
gcactcatcg ttgctctttt ctcttcttc ttcgctcttc ctcgctcttt acaggggaat      120
aataagtgtg gtcttcttcc tcatgcatc tactggatct caagtaaacy catcgtcaca      180
cctaattggtc tcatctctgg ttctgtggag gtgaaggagg gaattattgt gtcggtgggtg      240
aaggaagttg attggcataa gagtcaaagg agtcgagtga aagtgattga ttatggagaa      300
gctgtcctca tgcttgggtc cattgatgtg catgttcac ttgatgatcc tggaagaagt      360
gaatgggaag gttttccttc tggaactaag gctgctgctg ctgggggaat aactacattg      420
gttgacatgc ccttaaacag tttcccttca actgtatctc ctgaaacttt gaaactcaag      480
attgaagctg cgaaaaacag aatacatgtt gatgttgggt tctggggagg tctggtacct      540
gacaatgcac tcaactcaag tgctcttgag tctctcttag atgctggagt tcttggcttc      600
aagtccttta tgtgcccttc aggaatcaac gattttccaa tgacaaacat cactcatata      660
aaggaaggac tatctgtatt agctaaatac aaacgacctat tgcttgtaca cgcagagatc      720
gagagagact tagagattga agatggtagt gaaaatgata ctcgttctta tctgacttat      780
ttaaaaaacca ggcctacttc atggggaggag ggagcaatca gaaacctatt atcggttact      840
gaaaacacaa gaattgggtg ttctgcagaa ggagctcatc ttcattattgt acatttatct      900
gatgccagtt ctctcttggg ttgataaag gaagcaaaag gcaaaggaga cagtgttact      960
gttgaaacat gtccacatta cctagctttc tcagccgaag agattccaga aggtgatact      1020
cgtttcaaat gctcccctcc tatacgtgat ggggcaaata gagaaaaatt gtgggaagct      1080
ttgatggaag gagacattga tatgctgagc tctgatcatt cacctacaaa gcctgaactc      1140
aaacttatga gtgatggcaa ctctcttgaa gcttgggggtg ggatatcttc tttacagttt      1200
gttcttccta tcacatgggtc ttatggaaaa aagtatggag taacgctcga gcaggtaact      1260
tcttgggtga gtgataggcc ttccaaactc gctcgactac actctaaggg agcggttacg      1320
gttggaaaac acgcagatct tgttgtgtgg gaacctgaag ccgaatttga tgtagatgaa      1380
gatcatccaa ttcaactcaa acaccctagt atctcagctt atttgggaag aagattatca      1440
ggcaaagtgg ttctgacatt tgtgagaggg aacttgggtt ttggagaagg caagcatgct      1500
tctgatgctt gcgggtctct gcaacttgca actacttaac ttaaaaaggg atttaaaaga      1560
tcttgatctg caccatttaa acaaatgtaa atatgcgatt aagagttgct ctcatgttgc      1620
aagatggttg atgtaatgag tgagtctttt ttgccaattg taagtttaag actctctaaa      1680
tcttggttgg ggctttaagg ttagtggact catstatata ttgtysatgc aaataattta      1740
tatcgcttaa gtaaatgatg tataatttgt tgatgcaaata aatttaaaag tatac
```

(2) INFORMATION FOR SEQ ID NO:1620:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 512 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..512
(D) OTHER INFORMATION: / Ceres Seq. ID 1500759
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

```
Arg Asp Gln Glu Arg Asp Met Glu Arg Thr Leu Leu Gln Trp Arg Leu
1          5          10          15
Leu Pro Leu Leu Ala Leu Ile Val Ala Leu Phe Ser Phe Phe Ala
20          25          30
Ser Pro Arg Ser Leu Gln Gly Asn Asn Lys Cys Ser Leu Leu Pro His
35          40          45
Asp His Tyr Trp Ile Ser Ser Lys Arg Ile Val Thr Pro Asn Gly Leu
50          55          60
Ile Ser Gly Ser Val Glu Val Lys Gly Gly Ile Ile Val Ser Val Val
```

65					70					75				80
Lys	Glu	Val	Asp	Trp	His	Lys	Ser	Gln	Arg	Ser	Arg	Val	Lys	Val Ile
				85					90					95
Asp	Tyr	Gly	Glu	Ala	Val	Leu	Met	Pro	Gly	Leu	Ile	Asp	Val	His Val
			100					105					110	
His	Leu	Asp	Asp	Pro	Gly	Arg	Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser Gly
		115					120					125		
Thr	Lys	Ala	Ala	Ala	Ala	Gly	Gly	Ile	Thr	Thr	Leu	Val	Asp	Met Pro
		130				135					140			
Leu	Asn	Ser	Phe	Pro	Ser	Thr	Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu Lys
145					150					155				160
Ile	Glu	Ala	Ala	Lys	Asn	Arg	Ile	His	Val	Asp	Val	Gly	Phe	Trp Gly
				165					170					175
Gly	Leu	Val	Pro	Asp	Asn	Ala	Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser Leu
			180					185					190	
Leu	Asp	Ala	Gly	Val	Leu	Gly	Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser Gly
		195				200						205		
Ile	Asn	Asp	Phe	Pro	Met	Thr	Asn	Ile	Thr	His	Ile	Lys	Glu	Gly Leu
		210				215					220			
Ser	Val	Leu	Ala	Lys	Tyr	Lys	Arg	Pro	Leu	Leu	Val	His	Ala	Glu Ile
225					230					235				240
Glu	Arg	Asp	Leu	Glu	Ile	Glu	Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg Ser
			245						250					255
Tyr	Leu	Thr	Tyr	Leu	Lys	Thr	Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly Ala
			260					265					270	
Ile	Arg	Asn	Leu	Leu	Ser	Val	Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly Ser
		275					280					285		
Ala	Glu	Gly	Ala	His	Leu	His	Ile	Val	His	Leu	Ser	Asp	Ala	Ser Ser
		290				295					300			
Ser	Leu	Asp	Leu	Ile	Lys	Glu	Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val Thr
305					310					315				320
Val	Glu	Thr	Cys	Pro	His	Tyr	Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile Pro
			325						330					335
Glu	Gly	Asp	Thr	Arg	Phe	Lys	Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala Ala
		340						345					350	
Asn	Arg	Glu	Lys	Leu	Trp	Glu	Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp Met
		355					360					365		
Leu	Ser	Ser	Asp	His	Ser	Pro	Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met Ser
		370				375					380			
Asp	Gly	Asn	Phe	Leu	Lys	Ala	Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln Phe
385					390					395				400
Val	Leu	Pro	Ile	Thr	Trp	Ser	Tyr	Gly	Lys	Lys	Tyr	Gly	Val	Thr Leu
			405						410					415
Glu	Gln	Val	Thr	Ser	Trp	Trp	Ser	Asp	Arg	Pro	Ser	Lys	Leu	Ala Arg
		420						425					430	
Leu	His	Ser	Lys	Gly	Ala	Val	Thr	Val	Gly	Lys	His	Ala	Asp	Leu Val
		435					440					445		
Val	Trp	Glu	Pro	Glu	Ala	Glu	Phe	Asp	Val	Asp	Glu	Asp	His	Pro Ile
		450				455					460			
His	Phe	Lys	His	Pro	Ser	Ile	Ser	Ala	Tyr	Leu	Gly	Arg	Arg	Leu Ser
465					470					475				480
Gly	Lys	Val	Val	Ser	Thr	Phe	Val	Arg	Gly	Asn	Leu	Val	Phe	Gly Glu
			485					490						495
Gly	Lys	His	Ala	Ser	Asp	Ala	Cys	Gly	Ser	Leu	Gln	Leu	Ala	Thr Thr
			500					505					510	

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..506
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500760
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

Met	Glu	Arg	Thr	Leu	Leu	Gln	Trp	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Leu	
1				5					10					15		
Ile	Val	Ala	Leu	Phe	Ser	Phe	Phe	Phe	Ala	Ser	Pro	Arg	Ser	Leu	Gln	
			20					25					30			
Gly	Asn	Asn	Lys	Cys	Ser	Leu	Leu	Pro	His	Asp	His	Tyr	Trp	Ile	Ser	
		35					40					45				
Ser	Lys	Arg	Ile	Val	Thr	Pro	Asn	Gly	Leu	Ile	Ser	Gly	Ser	Val	Glu	
	50					55					60					
Val	Lys	Gly	Gly	Ile	Ile	Val	Ser	Val	Val	Lys	Glu	Val	Asp	Trp	His	
65					70					75				80		
Lys	Ser	Gln	Arg	Ser	Arg	Val	Lys	Val	Ile	Asp	Tyr	Gly	Glu	Ala	Val	
				85					90					95		
Leu	Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val	His	Leu	Asp	Asp	Pro	Gly	
			100					105					110			
Arg	Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly	Thr	Lys	Ala	Ala	Ala	Ala	
		115					120					125				
Gly	Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro	Leu	Asn	Ser	Phe	Pro	Ser	
	130					135					140					
Thr	Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys	Ile	Glu	Ala	Ala	Lys	Asn	
145					150					155				160		
Arg	Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly	Gly	Leu	Val	Pro	Asp	Asn	
				165					170					175		
Ala	Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu	Leu	Asp	Ala	Gly	Val	Leu	
		180						185					190			
Gly	Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly	Ile	Asn	Asp	Phe	Pro	Met	
	195					200					205					
Thr	Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu	Ser	Val	Leu	Ala	Lys	Tyr	
	210					215					220					
Lys	Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile	Glu	Arg	Asp	Leu	Glu	Ile	
225					230					235				240		
Glu	Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser	Tyr	Leu	Thr	Tyr	Leu	Lys	
				245					250					255		
Thr	Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly	Ala	Ile	Arg	Asn	Leu	Leu	Ser	
		260						265					270			
Val	Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly	Ser	Ala	Glu	Gly	Ala	His	Leu	
		275					280					285				
His	Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser	Ser	Leu	Asp	Leu	Ile	Lys	
	290					295					300					
Glu	Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr	Val	Glu	Thr	Cys	Pro	His	
305				310						315				320		
Tyr	Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro	Glu	Gly	Asp	Thr	Arg	Phe	
				325					330					335		
Lys	Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala	Asn	Arg	Glu	Lys	Leu	Trp	
			340					345					350			
Glu	Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met	Leu	Ser	Ser	Asp	His	Ser	
	355					360						365				
Pro	Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser	Asp	Gly	Asn	Phe	Leu	Lys	
	370					375					380					
Ala	Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe	Val	Leu	Pro	Ile	Thr	Trp	
385					390					395				400		
Ser	Tyr	Gly	Lys	Lys	Tyr	Gly	Val	Thr	Leu	Glu	Gln	Val	Thr	Ser	Trp	
				405					410					415		
Trp	Ser	Asp	Arg	Pro	Ser	Lys	Leu	Ala	Arg	Leu	His	Ser	Lys	Gly	Ala	

420	425	430
Val Thr Val Gly Lys His Ala Asp Leu Val Val Trp Glu Pro Glu Ala		
435	440	445
Glu Phe Asp Val Asp Glu Asp His Pro Ile His Phe Lys His Pro Ser		
450	455	460
Ile Ser Ala Tyr Leu Gly Arg Arg Leu Ser Gly Lys Val Val Ser Thr		
465	470	475
Phe Val Arg Gly Asn Leu Val Phe Gly Glu Gly Lys His Ala Ser Asp		
485	490	495
Ala Cys Gly Ser Leu Gln Leu Ala Thr Thr		
500	505	

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val	His	Leu	Asp	Asp	Pro	Gly	Arg
1			5					10						15	
Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly	Thr	Lys	Ala	Ala	Ala	Ala	Gly
			20					25						30	
Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro	Leu	Asn	Ser	Phe	Pro	Ser	Thr
		35				40						45			
Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys	Ile	Glu	Ala	Ala	Lys	Asn	Arg
	50				55					60					
Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly	Gly	Leu	Val	Pro	Asp	Asn	Ala
65				70						75				80	
Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu	Leu	Asp	Ala	Gly	Val	Leu	Gly
			85					90						95	
Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly	Ile	Asn	Asp	Phe	Pro	Met	Thr
		100						105					110		
Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu	Ser	Val	Leu	Ala	Lys	Tyr	Lys
	115					120						125			
Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile	Glu	Arg	Asp	Leu	Glu	Ile	Glu
	130				135						140				
Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser	Tyr	Leu	Thr	Tyr	Leu	Lys	Thr
145				150						155				160	
Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly	Ala	Ile	Arg	Asn	Leu	Leu	Ser	Val
			165					170						175	
Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly	Ser	Ala	Glu	Gly	Ala	His	Leu	His
		180						185					190		
Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser	Ser	Leu	Asp	Leu	Ile	Lys	Glu
	195					200						205			
Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr	Val	Glu	Thr	Cys	Pro	His	Tyr
	210				215						220				
Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro	Glu	Gly	Asp	Thr	Arg	Phe	Lys
225				230						235				240	
Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala	Asn	Arg	Glu	Lys	Leu	Trp	Glu
			245						250					255	
Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met	Leu	Ser	Ser	Asp	His	Ser	Pro
		260						265					270		
Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser	Asp	Gly	Asn	Phe	Leu	Lys	Ala
	275						280						285		
Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe	Val	Leu	Pro	Ile	Thr	Trp	Ser
	290					295						300			

Tyr Gly Lys Lys Tyr Gly Val Thr Leu Glu Gln Val Thr Ser Trp Trp
305 310 315 320
Ser Asp Arg Pro Ser Lys Leu Ala Arg Leu His Ser Lys Gly Ala Val
325 330 335
Thr Val Gly Lys His Ala Asp Leu Val Val Trp Glu Pro Glu Ala Glu
340 345 350
Phe Asp Val Asp Glu Asp His Pro Ile His Phe Lys His Pro Ser Ile
355 360 365
Ser Ala Tyr Leu Gly Arg Arg Leu Ser Gly Lys Val Val Ser Thr Phe
370 375 380
Val Arg Gly Asn Leu Val Phe Gly Glu Gly Lys His Ala Ser Asp Ala
385 390 395 400
Cys Gly Ser Leu Gln Leu Ala Thr Thr
405

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

atacaaatca	taactcaaag	aaaaacaacc	cctcaacggt	cgatgtgtga	tcccattaga	60
gaagatggct	ctaacaaaag	aggcgccgtg	agtaaggaaa	aaaggccgta	tattcataga	120
gaatggctcg	gggccgatat	aatacgcgag	ttaacccgta	tcaatgtgca	ctttttgtgt	180
ctcttggcac	catttaacta	caaatgggaa	gcattacggt	tcggtttcgt	gctctacgcg	240
ttgacttcac	tcagcatcac	attctcatac	cataggaact	tgggctcacc	ggagctttaa	300
gcttccgaaa	tggcttgaat	atccttttag	ttattttgct	gtttttgctc	ttcaggggtga	360
tccgttgat	tgggtgagca	tacatagggt	tccatcacca	gttcacagat	tctgaccgtg	420
accacatag	ccctatcgaa	ggatttttgt	tcagtcatgt	gtggtggata	tgtgacactc	480
gttatatcaa	atataagtgt	ggaggacgta	acaacgtgat	ggacttgaag	cagcaatggt	540
tctattgggt	tctacgaatg	acaattgggt	tccacgtcct	aatgttttgg	actgtcctct	600
atctctatgg	tggtttacct	taccttacat	gcggcggggg	cgttggaggt	gtgattgggt	660
accacgtgac	atggctcgtg	aactcggcat	gccatatttg	gggttcgaga	tcattggaaga	720
ctaaagacac	atctcgtaac	gtttggtggc	taagcttatt	tacaatggga	gagagttggc	780
acaataatca	ccacgccttt	gagtcacg	cgaggcaagg	attggagttg	tggcagatag	840
acataacttg	gtatcttatt	cgactatttg	aggtttctcg	gttagccact	gacgtgaaat	900
tgccctcgga	attccagaaa	cagaaactgg	ctctgactcg	ttgatcatct	gcattgagaga	960
tttatcagaa	ttttatattt	ttagaaaatt	atcaaagtta	ctataaaaga	ggataatata	1020
gatgagagtt	tatgattggt	atagtcttat	tgatattttc	cactataaat	tgttgttttc	1080
tgtctttgga	gtaggattta	aatgcggcaa	aaaaaggtat	ctattttttt	ttttaataaa	1140
aggcttaagt	tg					

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

Met Asp Leu Lys Gln Gln Trp Phe Tyr Trp Phe Leu Arg Met Thr Ile
1 5 10 15
Gly Phe His Val Leu Met Phe Trp Thr Val Leu Tyr Leu Tyr Gly Gly

	20		25		30										
Leu	Pro	Tyr	Leu	Thr	Cys	Gly	Gly	Val	Gly	Gly	Val	Ile	Gly	Tyr	
	35						40				45				
His	Val	Thr	Trp	Leu	Val	Asn	Ser	Ala	Cys	His	Ile	Trp	Gly	Ser	Arg
	50					55					60				
Ser	Trp	Lys	Thr	Lys	Asp	Thr	Ser	Arg	Asn	Val	Trp	Trp	Leu	Ser	Leu
65					70					75					80
Phe	Thr	Met	Gly	Glu	Ser	Trp	His	Asn	Asn	His	His	Ala	Phe	Glu	Ser
				85					90					95	
Ser	Ala	Arg	Gln	Gly	Leu	Glu	Trp	Trp	Gln	Ile	Asp	Ile	Thr	Trp	Tyr
		100						105					110		
Leu	Ile	Arg	Leu	Phe	Glu	Val	Leu	Gly	Leu	Ala	Thr	Asp	Val	Lys	Leu
		115					120					125			
Pro	Ser	Glu	Phe	Gln	Lys	Gln	Lys	Leu	Ala	Leu	Thr	Arg			
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

Met	Thr	Ile	Gly	Phe	His	Val	Leu	Met	Phe	Trp	Thr	Val	Leu	Tyr	Leu
1			5					10					15		
Tyr	Gly	Gly	Leu	Pro	Tyr	Leu	Thr	Cys	Gly	Gly	Gly	Val	Gly	Gly	Val
			20					25				30			
Ile	Gly	Tyr	His	Val	Thr	Trp	Leu	Val	Asn	Ser	Ala	Cys	His	Ile	Trp
		35					40					45			
Gly	Ser	Arg	Ser	Trp	Lys	Thr	Lys	Asp	Thr	Ser	Arg	Asn	Val	Trp	Trp
	50					55				60					
Leu	Ser	Leu	Phe	Thr	Met	Gly	Glu	Ser	Trp	His	Asn	Asn	His	His	Ala
65					70					75					80
Phe	Glu	Ser	Ser	Ala	Arg	Gln	Gly	Leu	Glu	Trp	Trp	Gln	Ile	Asp	Ile
			85					90					95		
Thr	Trp	Tyr	Leu	Ile	Arg	Leu	Phe	Glu	Val	Leu	Gly	Leu	Ala	Thr	Asp
		100					105					110			
Val	Lys	Leu	Pro	Ser	Glu	Phe	Gln	Lys	Gln	Lys	Leu	Ala	Leu	Thr	Arg
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met	Phe	Trp	Thr	Val	Leu	Tyr	Leu	Tyr	Gly	Gly	Leu	Pro	Tyr	Leu	Thr
1					5				10				15		
Cys	Gly	Gly	Gly	Val	Gly	Gly	Val	Ile	Gly	Tyr	His	Val	Thr	Trp	Leu
			20					25					30		

Val Asn Ser Ala Cys His Ile Trp Gly Ser Arg Ser Trp Lys Thr Lys
35 40 45
Asp Thr Ser Arg Asn Val Trp Trp Leu Ser Leu Phe Thr Met Gly Glu
50 55 60
Ser Trp His Asn Asn His His Ala Phe Glu Ser Ser Ala Arg Gln Gly
65 70 75 80
Leu Glu Trp Trp Gln Ile Asp Ile Thr Trp Tyr Leu Ile Arg Leu Phe
85 90 95
Glu Val Leu Gly Leu Ala Thr Asp Val Lys Leu Pro Ser Glu Phe Gln
100 105 110
Lys Gln Lys Leu Ala Leu Thr Arg
115 120

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

acaagtcaca	acccaccat	gcattgcata	tctctttcgt	tatcctcaat	attctttttc	60
ctcttctctca	catcaaccat	tttgatttct	ccggtacaac	ccacaacctc	taagcctccg	120
gcaccacggc	cccacagaga	gctctccgcc	gattactact	ccaagaaatg	tcctcagctt	180
gaaactctcg	tccgttccgt	cacttctcag	cggttcaaag	aagtcccat	ctcagctcca	240
gccaccattc	gcctcttctt	tcacgactgc	ttcgttgagg	gttgatgatg	gtcgatattg	300
atagaaacaa	agaaaggaag	caagaaatta	gcagagagag	aagcatatga	gaataaggaa	360
ttgagagagg	aaggatttga	tagtatcatc	aaggcgaagg	ccttggttga	gtctcattgc	420
ccttctctcg	tctcttctct	tgatattctc	gctattgccg	ctcgagattt	cattcatctg	480
gcagggtggc	cttactatca	agtgaaaaaa	ggaaggtggg	acggaaaaag	atcaacggca	540
aagaacgtcc	ctccaaacat	acctcgatca	aactccaccg	ttgatcaact	catcaagctc	600
ttcgcgtcca	aaggactaac	cgtagaggaa	ctcgtcgtcc	tttctggttc	ccacaccatc	660
ggttcgccca	ttgtaaaaaa	ttccttggtc	gtctctacga	ctacaaaggc	acaaaacgac	720
ccgacccgag	tcttgaccaa	agattactaa	aagagctccg	gatgtcttgt	cctttttccg	780
gcggaagctc	tggagtcgtc	cttccgctcg	acgctacaac	tccgtttgtg	tttgataatg	840
gatatttcac	aggtctagga	accaacatgg	gccttctcgg	gtcggaccaa	gctttgttcc	900
ttgacccgag	gacgaagccc	attgcacttg	agatggcaag	agataagcag	aagtttctca	960
aggcgtttgg	agacgctatg	gataaaatgg	gttccattgg	tgtaaagaga	gggaagagac	1020
atgggggaaat	acgtacggat	tgctcagagt	ttttatagat	tttctttatt	gtcttgtctg	1080
atgggttttg	tcttgatctt	gatgtgttct	gtgtcatgtg	tcctttaatt	tattagcatt	1140
ttcgtgattg	ttttgttgat	agtataaggt	attttttt			

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

Thr Ser His Asn Pro Thr Met His Val Ile Ser Leu Ser Leu Ser Ser
1 5 10 15
Ile Phe Phe Phe Leu Phe Leu Thr Ser Thr Ile Leu Ile Ser Pro Val
20 25 30
Gln Pro Thr Thr Ser Lys Pro Pro Ala Pro Arg Pro His Arg Glu Leu

(XI) SEQUENCE DISCONTINUITY																
Met	His	Val	Ile		Ser	Leu	Ser	Leu	Ser		Ile	Phe	Phe	Phe	Leu	Phe
1				5					10						15	
Leu	Thr	Ser	Thr	Ile	Leu	Ile	Ser	Pro	Val	Gln	Pro	Thr	Thr	Ser	Lys	
			20					25					30			
Pro	Pro	Ala	Pro	Arg	Pro	His	Arg	Glu	Leu	Ser	Ala	Asp	Tyr	Tyr	Ser	
		35					40					45				
Lys	Lys	Cys	Pro	Gln	Leu	Glu	Thr	Leu	Val	Gly	Ser	Val	Thr	Ser	Gln	
	50					55					60					
Arg	Phe	Lys	Glu	Val	Pro	Ile	Ser	Ala	Pro	Ala	Thr	Ile	Arg	Leu	Phe	
65				70						75					80	
Phe	His	Asp	Cys	Phe	Val	Glu	Gly	Cys	Asp	Gly	Ser	Ile	Leu	Ile	Glu	
			85						90					95		
Thr	Lys	Lys	Gly	Ser	Lys	Lys	Leu	Ala	Glu	Arg	Glu	Ala	Tyr	Glu	Asn	
			100					105					110			
Lys	Glu	Leu	Arg	Glu	Glu	Gly	Phe	Asp	Ser	Ile	Ile	Lys	Ala	Lys	Ala	
		115				120						125				
Leu	Val	Glu	Ser	His	Cys	Pro	Ser	Leu	Val	Ser	Xaa	Ser	Asp	Ile	Leu	
	130					135					140					
Ala	Ile	Ala	Ala	Arg	Asp	Phe	Ile	His	Leu	Ala	Gly	Gly	Pro	Tyr	Tyr	
145				150						155					160	
Gln	Val	Lys	Lys	Gly	Arg	Trp	Asp	Gly	Lys	Arg	Ser	Thr	Ala	Lys	Asn	
			165						170					175		

Val Pro Pro Asn Ile Pro Arg Ser Asn Ser Thr Val Asp Gln Leu Ile
180 185 190
Lys Leu Phe Ala Ser Lys Gly Leu Thr Val Glu Glu Leu Val Val Leu
195 200 205
Ser Gly Ser His Thr Ile Gly Ser Pro Ile Val Lys Ile Ser Leu Val
210 215 220
Val Ser Thr Thr Thr Lys Ala Gln Asn Asp Pro Thr Arg Val Leu Thr
225 230 235 240
Lys Asp Tyr

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

aaaaacacaa	acgtaacaag	gattcagact	ctctctagac	gatgcaagcc	aaaatcaatt	60
ctttcttcaa	gccctcctct	tcttcttcta	tcgctgcctc	agtaacaaca	gacacagacg	120
atrgsttttag	ctgtctggga	gaacaatcgg	aacgccatcg	tcaacaccta	ccagcgctcga	180
tctgcgatta	ccgaaagaag	tgaagtgcct	aaaggatgca	tcgaaaagac	gctgaagaaa	240
ggatcttctt	ctgtacctaa	aaatcacaaa	aagaagcgta	attatacaca	attccacata	300
gagttgggcc	aatctgattt	tcttctcaga	cattgcgcag	aatgtggagc	taagtatgct	360
cctggagatg	aattagatga	gaagaacct	caaagttttc	acaaggacta	tatgtatgga	420
ctccctttta	agggttggca	gaacgagaaa	gcgtttacat	cacctttgtt	catcaagaac	480
cgcatacgta	tggatatcaga	aaatgattcc	cctgcacaca	gaaacaaggt	gcaagagggt	540
gtgaaaaatga	tggagggttg	gttgggtgag	gattggattc	ttcaccaaca	ttgtaagggt	600
tatctattca	tatcctctca	gaggatctct	ggatgtctag	ttgctgaacc	aattaaggaa	660
gcatttaagc	tcatagcttc	tcttgatgat	gaaagacagt	tacaaaaaga	gagctcatcc	720
tcgccttcaa	cctccattca	gtttggaaac	attgttctac	aaagagaggt	atcgaaaaga	780
tgtcgaacat	cagatgatag	attagataac	ggagtcattg	tatgtgaaga	agaagctaaa	840
ccagctgttt	gtgggattag	agcgatttgg	gtctcacctt	ctaataagaag	aaaaggcata	900
gccacatggt	tactcgatac	cacgagggaa	agctttcgca	acaatgggtg	catgctggag	960
aaatctcagt	tagcattttc	acaaccaacc	tccataggaa	gatcttttgg	atctaaatat	1020
tttggaactt	gttcattctt	actttacaaa	gctcagctaa	ttgatactca	cttttcttaa	1080
acggcatagg	tttcatcaca	tcacaaccat	catcttcaact	gtc		

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..222
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

Met	Tyr	Gly	Leu	Pro	Phe	Lys	Gly	Trp	Gln	Asn	Glu	Lys	Ala	Phe	Thr
1				5				10						15	
Ser	Pro	Leu	Phe	Ile	Lys	Asn	Arg	Ile	Val	Met	Val	Ser	Glu	Asn	Asp
				20				25					30		
Ser	Pro	Ala	His	Arg	Asn	Lys	Val	Gln	Glu	Val	Val	Lys	Met	Met	Glu
				35				40					45		
Val	Glu	Leu	Gly	Glu	Asp	Trp	Ile	Leu	His	Gln	His	Cys	Lys	Val	Tyr
				50				55					60		

Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val Ala Glu Pro
65 70 75 80
Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp Glu Arg Gln
85 90 95
Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser Thr Ser Ile Gln Phe Gly
100 105 110
Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg Thr Ser Asp
115 120 125
Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu Ala Lys Pro
130 135 140
Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser Asn Arg Arg
145 150 155 160
Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu Ser Phe Arg
165 170 175
Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe Ser Gln Pro
180 185 190
Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly Thr Cys Ser
195 200 205
Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..196

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

Met Val Ser Glu Asn Asp Ser Pro Ala His Arg Asn Lys Val Gln Glu
1 5 10 15
Val Val Lys Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His
20 25 30
Gln His Cys Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly
35 40 45
Cys Leu Val Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser
50 55 60
Pro Asp Asp Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser
65 70 75 80
Thr Ser Ile Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys
85 90 95
Arg Cys Arg Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys
100 105 110
Glu Glu Glu Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val
115 120 125
Ser Pro Ser Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr
130 135 140
Thr Arg Glu Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln
145 150 155 160
Leu Ala Phe Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys
165 170 175
Tyr Phe Gly Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp
180 185 190
Thr His Phe Ser
195

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..177
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

Met	Met	Glu	Val	Glu	Leu	Gly	Glu	Asp	Trp	Ile	Leu	His	Gln	His	Cys
1			5						10					15	
Lys	Val	Tyr	Leu	Phe	Ile	Ser	Ser	Gln	Arg	Ile	Ser	Gly	Cys	Leu	Val
			20					25					30		
Ala	Glu	Pro	Ile	Lys	Glu	Ala	Phe	Lys	Leu	Ile	Ala	Ser	Pro	Asp	Asp
			35				40					45			
Glu	Arg	Gln	Leu	Gln	Lys	Glu	Ser	Ser	Ser	Ser	Pro	Ser	Thr	Ser	Ile
			50			55					60				
Gln	Phe	Gly	Asn	Ile	Val	Leu	Gln	Arg	Glu	Val	Ser	Lys	Arg	Cys	Arg
65				70					75					80	
Thr	Ser	Asp	Asp	Arg	Leu	Asp	Asn	Gly	Val	Ile	Val	Cys	Glu	Glu	Glu
			85					90					95		
Ala	Lys	Pro	Ala	Val	Cys	Gly	Ile	Arg	Ala	Ile	Trp	Val	Ser	Pro	Ser
			100					105					110		
Asn	Arg	Arg	Lys	Gly	Ile	Ala	Thr	Trp	Leu	Leu	Asp	Thr	Thr	Arg	Glu
			115				120					125			
Ser	Phe	Arg	Asn	Asn	Gly	Cys	Met	Leu	Glu	Lys	Ser	Gln	Leu	Ala	Phe
			130			135					140				
Ser	Gln	Pro	Thr	Ser	Ile	Gly	Arg	Ser	Phe	Gly	Ser	Lys	Tyr	Phe	Gly
145				150					155					160	
Thr	Cys	Ser	Phe	Leu	Tyr	Lys	Ala	Gln	Leu	Ile	Asp	Thr	His	Phe	
			165					170					175		

Ser

(2) INFORMATION FOR SEQ ID NO:1634:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1452 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

aagcattttg	cattcttggt	tcttggtttt	gtgttttagt	tttgagagaa	aatgggacag	60
attccgaggt	ttctttcttg	gaggaatatg	ttggctctct	cgttggccat	caacttcagc	120
ttgattctaa	agattttgaa	gggtgataga	gaacgaggag	attcatggga	cagaacagcg	180
tatgttagca	tatggcccg	ggtatccacc	acggcttcag	aatcttcttc	gttgtcttca	240
gcatcttgca	actatagcaa	gattgaagaa	gacgatgata	gaattatcaa	tctcaaattt	300
gggtgatccaa	cggtgtatga	gagatattgg	caggaaaatg	gagaggtgac	aacaatggtg	360
atacctggat	ggcaatctct	tagctatttt	tcagatgaaa	acaacctctg	ttggtttctt	420
gagccagagc	ttgccaaaga	gattgtgagg	gtgcataagg	ttgttgggaa	tgctgtaacg	480
caagaccgct	tcattgttgt	tggcactggc	tcaacacaat	tgtatcaggc	tgctctctat	540
gctctctccc	cacatgatga	ctccggtccc	attaatgtcg	tgtcagccgc	accctattat	600
agtcataccc	cgttgattac	agactgcctc	aaatcagggt	tatatcgatg	gggtggagat	660
gcaaagacgt	acaaagaaga	tggtccatac	attgaacttg	ttacatctcc	aaacaaccct	720
gatgggttct	tgagagaatc	agtagtgaac	agtactgaag	gtatattgat	ccatgatttg	780
gcttactatt	ggccacagta	tacaccgata	acataaccag	ctgatcacga	tgttatgctc	840
ttcactgctt	caaagagcac	tggccatgca	gggatacgga	ttggvtgggc	tttggtgaaa	900
gacagagaga	cggctaggaa	aatgatagag	tacattgaac	tcaacacgat	tggggtttca	960

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aaggactcac agcttagagt agccaaggtt cttaaggttg tgtcagacag ttgtgggaat 1020
gtaacgggca aatcttttctt tgaccatagt tatgatgcta tgtatgagag gtggaaacta 1080
ttgaaacaag cagcaaagga tactaaacgt ttcagtgttc ctgatttcgt ctctcaacgt 1140
tgcaatttct ttggcagggt ctttgagcca caaccagcat ttgcatggtt taagtgtgaa 1200
gaagggatag tggattgtga gaagtttctt agagaggaga agaagattct aactaaaagt 1260
ggaaagtact tcggagatga gctaagtaat gtgaggataa gcatgttgga tagagatact 1320
aactttaata ttttccttca caggattaca tcttccttta attcaacttt gtaagtgcac 1380
atgcatgtga ttatgatcga ttgtcataac ttgcaacaag tgttttgctc cataaatatt 1440
attggaaatt tg
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(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..254

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

```
Met Gly Gln Ile Pro Arg Phe Leu Ser Trp Arg Asn Met Leu Val Leu
1          5          10          15
Ser Leu Ala Ile Asn Phe Ser Leu Ile Leu Lys Ile Leu Lys Gly Asp
          20          25          30
Arg Glu Arg Gly Asp Ser Trp Asp Arg Thr Ala Tyr Val Ser Ile Trp
          35          40          45
Pro Val Val Ser Thr Thr Ala Ser Glu Ser Ser Ser Leu Ser Ser Ala
          50          55          60
Ser Cys Asn Tyr Ser Lys Ile Glu Glu Asp Asp Asp Arg Ile Ile Asn
65          70          75          80
Leu Lys Phe Gly Asp Pro Thr Val Tyr Glu Arg Tyr Trp Gln Glu Asn
          85          90          95
Gly Glu Val Thr Thr Met Val Ile Pro Gly Trp Gln Ser Leu Ser Tyr
          100          105          110
Phe Ser Asp Glu Asn Asn Leu Cys Trp Phe Leu Glu Pro Glu Leu Ala
          115          120          125
Lys Glu Ile Val Arg Val His Lys Val Val Gly Asn Ala Val Thr Gln
          130          135          140
Asp Arg Phe Ile Val Val Gly Thr Gly Ser Thr Gln Leu Tyr Gln Ala
145          150          155          160
Ala Leu Tyr Ala Leu Ser Pro His Asp Asp Ser Gly Pro Ile Asn Val
          165          170          175
Val Ser Ala Ala Pro Tyr Tyr Ser Thr Tyr Pro Leu Ile Thr Asp Cys
          180          185          190
Leu Lys Ser Gly Leu Tyr Arg Trp Gly Gly Asp Ala Lys Thr Tyr Lys
          195          200          205
Glu Asp Gly Pro Tyr Ile Glu Leu Val Thr Ser Pro Asn Asn Pro Asp
210          215          220
Gly Phe Leu Arg Glu Ser Val Val Asn Ser Thr Glu Gly Ile Leu Ile
225          230          235          240
His Asp Leu Ala Tyr Trp Pro Gln Tyr Thr Pro Ile Thr
          245          250
```

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1500795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

```
Met Leu Val Leu Ser Leu Ala Ile Asn Phe Ser Leu Ile Leu Lys Ile
 1          5          10          15
Leu Lys Gly Asp Arg Glu Arg Gly Asp Ser Trp Asp Arg Thr Ala Tyr
 20          25          30
Val Ser Ile Trp Pro Val Val Ser Thr Thr Ala Ser Glu Ser Ser Ser
 35          40          45
Leu Ser Ser Ala Ser Cys Asn Tyr Ser Lys Ile Glu Glu Asp Asp Asp
 50          55          60
Arg Ile Ile Asn Leu Lys Phe Gly Asp Pro Thr Val Tyr Glu Arg Tyr
 65          70          75          80
Trp Gln Glu Asn Gly Glu Val Thr Thr Met Val Ile Pro Gly Trp Gln
 85          90          95
Ser Leu Ser Tyr Phe Ser Asp Glu Asn Asn Leu Cys Trp Phe Leu Glu
 100         105         110
Pro Glu Leu Ala Lys Glu Ile Val Arg Val His Lys Val Val Gly Asn
 115         120         125
Ala Val Thr Gln Asp Arg Phe Ile Val Val Gly Thr Gly Ser Thr Gln
 130         135         140
Leu Tyr Gln Ala Ala Leu Tyr Ala Leu Ser Pro His Asp Asp Ser Gly
 145         150         155         160
Pro Ile Asn Val Val Ser Ala Ala Pro Tyr Tyr Ser Thr Tyr Pro Leu
 165         170         175
Ile Thr Asp Cys Leu Lys Ser Gly Leu Tyr Arg Trp Gly Gly Asp Ala
 180         185         190
Lys Thr Tyr Lys Glu Asp Gly Pro Tyr Ile Glu Leu Val Thr Ser Pro
 195         200         205
Asn Asn Pro Asp Gly Phe Leu Arg Glu Ser Val Val Asn Ser Thr Glu
 210         215         220
Gly Ile Leu Ile His Asp Leu Ala Tyr Tyr Trp Pro Gln Tyr Thr Pro
 225         230         235         240
Ile Thr
```

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1500796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

```
Met Leu Phe Thr Ala Ser Lys Ser Thr Gly His Ala Gly Ile Arg Ile
 1          5          10          15
Xaa Trp Ala Leu Val Lys Asp Arg Glu Thr Ala Arg Lys Met Ile Glu
 20          25          30
Tyr Ile Glu Leu Asn Thr Ile Gly Val Ser Lys Asp Ser Gln Leu Arg
 35          40          45
Val Ala Lys Val Leu Lys Val Val Ser Asp Ser Cys Gly Asn Val Thr
 50          55          60
Gly Lys Ser Phe Phe Asp His Ser Tyr Asp Ala Met Tyr Glu Arg Trp
 65          70          75          80
Lys Leu Leu Lys Gln Ala Ala Lys Asp Thr Lys Arg Phe Ser Val Pro
 85          90          95
Asp Phe Val Ser Gln Arg Cys Asn Phe Phe Gly Arg Val Phe Glu Pro
```

100	105	110
Gln Pro Ala Phe Ala Trp Phe Lys Cys Glu Glu Gly Ile Val Asp Cys		
115	120	125
Glu Lys Phe Leu Arg Glu Glu Lys Lys Ile Leu Thr Lys Ser Gly Lys		
130	135	140
Tyr Phe Gly Asp Glu Leu Ser Asn Val Arg Ile Ser Met Leu Asp Arg		
145	150	155
Asp Thr Asn Phe Asn Ile Phe Leu His Arg Ile Thr Ser Ser Phe Asn		
165	170	175
Ser Thr Leu		

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

aactaaatca	gaagattact	actaaacaga	gtcttttttg	acttgccaaa	aacacatctg	60
tctctctctc	tctttgcgga	tctgaaatgg	cgattcctgt	tatcgatttc	tccaaactca	120
atggtgaaga	aagagagaag	acactgtctg	aaatcgctag	agcttgcgaa	gagtggggat	180
tttttcagct	ggtgaaccat	ggtattccat	tggagcttct	aaataagggtg	aagaagctga	240
gctcagattg	ctacaaaaca	gagagagaag	aagcattcaa	gacttctaata	cccgtgaagt	300
tgctcaacga	attggttcaa	aagaactctg	gcgagaagct	agaaaacgtg	gactgggaag	360
atgtcttcac	tctcttggac	cataaccaaa	acgaatggcc	atccaaaatt	aaagagacta	420
tgggagaata	cagagaagaa	gtgaggaagc	tagcgagcaa	gatgatggaa	gtgatggatg	480
agaatttggg	tttgccataa	ggttacataa	agaaagcttt	caatgaagga	atggaagatg	540
gagaagagac	agctttcttt	gggactaaag	tcagccatta	ccctccttgt	cctcatcctg	600
agctagtcaa	tggccttcga	gctcatactg	atgcaggagg	tgtcgttttg	cttttccaag	660
acgatgaata	tgatggcctt	caggtcttga	aagacggcga	gtggatcgat	gttcagcctc	720
tacctaattg	cattgttatc	aacactgggtg	atcagattga	agttcttagc	aacggaaggt	780
acaagagtgc	gtggcacagg	gtgggtggcg	gggaggaagg	aaacagaagg	tctatagctt	840
ccttctacaa	tccgtcgtac	aaggcggcga	tagggccagc	cacggtggcg	gaagaggaag	900
gaagtggagaa	gaagtatcca	aagtttgtgt	ttggagatta	catggatggt	tatgcaaacc	960
agaagttcat	gcctaaagag	cctcgttttc	tagctgtaaa	gtctctctaa	atgtactatt	1020
ttattttatt	ttacagtact	atcactgttt	tatctacacc	cattatgtat	tttctcttaa	1080
gctataaatg	ccaaattata	tagttaaaaa	tttggcatct	gctctccagg	ctttatat	1140
ttttgttttt	ttttgttttg	ccatgtgatg	tatgaatctt	tcttgtgtga	cctatgttct	1200
tagtttttga	atataaatgt	gtgtgccttt	ttctt			

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

Met	Ala	Ile	Pro	Val	Ile	Asp	Phe	Ser	Lys	Leu	Asn	Gly	Glu	Glu	Arg
1				5					10					15	
Glu	Lys	Thr	Leu	Ser	Glu	Ile	Ala	Arg	Ala	Cys	Glu	Glu	Trp	Gly	Phe
			20					25					30		
Phe	Gln	Leu	Val	Asn	His	Gly	Ile	Pro	Leu	Glu	Leu	Leu	Asn	Lys	Val

35	40	45
Lys Lys Leu Ser Ser Asp Cys Tyr Lys Thr Glu Arg Glu Glu Ala Phe		
50	55	60
Lys Thr Ser Asn Pro Val Lys Leu Leu Asn Glu Leu Val Gln Lys Asn		
65	70	75
Ser Gly Glu Lys Leu Glu Asn Val Asp Trp Glu Asp Val Phe Thr Leu		
85	90	95
Leu Asp His Asn Gln Asn Glu Trp Pro Ser Lys Ile Lys Glu Thr Met		
100	105	110
Gly Glu Tyr Arg Glu Glu Val Arg Lys Leu Ala Ser Lys Met Met Glu		
115	120	125
Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile Lys Lys Ala		
130	135	140
Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe Phe Gly Thr		
145	150	155
Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu Val Asn Gly		
165	170	175
Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu Phe Gln Asp		
180	185	190
Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu Trp Ile Asp		
195	200	205
Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly Asp Gln Ile		
210	215	220
Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val Val		
225	230	235
Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn Pro		
245	250	255
Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Gly		
260	265	270
Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp Val		
275	280	285
Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala Val		
290	295	300
Lys Ser Leu		
305		

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1500799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

Met Gly Glu Tyr Arg Glu Glu Val Arg Lys Leu Ala Ser Lys Met Met		
1	5	10
Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile Lys Lys		
20	25	30
Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe Phe Gly		
35	40	45
Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu Val Asn		
50	55	60
Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu Phe Gln		
65	70	75
Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu Trp Ile		
85	90	95
Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly Asp Gln		
100	105	110

Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val
115 120 125
Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn
130 135 140
Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Glu
145 150 155 160
Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp
165 170 175
Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala
180 185 190
Val Lys Ser Leu
195

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Met Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile
1 5 10 15
Lys Lys Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe
20 25 30
Phe Gly Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu
35 40 45
Val Asn Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu
50 55 60
Phe Gln Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu
65 70 75 80
Trp Ile Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly
85 90 95
Asp Gln Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His
100 105 110
Arg Val Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe
115 120 125
Tyr Asn Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu
130 135 140
Glu Glu Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr
145 150 155 160
Met Asp Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe
165 170 175
Leu Ala Val Lys Ser Leu
180

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..619
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

acaccggcgt ttggctgmsa tcacgcagat gatacacact gcaagcttga tacacgacga

tgtgttagac	gagagtgaca	tgccaagagg	aaaggaaaca	gttcatgagc	ttttcggcac	120
aagagtagcg	gtgctagctg	gagatttcat	gtttgctcaa	gcgtcatggg	acttagcaaa	180
tctcgagaat	cttgaagtta	ttaagctcat	cagtcagggtg	atcaaagact	ttgcaagcgg	240
agagataaaag	caggcggtcca	gcttatttga	ctgcgacacc	aagctcgacg	agtacttact	300
caaaagtttc	tacaagacag	cctctttagt	ggctgcgagc	accaaaggag	ctgccatttt	360
cagcagagtt	gagcctgatg	tgacagaaca	aatgtacgag	tttggaaga	atctcgggtct	420
ctctttccag	atagttgatg	atattttgga	tttcactcag	tcgacagagc	agctcgggaa	480
gccagcaggg	agtgatttgg	ctaaaggtaa	cttaacagca	cctgtgattt	tcgctctgga	540
gagggagcca	aggctaagag	agatcattga	gtcagagttt	tgtgaggcgg	gttctctgga	600
agaagcgatt	gaagcgggtg					

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1500802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

His	Arg	Arg	Leu	Ala	Xaa	Ile	Ile	Glu	Met	Ile	His	Thr	Ala	Ser	Leu
1			5					10						15	
Ile	His	Asp	Asp	Val	Leu	Asp	Glu	Ser	Asp	Met	Arg	Arg	Gly	Lys	Glu
			20					25						30	
Thr	Val	His	Glu	Leu	Phe	Gly	Thr	Arg	Val	Ala	Val	Leu	Ala	Gly	Asp
		35					40						45		
Phe	Met	Phe	Ala	Gln	Ala	Ser	Trp	Tyr	Leu	Ala	Asn	Leu	Glu	Asn	Leu
	50					55					60				
Glu	Val	Ile	Lys	Leu	Ile	Ser	Gln	Val	Ile	Lys	Asp	Phe	Ala	Ser	Gly
65				70					75					80	
Glu	Ile	Lys	Gln	Ala	Ser	Ser	Leu	Phe	Asp	Cys	Asp	Thr	Lys	Leu	Asp
			85						90					95	
Glu	Tyr	Leu	Leu	Lys	Ser	Phe	Tyr	Lys	Thr	Ala	Ser	Leu	Val	Ala	Ala
		100						105					110		
Ser	Thr	Lys	Gly	Ala	Ala	Ile	Phe	Ser	Arg	Val	Glu	Pro	Asp	Val	Thr
		115					120					125			
Glu	Gln	Met	Tyr	Glu	Phe	Gly	Lys	Asn	Leu	Gly	Leu	Ser	Phe	Gln	Ile
	130					135					140				
Val	Asp	Asp	Ile	Leu	Asp	Phe	Thr	Gln	Ser	Thr	Glu	Gln	Leu	Gly	Lys
145				150						155				160	
Pro	Ala	Gly	Ser	Asp	Leu	Ala	Lys	Gly	Asn	Leu	Thr	Ala	Pro	Val	Ile
			165					170						175	
Phe	Ala	Leu	Glu	Arg	Glu	Pro	Arg	Leu	Arg	Glu	Ile	Ile	Glu	Ser	Glu
		180						185					190		
Phe	Cys	Glu	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Glu	Ala	Val			
	195					200					205				

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1500803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Met Ile His Thr Ala Ser Leu Ile His Asp Asp Val Leu Asp Glu Ser

```

1           5           10           15
Asp Met Arg Arg Gly Lys Glu Thr Val His Glu Leu Phe Gly Thr Arg
          20          25          30
Val Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ala Ser Trp Tyr
          35          40          45
Leu Ala Asn Leu Glu Asn Leu Glu Val Ile Lys Leu Ile Ser Gln Val
          50          55          60
Ile Lys Asp Phe Ala Ser Gly Glu Ile Lys Gln Ala Ser Ser Leu Phe
65          70          75          80
Asp Cys Asp Thr Lys Leu Asp Glu Tyr Leu Leu Lys Ser Phe Tyr Lys
          85          90          95
Thr Ala Ser Leu Val Ala Ala Ser Thr Lys Gly Ala Ala Ile Phe Ser
          100         105         110
Arg Val Glu Pro Asp Val Thr Glu Gln Met Tyr Glu Phe Gly Lys Asn
          115         120         125
Leu Gly Leu Ser Phe Gln Ile Val Asp Asp Ile Leu Asp Phe Thr Gln
          130         135         140
Ser Thr Glu Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Ala Lys Gly
145         150         155         160
Asn Leu Thr Ala Pro Val Ile Phe Ala Leu Glu Arg Glu Pro Arg Leu
          165         170         175
Arg Glu Ile Ile Glu Ser Glu Phe Cys Glu Ala Gly Ser Leu Glu Glu
          180         185         190
Ala Ile Glu Ala Val
          195
```

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1500804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

```

Met Arg Arg Gly Lys Glu Thr Val His Glu Leu Phe Gly Thr Arg Val
1           5           10           15
Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ala Ser Trp Tyr Leu
          20          25          30
Ala Asn Leu Glu Asn Leu Glu Val Ile Lys Leu Ile Ser Gln Val Ile
          35          40          45
Lys Asp Phe Ala Ser Gly Glu Ile Lys Gln Ala Ser Ser Leu Phe Asp
          50          55          60
Cys Asp Thr Lys Leu Asp Glu Tyr Leu Leu Lys Ser Phe Tyr Lys Thr
65          70          75          80
Ala Ser Leu Val Ala Ala Ser Thr Lys Gly Ala Ala Ile Phe Ser Arg
          85          90          95
Val Glu Pro Asp Val Thr Glu Gln Met Tyr Glu Phe Gly Lys Asn Leu
          100         105         110
Gly Leu Ser Phe Gln Ile Val Asp Asp Ile Leu Asp Phe Thr Gln Ser
          115         120         125
Thr Glu Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Ala Lys Gly Asn
          130         135         140
Leu Thr Ala Pro Val Ile Phe Ala Leu Glu Arg Glu Pro Arg Leu Arg
145         150         155         160
Glu Ile Ile Glu Ser Glu Phe Cys Glu Ala Gly Ser Leu Glu Glu Ala
          165         170         175
Ile Glu Ala Val
          180
```

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1776
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

```
gtctcatcac ttcccacttt cctctctgca tttgttgtct ctctctcctg aaaacccttg      60
aattttgcta cacgatctct gaaacgtgtc tctttgactg acttcaatct tctttatcac      120
ttaccgtttc tgggttttat gaagcaactg agctaataaa aagcttcttc ttagactcgg      180
aagaagaaaa aaaacagaat ctttattgtt taaagcttcc aaattcgaga agagaatttg      240
aaacgaccaa gttcaggata ttcgtttctt cgtctacttt ggtctcttcc tcttctcttt      300
cgaaaagggg ttattctgtc ttaaaagaaa cctttttgag agggtaaaaa aagcttcaat      360
tttcagagaa acacaaaagg cagaaacaga gaaaaacaaa tcatctaatt catgaaacag      420
ggttcaatga atagatcgtg tctctgtagt gtcttaatca ccactgctct gatttgggtg      480
gcttacttca tttgcaatgc ttatcttgct aaagacttta aagagaagtt gctgaagtgg      540
gaaatcactg ataagatgca taacagtact gataagatgc agaatgcaac aacaaccagt      600
acatgcaaga atttcaataa gccagtgggt actgaagcac taccgcaagg aattatcgag      660
aaaacatcga acctggaaac acaacatcta tgggaactacg atgacacaaa aaagagaagg      720
cctaaccatt cgatgagttt gttagccatg gcggtcggta tcaagcaaaa ggagctagtt      780
aacaaagtta tccaaaagtt tcctcctcga gatttcgcgg tcatgctttt tcattatgat      840
ggtgttgtcg atgactggaa gcagtatcca tgggaataatc atgcgattca tgtttccgtg      900
atgaatcaaaa caaaatggtg gttcgccaaag cgattcttgc atcccgatat agttgcagag      960
tacgagtata tatttctttg ggacgaagat cttggtgttg gtcatttcaa tcctcaacga      1020
tatctatcta ttgtcaaaga agaggggctt gagatatcgc aacctgctct tgacacttca      1080
aatcagaag tgcatcatcc tataaccgct cgtcaaaaaa aatcaaaaag tcatagaaga      1140
atgtataaat acaaaggtag cgggcgatgt gatgaaccata gcaccaatcc tccttgcac      1200
gggtgggtgg aaatgatggc acctgttttc tctagagctg catggagatg ttcttgggtat      1260
atgattcaga atgatttgat ccattgcttg ggtctggata cgcagcttgg ttattgtgct      1320
caaggtgacc gaaagaaaaa tgcggtgtgt gttgatgcgg agtacataat tcattatggt      1380
cttccaacac tcggtgtggt tgaaaccgct tcaagcgctt tgcggaatga gacagactcg      1440
aatcaacgg aatcattaga gtctcgtgaa gtggataata gaccagaagt gaggatgaaa      1500
tcatttggg agatgaagag attcaaggaa cgttggaaga aagctgtgag ggatgataca      1560
tggtgggttg atccgtattg aaatccgagc ggtttaagta aaccgaatcg aaccggattc      1620
ttttccttgt tgagtgtgct ttgtggtcca ttgtatacca ttattttggt acatagattt      1680
tgttttactt cgagaaaaat tagtgtattt atgtgtttta tggaccacag tgtagattta      1740
acattttgga gcattataca aaagtgtttt tgtgcc
```

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

```
Met Lys Gln Gly Ser Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile
1           5           10           15
Thr Thr Ala Leu Ile Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu
20           25           30
Ala Lys Asp Phe Lys Glu Lys Leu Leu Lys Trp Glu Ile Thr Asp Lys
35           40           45
Met His Asn Ser Thr Asp Lys Met Gln Asn Ala Thr Thr Thr Ser Thr
```

50		55		60	
Cys Lys Asn Phe Asn Lys Pro Val Gly Thr Glu Ala Leu Pro Gln Gly					
65		70		75	80
Ile Ile Glu Lys Thr Ser Asn Leu Glu Thr Gln His Leu Trp Asn Tyr					
	85		90		95
Asp Asp Thr Lys Lys Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala					
	100		105		110
Met Ala Val Gly Ile Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln					
	115		120		125
Lys Phe Pro Pro Arg Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly					
	130		135		140
Val Val Asp Asp Trp Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His					
145		150		155	160
Val Ser Val Met Asn Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu					
	165		170		175
His Pro Asp Ile Val Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu					
	180		185		190
Asp Leu Gly Val Gly His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val					
	195		200		205
Lys Glu Glu Gly Leu Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys					
	210		215		220
Ser Glu Val His His Pro Ile Thr Ala Arg Gln Lys Lys Ser Lys Val					
225		230		235	240
His Arg Arg Met Tyr Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His					
	245		250		255
Ser Thr Asn Pro Pro Cys Ile Gly Trp Val Glu Met Met Ala Pro Val					
	260		265		270
Phe Ser Arg Ala Ala Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp					
	275		280		285
Leu Ile His Ala Trp Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln					
	290		295		300
Gly Asp Arg Lys Lys Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile					
305		310		315	320
His Tyr Gly Leu Pro Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala					
	325		330		335
Leu Arg Asn Glu Thr Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg					
	340		345		350
Glu Val Asp Asn Arg Pro Glu Val Arg Met Lys Ser Phe Val Glu Met					
	355		360		365
Lys Arg Phe Lys Glu Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys					
	370		375		380
Trp Val Asp Pro Tyr					
385					

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile Thr Thr Ala Leu Ile		
1	5	10
Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu Ala Lys Asp Phe Lys		
	20	30
Glu Lys Leu Leu Lys Trp Glu Ile Thr Asp Lys Met His Asn Ser Thr		
	35	45

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Asp Lys Met Gln Asn Ala Thr Thr Thr Ser Thr Cys Lys Asn Phe Asn
50          55          60
Lys Pro Val Gly Thr Glu Ala Leu Pro Gln Gly Ile Ile Glu Lys Thr
65          70          75          80
Ser Asn Leu Glu Thr Gln His Leu Trp Asn Tyr Asp Asp Thr Lys Lys
85          90          95
Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala Met Ala Val Gly Ile
100         105         110
Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln Lys Phe Pro Pro Arg
115         120         125
Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly Val Val Asp Asp Trp
130         135         140
Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His Val Ser Val Met Asn
145         150         155         160
Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu His Pro Asp Ile Val
165         170         175
Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu Asp Leu Gly Val Gly
180         185         190
His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val Lys Glu Glu Gly Leu
195         200         205
Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys Ser Glu Val His His
210         215         220
Pro Ile Thr Ala Arg Gln Lys Lys Ser Lys Val His Arg Arg Met Tyr
225         230         235         240
Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His Ser Thr Asn Pro Pro
245         250         255
Cys Ile Gly Trp Val Glu Met Met Ala Pro Val Phe Ser Arg Ala Ala
260         265         270
Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp Leu Ile His Ala Trp
275         280         285
Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln Gly Asp Arg Lys Lys
290         295         300
Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile His Tyr Gly Leu Pro
305         310         315         320
Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala Leu Arg Asn Glu Thr
325         330         335
Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg Glu Val Asp Asn Arg
340         345         350
Pro Glu Val Arg Met Lys Ser Phe Val Glu Met Lys Arg Phe Lys Glu
355         360         365
Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys Trp Val Asp Pro Tyr
370         375         380

```

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

```

Met His Asn Ser Thr Asp Lys Met Gln Asn Ala Thr Thr Thr Ser Thr
1          5          10          15
Cys Lys Asn Phe Asn Lys Pro Val Gly Thr Glu Ala Leu Pro Gln Gly
20         25         30
Ile Ile Glu Lys Thr Ser Asn Leu Glu Thr Gln His Leu Trp Asn Tyr

```

(A1) SEQUENCE ALIGNMENT: 1200 bp						
aacctccact	gttaataaac	tcaaacctct	gcaattgtct	tcttctcttc	aactccatca	60
tctccaccac	cggcattctc	gccggaatcc	aatggagctt	accagcttcc	atcgctcttc	120
tctcttattc	ctcatctcac	taacattgat	cattctcccg	acgacaacaa	cttcaatcgg	180
agtaaaactac	ggtcaaatacg	gagacaacct	cccctcccca	accgacgtaa	tcccactaat	240
aaaatcaatc	ggagcaacaa	aagtaaaact	ctacgacgca	aatccacaaa	tcctcaaagc	300
tttctccaac	accggaatcg	aattcatcat	cggactcggc	aacgaatacc	tctccaaaat	360
gaaagatcct	tcaaaaagcct	taacatggat	caaacaaaac	gttactccat	ttttacctgc	420
gactaacatc	acatgcataa	ctatcggtaa	cgaaatcttc	gctctcaacg	actcttcaact	480
cactaccaat	ctcctcccag	cgatgcaagg	agttcactct	gctttaatca	cgcgcgggtct	540
ctc						

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

Thr	Ser	Thr	Val	Asn	Lys	Leu	Lys	Pro	Leu	Gln	Leu	Ser	Ser	Ser	Leu	
1				5					10					15		
Gln	Leu	His	His	Leu	His	His	Arg	His	Ser	Arg	Arg	Asn	Pro	Met	Glu	
			20					25					30			
Leu	Thr	Ser	Phe	His	Arg	Ser	Ser	Leu	Leu	Phe	Leu	Ile	Ser	Leu	Thr	
		35					40					45				
Leu	Ile	Ile	Leu	Pro	Thr	Thr	Thr	Thr	Ser	Ile	Gly	Val	Asn	Tyr	Gly	
	50					55					60					
Gln	Ile	Gly	Asp	Asn	Leu	Pro	Ser	Pro	Thr	Asp	Val	Ile	Pro	Leu	Ile	
65				70						75				80		
Lys	Ser	Ile	Gly	Ala	Thr	Lys	Val	Lys	Leu	Tyr	Asp	Ala	Asn	Pro	Gln	
			85						90				95			
Ile	Leu	Lys	Ala	Phe	Ser	Asn	Thr	Gly	Ile	Glu	Phe	Ile	Ile	Gly	Leu	
			100					105					110			
Gly	Asn	Glu	Tyr	Leu	Ser	Lys	Met	Lys	Asp	Pro	Ser	Lys	Ala	Leu	Thr	
	115					120						125				
Trp	Ile	Lys	Gln	Asn	Val	Thr	Pro	Phe	Leu	Pro	Ala	Thr	Asn	Ile	Thr	
	130					135					140					
Cys	Ile	Thr	Ile	Gly	Asn	Glu	Ile	Leu	Ala	Leu	Asn	Asp	Ser	Ser	Leu	
145					150					155				160		
Thr	Thr	Asn	Leu	Leu	Pro	Ala	Met	Gln	Gly	Val	His	Ser	Ala	Leu	Ile	
			165					170						175		
Thr	Ala	Gly	Leu													
			180													

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

Met	Glu	Leu	Thr	Ser	Phe	His	Arg	Ser	Ser	Leu	Leu	Phe	Leu	Ile	Ser	
1				5					10					15		
Leu	Thr	Leu	Ile	Ile	Leu	Pro	Thr	Thr	Thr	Thr	Ser	Ile	Gly	Val	Asn	
			20					25					30			
Tyr	Gly	Gln	Ile	Gly	Asp	Asn	Leu	Pro	Ser	Pro	Thr	Asp	Val	Ile	Pro	
	35					40					45					
Leu	Ile	Lys	Ser	Ile	Gly	Ala	Thr	Lys	Val	Lys	Leu	Tyr	Asp	Ala	Asn	
	50					55				60						
Pro	Gln	Ile	Leu	Lys	Ala	Phe	Ser	Asn	Thr	Gly	Ile	Glu	Phe	Ile	Ile	
65				70						75				80		
Gly	Leu	Gly	Asn	Glu	Tyr	Leu	Ser	Lys	Met	Lys	Asp	Pro	Ser	Lys	Ala	
			85					90					95			
Leu	Thr	Trp	Ile	Lys	Gln	Asn	Val	Thr	Pro	Phe	Leu	Pro	Ala	Thr	Asn	

100 105 110
Ile Thr Cys Ile Thr Ile Gly Asn Glu Ile Leu Ala Leu Asn Asp Ser
115 120 125
Ser Leu Thr Thr Asn Leu Leu Pro Ala Met Gln Gly Val His Ser Ala
130 135 140
Leu Ile Thr Ala Gly Leu
145 150

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

caagtgatca aacaaaaaav gaccaagtct ttttggtwtt tcagatcgag aaaaaatgtg	60
gttgcaaggt ttgaagtaat cttgcaatgg attctttgac tggatttaga atggaaccca	120
aatggcaaat tgatcctcag cttctctttg ttggtccaaa gattggtgaa ggagctcatg	180
ctaaagtcta tgagggaaaa tacaagaatc agacagttgc tataaagata gttcacagag	240
gagaaacacc agaagagatt gctaaaagag attcaagatt ccttagagaa gtagaaatgc	300
tctcagctgt tcaacacaag aatttgggtca agttcattgg tgcttgcaag gagcctgtaa	360
tggtgatagt tacagaactt cttcaaggcg gtacattgcg taaatatcta ttaaaacttga	420
gacccgcatg tttggagact cgtgtggcta tcggttttgc gcttgatatt gctcgtggta	480
tggaatgctt gcattcccat gggatcattc accgtgatct caaacccgag aacttgcttt	540
taactgcaga ccataaaaca gtaaaactag cagattttgg attagcaaga gaagagtcac	600
tgactgagat gatgacggct gagacaggaa cataccgatg gatggcacct gagttgtaca	660
gcacgggt	

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

Met Asp Ser Leu Thr Gly Phe Arg Met Glu Pro Lys Trp Gln Ile Asp	
1 5 10 15	
Pro Gln Leu Leu Phe Val Gly Pro Lys Ile Gly Glu Gly Ala His Ala	
20 25 30	
Lys Val Tyr Glu Gly Lys Tyr Lys Asn Gln Thr Val Ala Ile Lys Ile	
35 40 45	
Val His Arg Gly Glu Thr Pro Glu Glu Ile Ala Lys Arg Asp Ser Arg	
50 55 60	
Phe Leu Arg Glu Val Glu Met Leu Ser Arg Val Gln His Lys Asn Leu	
65 70 75 80	
Val Lys Phe Ile Gly Ala Cys Lys Glu Pro Val Met Val Ile Val Thr	
85 90 95	
Glu Leu Leu Gln Gly Gly Thr Leu Arg Lys Tyr Leu Leu Asn Leu Arg	
100 105 110	
Pro Ala Cys Leu Glu Thr Arg Val Ala Ile Gly Phe Ala Leu Asp Ile	
115 120 125	
Ala Arg Gly Met Glu Cys Leu His Ser His Gly Ile Ile His Arg Asp	
130 135 140	

Leu Lys Pro Glu Asn Leu Leu Leu Thr Ala Asp His Lys Thr Val Lys
145 150 155 160
Leu Ala Asp Phe Gly Leu Ala Arg Glu Glu Ser Leu Thr Glu Met Met
165 170 175
Thr Ala Glu Thr Gly Thr Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser
180 185 190
Thr

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..185

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Glu Pro Lys Trp Gln Ile Asp Pro Gln Leu Leu Phe Val Gly Pro
1 5 10 15
Lys Ile Gly Glu Gly Ala His Ala Lys Val Tyr Glu Gly Lys Tyr Lys
20 25 30
Asn Gln Thr Val Ala Ile Lys Ile Val His Arg Gly Glu Thr Pro Glu
35 40 45
Glu Ile Ala Lys Arg Asp Ser Arg Phe Leu Arg Glu Val Glu Met Leu
50 55 60
Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala Cys Lys
65 70 75 80
Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly Thr Leu
85 90 95
Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr Arg Val
100 105 110
Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys Leu His
115 120 125
Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
130 135 140
Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu Ala Arg
145 150 155 160
Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr Tyr Arg
165 170 175
Trp Met Ala Pro Glu Leu Tyr Ser Thr
180 185

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..123

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Leu Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala
1 5 10 15
Cys Lys Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly
20 25 30
Thr Leu Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr

```

      35              40              45
Arg Val Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys
  50              55              60
Leu His Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu
  65              70              75              80
Leu Leu Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu
      85              90              95
Ala Arg Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr
      100              105              110
Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser Thr
      115              120
```

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1887
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

```

cacacattct tgcagaaggt tttagaatca caaagcataa ctcacctacc cctaaaccaa      60
ctccaatttc tctcctcctc tattaatatct ttctcaatca tctttctttg agtcttttgc      120
cttggaatcc tgatcatggc gtcttctctc acttccaaat ccattcctcg gatgcaccaa      180
accgcttct tcttcttttc tatccgctcg agctccgctg tctctcttct cccgcccgtt      240
agatatctct ccattcacaa accaggaaga acttccggca gtcgtgggga ttgaagaaga      300
gtgatctgat gctaaatggg tctgagattc gtcctgtgaa ggtaggggct tctgtttcca      360
cggcgagaaa agcttcggag attgtgcttc aaccattag agaaatctcg ggtctcatta      420
agcttccctg ctccaagtct ctctctaata gaattctgct tctcgctgct ctatctgagg      480
gaactacttg agtggacaac ttgttgaaca gtgatgacat caattacatg cttgatgcgt      540
tgaagatatt gggacttaat gtggaaactc acagtgaaaa caatcgtgct gtagttgaag      600
gatgtggcgg ggtatttcca gcttccattg attccaagag tgatatcgaa ctttacctcg      660
gcaatgcagg aacagcaatg cgtccactta ccgccgcagt tactgctgca ggtggcaacg      720
caagtatatg ccttgatggg gtgcctcaga tgagagagag acctataggg gatttggttg      780
ttggtcttaa gcagcttgg gtgatgttg aatgtactct tggcactaac tgccctcctg      840
ttcgtgtcaa cgctaattgg ggccttccct gtggaaagggt gaagctttct ggatctatta      900
ttagaattgt cgataaattg atttctgttc cgtatgttga aatgacattg aagttgatgg      960
aacgttttgg ggtaagtgt gagcatagt aaagctggga tcgtttcttt gttaagggtg      1020
ggcaaaaata caagtcgccg ggtaatgctt acgtagaagg tgatgcttct agtgctagtt      1080
atttcttggc tgggtgtgcc attaccggtg aaactgtcac tgttgaagggt tgtggaacga      1140
ccagtttgca gggagatgtg aaatttgccg aggttcttga gaaaatggga tgtaaagtgt      1200
cctggacaga gaacagtgtg actgtgacag ggccgtctag agatgctttt ggaatgagac      1260
acttgccggc tattgatgtc aacatgaaca aaatgcctga tgtagcaatg actcttgccg      1320
tcgttgctct ctttgccgat ggtccaacca ccattagaga tgtggctagc tggagagtaa      1380
aggagacgga aaggatgatt gccatttgca cagagcttag aaaactggga gctacagtgg      1440
aagaaggttc agattattgt gtgattactc cgccgaaaaa ggtgaaaccg gcagagattg      1500
atacatatga tgatcataga atggcaatgg cattctctct tgcagcttgt gctgatgttc      1560
caatcaccat caatgacccc ggttgaccca ggaaaacctt ccccgactac ttccaagtcc      1620
ttgaaagaat cacaaagcat taaacaaaaa aactctaaaa tctccactgt tttttcttct      1680
gatccaagct tatctgtttc catttttctt gtctctgtaa cattattaga aagcaagagt      1740
agtgtttgtt tgtgtgtacc tgaactgagt gagatttgag atgcaatcat tgaatcggct      1800
ttggtatatc attttactct gttttcc
```

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1500829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

Met	Leu	Asn	Gly	Ser	Glu	Ile	Arg	Pro	Val	Lys	Val	Arg	Ala	Ser	Val
1				5					10					15	
Ser	Thr	Ala	Glu	Lys	Ala	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Arg	Glu
		20						25					30		
Ile	Ser	Gly	Leu	Ile	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg
		35					40					45			
Ile	Leu	Leu	Leu	Ala	Ala	Leu	Ser	Glu	Gly	Thr	Thr	Val	Val	Asp	Asn
	50					55					60				
Leu	Leu	Asn	Ser	Asp	Asp	Ile	Asn	Tyr	Met	Leu	Asp	Ala	Leu	Lys	Ile
65				70						75				80	
Leu	Gly	Leu	Asn	Val	Glu	Thr	His	Ser	Glu	Asn	Asn	Arg	Ala	Val	Val
			85						90					95	
Glu	Gly	Cys	Gly	Gly	Val	Phe	Pro	Ala	Ser	Ile	Asp	Ser	Lys	Ser	Asp
		100						105					110		
Ile	Glu	Leu	Tyr	Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr
	115					120						125			
Ala	Ala	Val	Thr	Ala	Ala	Gly	Gly	Asn	Ala	Ser	Tyr	Val	Leu	Asp	Gly
	130					135					140				
Val	Pro	Gln	Met	Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu
145					150					155				160	
Lys	Gln	Leu	Gly	Ala	Asp	Val	Glu	Cys	Thr	Leu	Gly	Thr	Asn	Cys	Pro
			165					170					175		
Pro	Val	Arg	Val	Asn	Ala	Asn	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys
		180					185					190			
Leu	Ser	Gly	Ser	Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala
	195						200					205			
Ala	Pro	Leu	Ala	Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Val	Asp	Lys	Leu
	210				215						220				
Ile	Ser	Val	Pro	Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe
225				230						235				240	
Gly	Val	Ser	Ala	Glu	His	Ser	Glu	Ser	Trp	Asp	Arg	Phe	Phe	Val	Lys
			245					250						255	
Gly	Gly	Gln	Lys	Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Tyr	Val	Glu	Gly	Asp
		260						265					270		
Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Glu
	275					280						285			
Thr	Val	Thr	Val	Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val
	290					295					300				
Lys	Phe	Ala	Glu	Val	Leu	Glu	Lys	Met	Gly	Cys	Lys	Val	Ser	Trp	Thr
305				310						315				320	
Glu	Asn	Ser	Val	Thr	Val	Thr	Gly	Pro	Ser	Arg	Asp	Ala	Phe	Gly	Met
			325					330					335		
Arg	His	Leu	Arg	Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val
		340					345						350		
Ala	Met	Thr	Leu	Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Thr
	355						360					365			
Ile	Arg	Asp	Val	Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile
	370				375						380				
Ala	Ile	Cys	Thr	Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Glu	Glu	Gly
385				390						395				400	
Ser	Asp	Tyr	Cys	Val	Ile	Thr	Pro	Pro	Lys	Lys	Val	Lys	Pro	Ala	Glu
			405						410					415	
Ile	Asp	Thr	Tyr	Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala
		420					425					430			
Ala	Cys	Ala	Asp	Val	Pro	Ile	Thr	Ile	Asn	Asp	Pro	Gly	Cys	Thr	Arg

	435		440		445	
Lys	Thr	Phe	Pro	Asp	Tyr	Phe
						Gln
						Val
						Leu
						Glu
						Arg
						Ile
						Thr
						Lys
						His
450						460

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

Met	Leu	Asp	Ala	Leu	Lys	Ile	Leu	Gly	Leu	Asn	Val	Glu	Thr	His	Ser
1				5					10					15	
Glu	Asn	Asn	Arg	Ala	Val	Val	Glu	Gly	Cys	Gly	Gly	Val	Phe	Pro	Ala
			20					25					30		
Ser	Ile	Asp	Ser	Lys	Ser	Asp	Ile	Glu	Leu	Tyr	Leu	Gly	Asn	Ala	Gly
			35				40					45			
Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr	Ala	Ala	Gly	Gly	Asn
			50			55				60					
Ala	Ser	Tyr	Val	Leu	Asp	Gly	Val	Pro	Gln	Met	Arg	Glu	Arg	Pro	Ile
65					70				75					80	
Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	Gly	Ala	Asp	Val	Glu	Cys
				85					90					95	
Thr	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Val	Asn	Ala	Asn	Gly	Gly
			100					105					110		
Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	Ile	Ser	Ser	Gln	Tyr
			115				120					125			
Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	Leu	Gly	Asp	Val	Glu
			130			135					140				
Ile	Glu	Ile	Val	Asp	Lys	Leu	Ile	Ser	Val	Pro	Tyr	Val	Glu	Met	Thr
145					150				155					160	
Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Ala	Glu	His	Ser	Glu	Ser
				165					170					175	
Trp	Asp	Arg	Phe	Phe	Val	Lys	Gly	Gly	Gln	Lys	Tyr	Lys	Ser	Pro	Gly
			180				185						190		
Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala
			195				200					205			
Gly	Ala	Ala	Ile	Thr	Gly	Glu	Thr	Val	Thr	Val	Glu	Gly	Cys	Gly	Thr
			210			215					220				
Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	Val	Leu	Glu	Lys	Met
225					230					235				240	
Gly	Cys	Lys	Val	Ser	Trp	Thr	Glu	Asn	Ser	Val	Thr	Val	Thr	Gly	Pro
				245					250					255	
Ser	Arg	Asp	Ala	Phe	Gly	Met	Arg	His	Leu	Arg	Ala	Ile	Asp	Val	Asn
			260					265					270		
Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	Ala	Val	Val	Ala	Leu
			275				280						285		
Phe	Ala	Asp	Gly	Pro	Thr	Thr	Ile	Arg	Asp	Val	Ala	Ser	Trp	Arg	Val
			290			295					300				
Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys	Thr	Glu	Leu	Arg	Lys	Leu
305					310				315					320	
Gly	Ala	Thr	Val	Glu	Glu	Gly	Ser	Asp	Tyr	Cys	Val	Ile	Thr	Pro	Pro
				325					330					335	
Lys	Lys	Val	Lys	Pro	Ala	Glu	Ile	Asp	Thr	Tyr	Asp	Asp	His	Arg	Met
			340					345					350		

Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile
355 360 365
Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val
370 375 380
Leu Glu Arg Ile Thr Lys His
385 390

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

Met Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Ser
1 5 10 15
Tyr Val Leu Asp Gly Val Pro Gln Met Arg Glu Arg Pro Ile Gly Asp
20 25 30
Leu Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu
35 40 45
Gly Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro
50 55 60
Gly Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr
65 70 75 80
Ala Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu
85 90 95
Ile Val Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys
100 105 110
Leu Met Glu Arg Phe Gly Val Ser Ala Glu His Ser Glu Ser Trp Asp
115 120 125
Arg Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala
130 135 140
Tyr Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala
145 150 155 160
Ala Ile Thr Gly Glu Thr Val Thr Val Glu Gly Cys Gly Thr Thr Ser
165 170 175
Leu Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys
180 185 190
Lys Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly Pro Ser Arg
195 200 205
Asp Ala Phe Gly Met Arg His Leu Arg Ala Ile Asp Val Asn Met Asn
210 215 220
Lys Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala
225 230 235 240
Asp Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu
245 250 255
Thr Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala
260 265 270
Thr Val Glu Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Lys Lys
275 280 285
Val Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met
290 295 300
Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile Asn Asp
305 310 315 320
Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu
325 330 335
Arg Ile Thr Lys His

(2) INFORMATION FOR SEQ ID NO:1661:

(A) LENGTH: 1673 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1673

(D) OTHER INFORMATION: / Ceres Seq. ID 1500832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:101				
aacgaggtctg	tggagaaaaag	aaccaaaaagt	gactgttggt	agagatgagg aatgcagagc 60
tcatacttcot	cccaacaccca	actgttggtc	atcttgttcc	gtttcttgaa tttgctaggc 120
gtctcattga	gcaggatgat	aaaatccgta	tcaccttcct	cttgatgaag caacaaggtc 180
agtctcatct	ggattcctat	gttaagacaa	tttcctcgtc	tctgccgttt gttagattta 240
ttgatgtccc	tgagttagag	gagaaaccaa	cacttggtac	acagtctgtg gaagcctatg 300
gtgtacgatt	ttattgaaac	aaatgtccct	cttgtgcaaa	atataatcat gggtaacctta 360
tcttctcctg	cattttgatgg	agttacggtc	aagggatctg	ttgtgtgatt tttctgtctc 420
ccgatgatgg	atgttgcaaa	agatgcaagt	cttccttttt	atgtgtttct gacttcaaatt 480
tcgggattcc	tagctatgat	gcagtatctg	gcatatggac	ataagaaaga tacctcagtt 540
tttgcaagaa	actctgaaga	aatgttgtca	attcctggat	ttgtaaaccg tgtcccagcc 600
aaagtactgc	cgtcagctct	gtttattgag	gatggttatg	atgctgacgt taaactggct 660
atattgttta	caaaggctaa	tggaatccta	gtgaatacct	cctttgatat tgagcctacc 720
tctctgaatc	atthttcttga	agaagagaat	tacccttctg	tttatgtgtg ttgcccata 780
tttaaacccga	aggcccattc	tcattccgat	caagacctcg	ctgtgtgtga cgagtcgatg 840
aaatggcttg	atgtccaacc	cgaggcatca	gttgtattcc	tttgttttgg gagtatgggt 900
agcttaagag	gtcctctagt	gaaggaaata	gcacatggac	ttgagctatg tcagtataga 960
ttcctctggt	cactccgcac	agaagaagtg	acaaatgatg	atcctttgcc agadggattc 1020
atggaccgtg	tcagtgggacg	gggaatgata	tgcggttggt	ctcctcaggt ggaaatactg 1080
gcccataaag	cagtggggagg	ttttgttttc	catttgtggat	ggaactcaat agtagagagt 1140
ttatggtttg	gtgtgccaat	tgtgacatgg	cccaatgtat	gcagagcaac agctcaatgc 1200
gtttctgatg	gtgaaggaaac	tgaagctcgc	agtgagctg	aaactcgatt atagtgtaca 1260
tagtggtgag	attgtaaagt	caaacgagat	agagacagcg	atthcttgtg taatgaacaa 1320
cgataataat	gttgtgagga	aacgagtgat	ggatatctcg	cagatgatcc agagagctac 1380
gaagaatggt	ggatcttcgt	ttgccgcaat	tgagaaattc	atacatgacg tgataggaac 1440
caggacttag	cctttcttat	cggattcttc	ataaactgta	acctgattat gcaacagtc 1500
tttgaatctg	ctttgtttct	aatatttttt	tctattcttt	tgtcatcagc tttgtcttta 1560
actttgtctg	tgttgattcc	tttatctaac	aagctgtgag	tttctttgtt agccaatgct 1620
gcattttctc	tgttatggat	tttgttcaaa	attgggtaca	tctcttattc ttt

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1500833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

(A1) SEQUENCE DESCRIPTION															
Met	Val	Tyr	Asp	Phe	Ile	Glu	Thr	Asn	Val	Pro	Leu	Val	Gln	Asn	Ile
1				5					10					15	
Ile	Met	Gly	Ile	Leu	Ser	Ser	Pro	Ala	Phe	Asp	Gly	Val	Thr	Val	Lys
			20					25					30		
Gly	Phe	Val	Ala	Asp	Phe	Phe	Cys	Leu	Pro	Met	Ile	Asp	Val	Ala	Lys
			35				40					45			
Asp	Ala	Ser	Leu	Pro	Phe	Tyr	Val	Phe	Leu	Thr	Ser	Asn	Ser	Gly	Phe
	50					55				60					

Leu Ala Met Met Gln Tyr Leu Ala Tyr Gly His Lys Lys Asp Thr Ser
65 70 75 80
Val Phe Ala Arg Asn Ser Glu Glu Met Leu Ser Ile Pro Gly Phe Val
85 90 95
Asn Pro Val Pro Ala Lys Val Leu Pro Ser Ala Leu Phe Ile Glu Asp
100 105 110
Gly Tyr Asp Ala Asp Val Lys Leu Ala Ile Leu Phe Thr Lys Ala Asn
115 120 125
Gly Ile Leu Val Asn Thr Ser Phe Asp Ile Glu Pro Thr Ser Leu Asn
130 135 140
His Phe Leu Glu Glu Glu Asn Tyr Pro Ser Val Tyr Ala Val Gly Pro
145 150 155 160
Ile Phe Asn Pro Lys Ala His Pro His Pro Asp Gln Asp Leu Ala Cys
165 170 175
Cys Asp Glu Ser Met Lys Trp Leu Asp Ala Gln Pro Glu Ala Ser Val
180 185 190
Val Phe Leu Cys Phe Gly Ser Met Gly Ser Leu Arg Gly Pro Leu Val
195 200 205
Lys Glu Ile Ala His Gly Leu Glu Leu Cys Gln Tyr Arg Phe Leu Trp
210 215 220
Ser Leu Arg Thr Glu Glu Val Thr Asn Asp Asp Leu Leu Pro Xaa Gly
225 230 235 240
Phe Met Asp Arg Val Ser Gly Arg Gly Met Ile Cys Gly Trp Ser Pro
245 250 255
Gln Val Glu Ile Leu Ala His Lys Ala Val Gly Gly Phe Val Ser His
260 265 270
Cys Gly Trp Asn Ser Ile Val Glu Ser Leu Trp Phe Gly Val Pro Ile
275 280 285
Val Thr Trp Pro Asn Val Cys Arg Ala Thr Ala Gln Cys Val Ser Asp
290 295 300
Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala Glu Thr Arg Leu
305 310 315

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1500834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

Met Gly Ile Leu Ser Ser Pro Ala Phe Asp Gly Val Thr Val Lys Gly
1 5 10 15
Phe Val Ala Asp Phe Phe Cys Leu Pro Met Ile Asp Val Ala Lys Asp
20 25 30
Ala Ser Leu Pro Phe Tyr Val Phe Leu Thr Ser Asn Ser Gly Phe Leu
35 40 45
Ala Met Met Gln Tyr Leu Ala Tyr Gly His Lys Lys Asp Thr Ser Val
50 55 60
Phe Ala Arg Asn Ser Glu Glu Met Leu Ser Ile Pro Gly Phe Val Asn
65 70 75 80
Pro Val Pro Ala Lys Val Leu Pro Ser Ala Leu Phe Ile Glu Asp Gly
85 90 95
Tyr Asp Ala Asp Val Lys Leu Ala Ile Leu Phe Thr Lys Ala Asn Gly
100 105 110
Ile Leu Val Asn Thr Ser Phe Asp Ile Glu Pro Thr Ser Leu Asn His
115 120 125
Phe Leu Glu Glu Glu Asn Tyr Pro Ser Val Tyr Ala Val Gly Pro Ile

130	135	140
Phe Asn Pro Lys Ala His	Pro His Pro Asp Gln	Asp Leu Ala Cys Cys
145	150	155
Asp Glu Ser Met Lys Trp	Leu Asp Ala Gln Pro	Glu Ala Ser Val Val
165	170	175
Phe Leu Cys Phe Gly Ser	Met Gly Ser Leu Arg	Gly Pro Leu Val Lys
180	185	190
Glu Ile Ala His Gly Leu	Glu Leu Cys Gln Tyr	Arg Phe Leu Trp Ser
195	200	205
Leu Arg Thr Glu Glu Val	Thr Asn Asp Asp Leu	Leu Pro Xaa Gly Phe
210	215	220
Met Asp Arg Val Ser Gly	Arg Gly Met Ile Cys	Gly Trp Ser Pro Gln
225	230	235
Val Glu Ile Leu Ala His	Lys Ala Val Gly Gly	Phe Val Ser His Cys
245	250	255
Gly Trp Asn Ser Ile Val	Glu Ser Leu Trp Phe	Gly Val Pro Ile Val
260	265	270
Thr Trp Pro Asn Val Cys	Arg Ala Thr Ala Gln	Cys Val Ser Asp Gly
275	280	285
Glu Gly Thr Glu Ala Arg	Ser Gly Ala Glu Thr	Arg Leu
290	295	300

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1500835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

Met Ile Asp Val Ala Lys	Asp Ala Ser Leu Pro	Phe Tyr Val Phe Leu
1	5	10
Thr Ser Asn Ser Gly Phe	Leu Ala Met Met Gln Tyr	Leu Ala Tyr Gly
20	25	30
His Lys Lys Asp Thr Ser	Val Phe Ala Arg Asn Ser	Glu Glu Met Leu
35	40	45
Ser Ile Pro Gly Phe Val	Asn Pro Val Pro Ala Lys	Val Leu Pro Ser
50	55	60
Ala Leu Phe Ile Glu Asp	Gly Tyr Asp Ala Asp	Val Lys Leu Ala Ile
65	70	75
Leu Phe Thr Lys Ala Asn	Gly Ile Leu Val Asn Thr	Ser Phe Asp Ile
85	90	95
Glu Pro Thr Ser Leu Asn	His Phe Leu Glu Glu	Glu Asn Tyr Pro Ser
100	105	110
Val Tyr Ala Val Gly Pro	Ile Phe Asn Pro Lys Ala	His Pro His Pro
115	120	125
Asp Gln Asp Leu Ala Cys	Cys Asp Glu Ser Met Lys	Trp Leu Asp Ala
130	135	140
Gln Pro Glu Ala Ser Val	Val Phe Leu Cys Phe Gly	Ser Met Gly Ser
145	150	155
Leu Arg Gly Pro Leu Val	Lys Glu Ile Ala His Gly	Leu Glu Leu Cys
165	170	175
Gln Tyr Arg Phe Leu Trp	Ser Leu Arg Thr Glu Glu	Val Thr Asn Asp
180	185	190
Asp Leu Leu Pro Xaa Gly	Phe Met Asp Arg Val Ser	Gly Arg Gly Met
195	200	205
Ile Cys Gly Trp Ser Pro	Gln Val Glu Ile Leu Ala	His Lys Ala Val
210	215	220

Gly Gly Phe Val Ser His Cys Gly Trp Asn Ser Ile Val Glu Ser Leu
225 230 235 240
Trp Phe Gly Val Pro Ile Val Thr Trp Pro Asn Val Cys Arg Ala Thr
245 250 255
Ala Gln Cys Val Ser Asp Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala
260 265 270
Glu Thr Arg Leu
275

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..566
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

actacgaatt tagcacatag cccgagctcc gatcatgtca tcttgctccg acgaagcgat	60
tcccggccaa ccaatcgctc tcggttggtg tcaactttgt ctagattact tagtcacagt	120
ggcgtctttt ccaattcccg atcaaaagat cccgagccaca agcttcaagg tccaaggagt	180
tggttaacact gggaatgctt taacatgtgt tgctcgtttg ggtttgctt gtcgaatctt	240
ggctaagggt gctgatgatt ctacgggcg atatatggta gaagaactcg aatctagcgg	300
tgtggatact tcgttttgta tgagtgtctaa agatggagct tcacatttta attacgtcat	360
tgtagataac caaacgaata ctctacttg tatttacact ccaggatatc ctcttttgct	420
accagatgac cttactgaat ctctacttct agatgttctt gatggagtaa gagttctata	480
tgtaaatgga aggtcccgtg aagccgaatt gcttcttgcg caaaaggcac atagcaagaa	540
atataccaat cttaattaat gcagag	

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

Met Ser Ser Cys Ser Asp Glu Ala Ile Pro Gly Gln Pro Ile Val Leu	
1 5 10 15	
Gly Cys Gly Gln Leu Cys Leu Asp Tyr Leu Val Thr Val Ala Ser Phe	
20 25 30	
Pro Ile Pro Asp Gln Lys Ile Arg Gly Thr Ser Phe Lys Val Gln Gly	
35 40 45	
Val Gly Asn Thr Gly Asn Ala Leu Thr Cys Val Ala Arg Leu Gly Leu	
50 55 60	
Pro Cys Arg Ile Leu Ala Lys Val Ala Asp Asp Ser His Gly Arg Tyr	
65 70 75 80	
Met Val Glu Glu Leu Glu Ser Ser Gly Val Asp Thr Ser Phe Cys Met	
85 90 95	
Ser Ala Lys Asp Gly Ala Ser His Phe Asn Tyr Val Ile Val Asp Asn	
100 105 110	
Gln Thr Asn Thr Arg Thr Cys Ile Tyr Thr Pro Gly Tyr Pro Pro Leu	
115 120 125	
Leu Pro Asp Asp Leu Thr Glu Ser Leu Leu Leu Asp Val Leu Asp Gly	
130 135 140	
Val Arg Val Leu Tyr Val Asn Gly Arg Ser Arg Glu Ala Glu Leu Leu	

160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..94

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500838

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 100															
Met	Val	Glu	Glu	Leu	Glu	Ser	Ser	Gly	Val	Asp	Thr	Ser	Phe	Cys	Met
1				5					10					15	
Ser	Ala	Lys	Asp	Gly	Ala	Ser	His	Phe	Asn	Tyr	Val	Ile	Val	Asp	Asn
			20					25					30		
Gln	Thr	Asn	Thr	Arg	Thr	Cys	Ile	Tyr	Thr	Pro	Gly	Tyr	Pro	Pro	Leu
		35					40					45			
Leu	Pro	Asp	Asp	Leu	Thr	Glu	Ser	Leu	Leu	Leu	Asp	Val	Leu	Asp	Gly
	50					55					60				
Val	Arg	Val	Leu	Tyr	Val	Asn	Gly	Arg	Ser	Arg	Glu	Ala	Glu	Leu	Leu
65				70						75					80
Leu	Ala	Gln	Lys	Ala	His	Ser	Lys	Lys	Tyr	Thr	Asn	Leu	Asn		
				85					90						

(2) INFORMATION FOR SEQ ID NO:1668:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- ```
{ix) FEATURE:
```

- (A) NAME/KEY: -

- (B) LOCATION: 1..581

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500847

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1000 |            |              |            |            |             |     |
|-------------------------------------------|------------|--------------|------------|------------|-------------|-----|
| aataaacaaa                                | aaattaatac | aacaagatcc   | tgctatgtcg | tccacggcga | gaaatatattc | 60  |
| tggcagcggg                                | aaccgaaagt | cgagtaggct   | gcagcggcgg | gctccaccgc | ctcttaagat  | 120 |
| aaacccttgc                                | gaacgaantt | ggaaagtggc   | tattcctctt | ctatcaccta | cggagtcgcc  | 180 |
| gccacagaaa                                | ccaccggcgg | taatgaagag   | ggaggagcaa | cgtgtgggta | aagaggcgga  | 240 |
| gaagccgccg                                | rtttttaaga | agtggcagca   | cccggcagct | ccgttttact | accagccagc  | 300 |
| accgtcatcg                                | aatcagccgt | ttgcatggcc   | aaattaacgg | tctcttaata | ttaggtctat  | 360 |
| cacacaaata                                | cataaatatt | tgaattctttt  | taattgtatg | ccgatcatat | tgacaaatag  | 420 |
| catattttat                                | ttttatttaa | catataaccatc | tttatgcagt | atgtatgttg | ggtttgatgt  | 480 |
| tgttatgtcc                                | ttgtaaccat | gaatttaaatc  | actaatatat | atagtgtatt | gtttcgtata  | 540 |
| ctgtgtaatg                                | ttgaagacac | tagctaagat   | cgcctgtaa  | t          |             |     |

(2) INFORMATION FOR SEQ ID NO:1669:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..111

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500848

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

Ile Asn Lys Lys Leu Ile Gln Gln Asp Pro Ala Met Ser Ser Thr Ala  
1 5 10 15  
Arg Asn Ile Ser Gly Ser Gly Asn Arg Lys Ser Ser Arg Leu Gln Arg  
20 25 30  
Arg Ala Pro Pro Pro Leu Lys Ile Asn Pro Cys Glu Arg Xaa Trp Lys  
35 40 45  
Val Ala Ile Pro Leu Leu Ser Pro Thr Glu Ser Pro Pro Gln Lys Pro  
50 55 60  
Pro Ala Val Met Lys Arg Glu Glu Gln Arg Trp Gly Lys Glu Ala Glu  
65 70 75 80  
Lys Pro Pro Xaa Phe Lys Lys Trp Gln His Pro Ala Ala Pro Phe Tyr  
85 90 95  
Tyr Gln Pro Ala Pro Ser Ser Asn Gln Pro Phe Ala Trp Pro Asn  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

Met Ser Ser Thr Ala Arg Asn Ile Ser Gly Ser Gly Asn Arg Lys Ser  
1 5 10 15  
Ser Arg Leu Gln Arg Arg Ala Pro Pro Leu Lys Ile Asn Pro Cys  
20 25 30  
Glu Arg Xaa Trp Lys Val Ala Ile Pro Leu Leu Ser Pro Thr Glu Ser  
35 40 45  
Pro Pro Gln Lys Pro Pro Ala Val Met Lys Arg Glu Glu Gln Arg Trp  
50 55 60  
Gly Lys Glu Ala Glu Lys Pro Pro Xaa Phe Lys Lys Trp Gln His Pro  
65 70 75 80  
Ala Ala Pro Phe Tyr Gln Pro Ala Pro Ser Ser Asn Gln Pro Phe  
85 90 95  
Ala Trp Pro Asn  
100

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

gcataatcag ctgtcaggtc agattccccg agatcttggg gagctctcct ttctgtcaac 60  
catgaacttc gccacaaca atctcgaagg tccaatgcc aagcgaacac aatttcaaag 120  
ccaaaactgt tcttcattca tggacaaccc caagctttac ggtcttgatg atatctgcag 180  
aaaaactcat gtcccaaatc ctgaccaca agaattagag aaagtatcag agccggaaga 240  
agagcaagtg attaaactgga catcagcagc aatagcgtat ggacctgggtg tgttttgcg 300  
attagtgatt ggacatatct tcatttcgca taagcaggag tggttaatgg aaaagtttcg 360  
tagaaacaag cccagagttg tcatcagaag cgctcgttga acacgtgcat atgtatgtgt 420  
ttgtgaaaaa ctctttcgtg tgcgttgtaa tgttctaata tatggttttg taataaacgt 480  
ctttgggtggc ggtacgtatt tgatacatat tggttttg

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1500855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

```
His Asn Gln Leu Ser Gly Gln Ile Pro Arg Asp Leu Gly Glu Leu Ser
1 5 10 15
Phe Leu Ser Thr Met Asn Phe Ala His Asn Asn Leu Glu Gly Pro Met
20 25 30
Pro Arg Gly Thr Gln Phe Gln Ser Gln Asn Cys Ser Ser Phe Met Asp
35 40 45
Asn Pro Lys Leu Tyr Gly Leu Asp Asp Ile Cys Arg Lys Thr His Val
50 55 60
Pro Asn Pro Arg Pro Gln Glu Leu Glu Lys Val Ser Glu Pro Glu Glu
65 70 75 80
Glu Gln Val Ile Asn Trp Thr Ser Ala Ala Ile Ala Tyr Gly Pro Gly
85 90 95
Val Phe Cys Gly Leu Val Ile Gly His Ile Phe Ile Ser His Lys Gln
100 105 110
Glu Trp Leu Met Glu Lys Phe Arg Arg Asn Lys Pro Arg Val Val Ile
115 120 125
Arg Ser Ala Arg
130
```

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1500856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

```
Met Asn Phe Ala His Asn Asn Leu Glu Gly Pro Met Pro Arg Gly Thr
1 5 10 15
Gln Phe Gln Ser Gln Asn Cys Ser Ser Phe Met Asp Asn Pro Lys Leu
20 25 30
Tyr Gly Leu Asp Asp Ile Cys Arg Lys Thr His Val Pro Asn Pro Arg
35 40 45
Pro Gln Glu Leu Glu Lys Val Ser Glu Pro Glu Glu Glu Gln Val Ile
50 55 60
Asn Trp Thr Ser Ala Ala Ile Ala Tyr Gly Pro Gly Val Phe Cys Gly
65 70 75 80
Leu Val Ile Gly His Ile Phe Ile Ser His Lys Gln Glu Trp Leu Met
85 90 95
Glu Lys Phe Arg Arg Asn Lys Pro Arg Val Val Ile Arg Ser Ala Arg
100 105 110
```

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500857  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:  
Met Pro Arg Gly Thr Gln Phe Gln Ser Gln Asn Cys Ser Ser Phe Met  
1 5 10 15  
Asp Asn Pro Lys Leu Tyr Gly Leu Asp Ile Cys Arg Lys Thr His  
20 25 30  
Val Pro Asn Pro Arg Pro Gln Glu Leu Glu Lys Val Ser Glu Pro Glu  
35 40 45  
Glu Glu Gln Val Ile Asn Trp Thr Ser Ala Ala Ile Ala Tyr Gly Pro  
50 55 60  
Gly Val Phe Cys Gly Leu Val Ile Gly His Ile Phe Ile Ser His Lys  
65 70 75 80  
Gln Glu Trp Leu Met Glu Lys Phe Arg Arg Asn Lys Pro Arg Val Val  
85 90 95  
Ile Arg Ser Ala Arg  
100

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..615  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

gataatattt cattttcrtc gtttctttct ttctaagttt cgatgtcagt tcctaattctc 60  
tatggcggtc atgatagcca aatggtaact ttggtggcct aatgtatgtc acgtaaatta 120  
tccacgtggc actcactttt ttgcatcttt ctcaaaatat atcaaaggag acttcataaa 180  
gaaagaatct ttagtggtgga gagactaaaa ggacaccaca agcttatttc ataagaaact 240  
tcaaattaga atcagaaaca agagcatcct tcttcattta cacaggtaaa ttaggtgtaa 300  
aaatggtgat gagaagtgtg gatctacgat cagataccgt tactagaccg acagatgcga 360  
tgcgagaagc aatgtgtaac gcagagggtg atgatgacgt cctcgatat gacccaacgg 420  
ctagacgtct tgaagaggag atggctaaga tgatggggaa agaggctgct ctgttcgtgc 480  
catccgggac aatggggaat ctgatcagcg tgatgggttca ctgcgacgtg agaggcagcg 540  
aggtgattct tggcgacaat tgtcacatcc atgtttacga gaatggaggg atatcgacta 600  
tcgggggagt gcatc

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

Met Val Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro  
1 5 10 15  
Thr Asp Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp

20 25 30  
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Met Ala  
35 40 45  
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met  
50 55 60  
Gly Asn Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu  
65 70 75 80  
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly  
85 90 95  
Ile Ser Thr Ile Gly Gly Val His  
100

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1500864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro Thr Asp  
1 5 10 15  
Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp Val Leu  
20 25 30  
Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Met Ala Lys Met  
35 40 45  
Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn  
50 55 60  
Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile  
65 70 75 80  
Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser  
85 90 95  
Thr Ile Gly Gly Val His  
100

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1500865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp Val Leu Gly  
1 5 10 15  
Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Met Ala Lys Met Met  
20 25 30  
Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn Leu  
35 40 45  
Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile Leu  
50 55 60  
Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser Thr  
65 70 75 80  
Ile Gly Gly Val His  
85



(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..643
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| atttttttagg | tttgttcagc | tgttttacgg  | agtcgctttt  | gagatatcga | tcttacgaag | 60  |
| aagcaaaaaat | ggcgggtccc | ttgctttacca | agaagggtgt  | gaagaagagg | tctactaagt | 120 |
| tcatcagacc  | ccagagtga  | cgtagaatca  | ccgtcaagga  | aagctggagg | aggccaaagg | 180 |
| gtattgattc  | aaggatgaga | agaaagttca  | aagggtgtgac | tttgatgccc | aatgttggtt | 240 |
| acggatctga  | caagaagact | cgtcactatc  | ttcccaatgg  | attcaagaaa | ttcgttggtc | 300 |
| acaacacaag  | tgagctcgag | ttggttgatga | tgcacaacag  | gacttactgt | gctgagattg | 360 |
| ctcacaacgt  | ctccactaag | aagagaaaagg | caattgttga  | gagagcttct | cagctagacg | 420 |
| ttgttggttac | caacaggctt | gctaggctcc  | gtagccaaga  | agacgagtga | agaagaatct | 480 |
| tgccgactac  | ttagttgttt | cttctgtttt  | gttgcatctc  | ctttttgtta | taagacgatt | 540 |
| tttgattact  | gctgtgtttg | tgtttggagt  | gaacaaacat  | gagttttggt | tttagtatga | 600 |
| aacagatcaa  | gttaagacct | tttgttaaag  | ctatttcgga  | ttc        |            |     |

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Leu | Gly | Leu | Phe | Ser | Cys | Phe | Thr | Glu | Ser | Leu | Leu | Arg | Tyr | Arg |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Tyr | Glu | Glu | Ala | Lys | Met | Ala | Val | Pro | Leu | Leu | Thr | Lys | Lys | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Lys | Lys | Arg | Ser | Thr | Lys | Phe | Ile | Arg | Pro | Gln | Ser | Asp | Arg | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Thr | Val | Lys | Glu | Ser | Trp | Arg | Arg | Pro | Lys | Gly | Ile | Asp | Ser | Arg |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Met | Arg | Arg | Lys | Phe | Lys | Gly | Val | Thr | Leu | Met | Pro | Asn | Val | Gly | Tyr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Ser | Asp | Lys | Lys | Thr | Arg | His | Tyr | Leu | Pro | Asn | Gly | Phe | Lys | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Phe | Val | Val | His | Asn | Thr | Ser | Glu | Leu | Glu | Leu | Leu | Met | Met | His | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Arg | Thr | Tyr | Cys | Ala | Glu | Ile | Ala | His | Asn | Val | Ser | Thr | Lys | Lys | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Ala | Ile | Val | Glu | Arg | Ala | Ser | Gln | Leu | Asp | Val | Val | Val | Thr | Asn |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Arg | Leu | Ala | Arg | Leu | Arg | Ser | Gln | Glu | Asp | Glu |     |     |     |     |     |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1500868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

```
Met Ala Val Pro Leu Leu Thr Lys Lys Val Val Lys Lys Arg Ser Thr
 1 5 10 15
Lys Phe Ile Arg Pro Gln Ser Asp Arg Arg Ile Thr Val Lys Glu Ser
 20 25 30
Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Met Arg Arg Lys Phe Lys
 35 40 45
Gly Val Thr Leu Met Pro Asn Val Gly Tyr Gly Ser Asp Lys Lys Thr
 50 55 60
Arg His Tyr Leu Pro Asn Gly Phe Lys Lys Phe Val Val His Asn Thr
65 70 75 80
Ser Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu
 85 90 95
Ile Ala His Asn Val Ser Thr Lys Lys Arg Lys Ala Ile Val Glu Arg
 100 105 110
Ala Ser Gln Leu Asp Val Val Val Thr Asn Arg Leu Ala Arg Leu Arg
 115 120 125
Ser Gln Glu Asp Glu
 130
```

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1500869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

```
Met Arg Arg Lys Phe Lys Gly Val Thr Leu Met Pro Asn Val Gly Tyr
 1 5 10 15
Gly Ser Asp Lys Lys Thr Arg His Tyr Leu Pro Asn Gly Phe Lys Lys
 20 25 30
Phe Val Val His Asn Thr Ser Glu Leu Glu Leu Leu Met Met His Asn
 35 40 45
Arg Thr Tyr Cys Ala Glu Ile Ala His Asn Val Ser Thr Lys Lys Arg
 50 55 60
Lys Ala Ile Val Glu Arg Ala Ser Gln Leu Asp Val Val Val Thr Asn
65 70 75 80
Arg Leu Ala Arg Leu Arg Ser Gln Glu Asp Glu
 85 90
```

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1500877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

tacctacccc ctgcgcttgc acaaaatcct tcttgatccg cacaggaagg tggaaggtcc

```
cggcagaaga acttggcggg cgaaaggcga aaccgacgtg ctcccrggcg ggcggcgaca 120
cggcatggag cgagagcgnc aggcagtggc gaggaacagg aaggtggtgc tgcgcgggta 180
catcgaccgc gcgcccaggg aggaagacat ggagctcgtc gacggcrgcg ccgtggagct 240
gcgcgtcccc gadggcggcg gcggccccgc ggtgctggtg aagaacctct acctatcctg 300
cgacccttac atgcgcggca ggatgcggga cttccgcaac tcctacatcc cgcccttcaa 360
acctggatca cctattgang ggtttggcgt ggggarggtg gtcgactcca ctcatccagg 420
attcagtgcc ggtgacgttg tttccgggat gactggatgg gaggactaca gtctgatcac 480
caatcctgaa cag
```

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

```
Thr Tyr Pro Leu Arg Leu His Lys Ile Leu Leu Asp Pro His Arg Lys
1 5 10 15
Val Glu Gly Pro Gly Arg Arg Thr Trp Arg Ala Lys Gly Glu Thr Asp
 20 25 30
Val Leu Xaa Gly Gly Arg Arg His Gly Met Glu Arg Glu Xaa Gln Ala
 35 40 45
Val Ala Arg Asn Arg Lys Val Val Leu Arg Gly Tyr Ile Asp Arg Ala
 50 55 60
Pro Arg Glu Glu Asp Met Glu Leu Val Asp Gly Xaa Ala Val Glu Leu
 65 70 75 80
Arg Val Pro Xaa Gly Gly Gly Gly Pro Ala Val Leu Val Lys Asn Leu
 85 90 95
Tyr Leu Ser Cys Asp Pro Tyr Met Arg Gly Arg Met Arg Asp Phe Arg
 100 105 110
Asn Ser Tyr Ile Pro Pro Phe Lys Pro Gly Ser Pro Ile Xaa Gly Phe
 115 120 125
Gly Val Gly Xaa Val Val Asp Ser Thr His Pro Gly Phe Ser Ala Gly
 130 135 140
Asp Val Val Ser Gly Met Thr Gly Trp Glu Asp Tyr Ser Leu Ile Thr
 145 150 155 160
Asn Pro Glu Gln
```

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1500879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

```
Met Glu Arg Glu Xaa Gln Ala Val Ala Arg Asn Arg Lys Val Val Leu
1 5 10 15
Arg Gly Tyr Ile Asp Arg Ala Pro Arg Glu Glu Asp Met Glu Leu Val
 20 25 30
Asp Gly Xaa Ala Val Glu Leu Arg Val Pro Xaa Gly Gly Gly Pro
 35 40 45
Ala Val Leu Val Lys Asn Leu Tyr Leu Ser Cys Asp Pro Tyr Met Arg
```

50 55 60  
Gly Arg Met Arg Asp Phe Arg Asn Ser Tyr Ile Pro Pro Phe Lys Pro  
65 70 75 80  
Gly Ser Pro Ile Xaa Gly Phe Gly Val Gly Xaa Val Val Asp Ser Thr  
85 90 95  
His Pro Gly Phe Ser Ala Gly Asp Val Val Ser Gly Met Thr Gly Trp  
100 105 110  
Glu Asp Tyr Ser Leu Ile Thr Asn Pro Glu Gln  
115 120

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1500880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

Met Glu Leu Val Asp Gly Xaa Ala Val Glu Leu Arg Val Pro Xaa Gly  
1 5 10 15  
Gly Gly Gly Pro Ala Val Leu Val Lys Asn Leu Tyr Leu Ser Cys Asp  
20 25 30  
Pro Tyr Met Arg Gly Arg Met Arg Asp Phe Arg Asn Ser Tyr Ile Pro  
35 40 45  
Pro Phe Lys Pro Gly Ser Pro Ile Xaa Gly Phe Gly Val Gly Xaa Val  
50 55 60  
Val Asp Ser Thr His Pro Gly Phe Ser Ala Gly Asp Val Val Ser Gly  
65 70 75 80  
Met Thr Gly Trp Glu Asp Tyr Ser Leu Ile Thr Asn Pro Glu Gln  
85 90 95

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..535

(D) OTHER INFORMATION: / Ceres Seq. ID 1500881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

aagtcagagg gacattgcat tggggaacta cagaaaaggg tccgaatcga atccgtggtg 60  
cactgccccct tcctccccc caagccgccg ccgccgccgt gaggactccg gcgaatggcg 120  
tcccgcgtcg cctcgggcct cctccgccgc cgcgccggcg ccacactagg cctcctaagg 180  
agttatgcac atgtcagaag ctacaacagt caactttcag ctttggtttc tgctacatct 240  
gaatgctcaa atctgccgag aagatgctat tacttaccta atccctctcc ataccaagtt 300  
tgagtaggt catttgcttc agacaacgga gacaagtttg aggctgttgt gcccttcatg 360  
ggtgaatctg taactgatgg aactcttgct aacttcttaa agaaacctgg agacagagtc 420  
gaggctgatg aacctatagc gcagattgaa actgataagg tcactataga tgtcgcaagt 480  
cctgargctg gtgttattga aaagctcatt gctagtgaag gcgacacagt tactc

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1500882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

```
Val Arg Gly Thr Leu His Trp Gly Thr Thr Glu Lys Gly Pro Asn Arg
1 5 10 15
Ile Arg Gly Ala Leu Pro Leu Pro Pro Pro Gln Ala Ala Ala Ala
20 25 30
Val Arg Thr Pro Ala Asn Gly Val Pro Arg Arg Leu Gly Pro Pro Pro
35 40 45
Pro Pro Arg Arg Arg His Thr Arg Pro Pro Lys Glu Leu Cys Thr Cys
50 55 60
Gln Lys Leu Gln Gln Ser Thr Phe Ser Phe Gly Phe Cys Tyr Ile
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

```
Met Ala Ser Arg Val Ala Ser Gly Leu Leu Arg Arg Arg Ala Gly Ala
1 5 10 15
Thr Leu Gly Leu Leu Arg Ser Tyr Ala His Val Arg Ser Tyr Asn Ser
20 25 30
Gln Leu Ser Ala Leu Val Ser Ala Thr Ser Glu Cys Ser Asn Leu Pro
35 40 45
Arg Arg Cys Tyr Tyr Leu Pro Asn Pro Ser Pro Tyr Gln Val Trp Ser
50 55 60
Arg Ser Phe Ala Ser Asp Asn Gly Asp Lys Phe Glu Ala Val Val Pro
65 70 75 80
Phe Met Gly Glu Ser Val Thr Asp Gly Thr Leu Ala Asn Phe Leu Lys
85 90 95
Lys Pro Gly Asp Arg Val Glu Ala Asp Glu Pro Ile Ala Gln Ile Glu
100 105 110
Thr Asp Lys Val Thr Ile Asp Val Ala Ser Pro Xaa Ala Gly Val Ile
115 120 125
Glu Lys Leu Ile Ala Ser Glu Gly Asp Thr Val Thr
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1500884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

```
ataccgcaac cagctattga gctactgcct ctgaccaagt cccaagctgc gctgcgcctg 60
ctatgtcgtc gtcctcgccc gtatcggcgg tctcatcagc cactgcgcgc cactgcgtgg 120
acgactgcct cggcatcgtg cagcttctta gcgatggcac cgtgacgcgc tccgsgacta 180
ctccgacatc cctctccttg gcgaggtgcc gtccaacctg cccgtccagt ggaaggacgt 240
```

cgtctacgac cccgcgcacg cgctccgcct ccgcatgtac aggccccaccg acaccgacgg 300  
cggcaggacg accaacaaca agctgccggt gctagtctac ttccacggcg gcggcttctg 360  
catctgcagc ttcgagatgc cccacttcca cgccggcggg ctccgcctcg ccgccgagct 420  
cccggcgctc gtgctctmcg ccgactacmg cctggggccc gagcaccgcc t

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Gln | Pro | Ala | Ile | Glu | Leu | Leu | Pro | Leu | Thr | Lys | Ser | Gln | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Arg | Leu | Leu | Cys | Arg | Arg | Pro | Arg | Pro | Tyr | Arg | Arg | Ser | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Pro | Leu | Arg | Arg | Thr | Ser | Trp | Thr | Thr | Ala | Ser | Ala | Ser | Cys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Ala | Met | Ala | Pro |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Ser | Ser | Pro | Val | Ser | Ala | Val | Ser | Ser | Ala | Thr | Ala | Pro |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Val | Val | Asp | Asp | Cys | Leu | Gly | Ile | Val | Gln | Leu | Leu | Ser | Asp | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Val | Thr | Arg | Ser | Xaa | Thr | Thr | Pro | Thr | Ser | Leu | Ser | Trp | Ala | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Arg | Pro | Thr | Cys | Pro | Ser | Ser | Gly | Arg | Thr | Ser | Ser | Thr | Thr | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Thr | Arg | Ser | Ala | Ser | Ala | Cys | Thr | Gly | Pro | Pro | Thr | Pro | Thr | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Arg | Pro | Thr | Ser | Cys | Arg | Cys |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

Met Tyr Arg Pro Thr Asp Thr Asp Gly Gly Arg Thr Thr Asn Asn Lys

1 5 10 15  
Leu Pro Val Leu Val Tyr Phe His Gly Gly Phe Cys Ile Cys Ser  
20 25 30  
Phe Glu Met Pro His Phe His Ala Gly Gly Leu Arg Leu Ala Ala Glu  
35 40 45  
Leu Pro Ala Leu Val Leu Xaa Ala Asp Tyr Xaa Leu Gly Pro Glu His  
50 55 60

Arg  
65

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| cttcgctgc  | ttttcctttc  | tctctctcc  | cctttcctct  | ccccaagcag | gcggggcgag | 60  |
| cgagcccagc | aggcgtctct  | cctctcgtcc | atccgtttcc  | tcctccccct | gcttcccggc | 120 |
| tcgcctccct | ccccctccctg | tgcgcctctt | ttcattgcgcg | aggagggacc | gtggggacca | 180 |
| ccaccaccag | caccaccacc  | tccatccgtg | cgcctctcgc  | tctcgtcgtg | ggtgctcctc | 240 |
| ctcctcctcc | tgtctccggg  | gcggggcgcc | tccttttcca  | cctcctgctg | gtgcmagggc | 300 |
| cgggagggcg | tmgcggaggt  | ggcgcgcatg | gggctcgcmg  | gggamgggtc | ggcggacacm | 360 |
| gcmcacctca | gtaataatga  | aaatrpgcgg | ttmatattatg | gagttgcgag | ttctcctggt | 420 |
| aaaagagcat | cgatggagga  | cttctatgag | gcaagaatag  | acgamgttga | tggagagaaa | 480 |
| attggaatgt | tcggtgtata  | tgatggtcac | ggaggagtcc  | gagcagctga | gtatgttaag | 540 |
| cagcaccttt | tcagcaattt  | aatcaaacac | ccaaagttca  | tcactgatac | c          |     |

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Leu | Leu | Phe | Leu | Ser | Pro | Leu | Ser | Pro | Phe | Leu | Ser | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Arg | Gly | Glu | Arg | Ala | Gln | Gln | Ala | Ser | Leu | Leu | Ser | Ser | Ile | Arg |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Leu | Leu | Pro | Leu | Leu | Pro | Gly | Ser | Pro | Pro | Ser | Pro | Pro | Cys | Ala |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Pro | Leu | Phe | Met | Arg | Glu | Glu | Gly | Pro | Trp | Gly | Pro | Pro | Pro | Pro | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Pro | Pro | Pro | Pro | Ser | Val | Arg | Leu | Ser | Leu | Ser | Leu | Val | Val | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Leu | Leu | Leu | Leu | Pro | Gly | Arg | Ala | Ala | Ser | Phe | Ser | Thr | Ser | Cys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Cys | Xaa | Gly | Arg | Glu | Gly | Xaa | Ala | Glu | Val | Ala | Arg | Met | Gly | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Xaa | Gly | Xaa | Gly | Ser | Ala | Asp | Xaa | Xaa | His | Leu | Ser | Asn | Asn | Glu | Asn |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Xaa | Arg | Xaa | Ile | Tyr | Gly | Val | Ala | Ser | Ser | Pro | Gly | Lys | Arg | Ala | Ser |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |

Met Glu Asp Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys  
145 150 155 160  
Ile Gly Met Phe Gly Val Tyr Asp Gly His Gly Gly Val Arg Ala Ala  
165 170 175  
Glu Tyr Val Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys  
180 185 190  
Phe Ile Thr Asp Thr  
195

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1500890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Phe Arg Cys Phe Ser Phe Leu Leu Ser Pro Leu Ser Ser Pro Gln Ala  
1 5 10 15  
Gly Gly Ala Ser Glu Pro Ser Arg Arg Leu Ser Ser Arg Pro Ser Val  
20 25 30  
Ser Ser Ser Pro Cys Phe Pro Ala Arg Leu Pro Pro Leu Pro Val Arg  
35 40 45  
Leu Phe Ser Cys Ala Arg Arg Asp Arg Gly Asp His His His Gln His  
50 55 60  
His His Leu His Pro Cys Ala Ser Arg Ser Arg Trp Trp Cys Ser Ser  
65 70 75 80  
Ser Ser Ser Cys Ser Arg Gly Gly Arg Pro Pro Phe Pro Pro Pro Ala  
85 90 95  
Gly Xaa Arg Ala Gly Arg Ala Xaa Arg Arg Trp Arg Ala Trp Gly Ser  
100 105 110  
Xaa Gly Xaa Gly Arg Arg Thr Xaa Xaa Thr Ser Val Ile Met Lys Xaa  
115 120 125  
Gly Gly Xaa Phe Met Glu Leu Arg Val Leu Leu Val Lys Glu His Arg  
130 135 140  
Trp Arg Thr Ser Met Arg Gln Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1500891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met Arg Glu Glu Gly Pro Trp Gly Pro Pro Pro Pro Ala Pro Pro Pro  
1 5 10 15  
Pro Ser Val Arg Leu Ser Leu Ser Leu Val Val Leu Leu Leu Leu Leu  
20 25 30  
Leu Leu Pro Gly Arg Ala Ala Ser Phe Ser Thr Ser Cys Trp Cys Xaa  
35 40 45  
Gly Arg Glu Gly Xaa Ala Glu Val Ala Arg Met Gly Leu Xaa Gly Xaa  
50 55 60  
Gly Ser Ala Asp Xaa Xaa His Leu Ser Asn Asn Glu Asn Xaa Arg Xaa



(2) INFORMATION FOR SEQ ID NO:1698:

(A) LENGTH: 654 base pairs

(C) STRANDEDNESS: sing

MOLECULE TYPE: DNA (gen

(1X) FEATURE.  
(A) NAM

(D) OTHER INFORMATION

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:100  
ggccgtc gccgtgtccac tttccccgtg cttctccgcc gt

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

FEATURE:

(B) LOCATION: 1..120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ala | Val | Ala | Cys | Pro | Leu | Ser | Pro | Cys | Phe | Ser | Ala | Val | Glu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Gln | Cys | Glu | Glu | Thr | Thr | Thr | Gln | Met | Ala | Ser | Arg | Trp | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Pro | Glu | Val | Tyr | Pro | Leu | Phe | Ala | Ala | Thr | Gly | Val | Ala | Val | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Cys | Gly | Phe | Gln | Leu | Phe | Arg | Asn | Ile | Thr | Gly | Asn | Pro | Glu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Val | Asn | Lys | Ala | Gly | Arg | Ala | Ala | Gly | Val | Leu | Glu | Asn | His | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Gly | Arg | Arg | Tyr | Ala | Met | His | Gly | Leu | Thr | Pro | Thr | Leu | Leu | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Leu | Ser | Ala | Ala | Leu | Ala | Ser | Leu | Phe | Leu | Leu | Asn | Tyr | Gln | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Thr | Cys | Thr | Leu | Ser | Gln |     |     |     |     |     |     |     |     |

115 120  
(2) INFORMATION FOR SEQ ID NO:1700:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..94  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500902  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:  
Met Ala Ser Arg Trp Val Arg Pro Glu Val Tyr Pro Leu Phe Ala Ala  
1 5 10 15  
Thr Gly Val Ala Val Gly Ile Cys Gly Phe Gln Leu Phe Arg Asn Ile  
20 25 30  
Thr Gly Asn Pro Glu Val Arg Val Asn Lys Ala Gly Arg Ala Ala Gly  
35 40 45  
Val Leu Glu Asn His Glu Glu Gly Arg Arg Tyr Ala Met His Gly Leu  
50 55 60  
Thr Pro Thr Leu Leu Trp Val Leu Ser Ala Ala Leu Ala Ser Leu Phe  
65 70 75 80  
Leu Leu Asn Tyr Gln Asp Ser Arg Thr Cys Thr Leu Ser Gln  
85 90

(2) INFORMATION FOR SEQ ID NO:1701:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500903  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:  
Met Gly Ser Phe Ser Ser Thr Gly Leu Thr Ile Ser Ser Lys Leu Pro  
1 5 10 15  
Arg Phe Ser Asp Met Tyr Thr Leu Thr Ile Ala Ser Ala Asp Pro Gln  
20 25 30  
Ser Ile Ser Ala Asn Lys Pro Val His Phe Thr Lys Ser Val Thr Lys  
35 40 45  
Trp Phe Thr Lys Glu Gly Val Leu Val Glu Gly Leu Phe Trp Lys Asp  
50 55 60  
Val Glu Lys Leu Ile Asp Asp Tyr Asn Ser Glu Arg Lys Ser Lys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1702:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 465 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..465  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500907  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:  
acacaacacc agtaagcaag caccgccagc acgcacaagc aggcaaagct ctcgaccatc 60  
gctctgaggg attaatggcg gcgggaggag gaggcggcgg catcgcgacg agaaggcccc 120

tgctgctgag gcgttcggcg ggcacctgga ggcggcggag atgacggagg cggaggaggga 180  
acacagcggc gtcaagtccc ggctgtcggg tctgctgtgg cacggcgggt cggcgtagca 240  
cgcggtggttc agctgcgcgt cgaaccaggt ggcgcagggt ctgctgacgc tgccctactc 300  
gttcgcgcac tggggatgct garcggcgtg ctgttccagc tcttctacgg cctgctgggc 360  
agctggacgg cgtacctgat cagcatcctg tacctggagt accgcacccg tcgggagcgc 420  
gagaaggccg cggacttccg gaaccacgtg atccagtggg tcgag

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1500908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

Thr Thr Pro Val Ser Lys His Arg Gln His Ala Gln Ala Gly Lys Ala  
1 5 10 15  
Leu Asp His Arg Ser Glu Gly Leu Met Ala Ala Gly Gly Gly Gly Gly  
20 25 30  
Gly Ile Ala Thr Arg Arg Pro Leu Leu Leu Arg Arg Ser Ala Gly Thr  
35 40 45  
Trp Arg Arg Arg Arg  
50

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1500909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

Met Thr Glu Ala Glu Glu His Ser Gly Val Lys Ser Arg Leu Ser  
1 5 10 15  
Gly Leu Leu Trp His Gly Gly Ser Ala Tyr Asp Ala Trp Phe Ser Cys  
20 25 30  
Ala Ser Asn Gln Val Ala Gln Val Leu Leu Thr Leu Pro Tyr Ser Phe  
35 40 45  
Ala His Trp Gly Cys  
50

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1500910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

Met Leu Xaa Gly Val Leu Phe Gln Leu Phe Tyr Gly Leu Leu Gly Ser  
1 5 10 15  
Trp Thr Ala Tyr Leu Ile Ser Ile Leu Tyr Leu Glu Tyr Arg Thr Arg

20 25 30  
Arg Glu Xaa Glu Lys Ala Ala Asp Phe Arg Asn His Val Ile Gln Trp  
35 40 45  
Phe Glu  
50

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..548
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gttacatccc accatttgct gttcaccttc cctcccgttt gcctcctctc gctgtctcgt | 60  |
| agcttctttt ctccggcgac ggctgggcga gggccgcga gtcgggccct tcgtcggcga  | 120 |
| cgagcatcca cctgcgcggc gcccacatct ccgctccttc cttactcgc gctcggcaca  | 180 |
| caggcgacgg cgggcgcggc gctcaggatc gggctatcac cgacggggtc cggcttctcc | 240 |
| gcccgcctct cgccactcgc ctgcgcacct cgcctccggt cctccgcaca ccggccggcg | 300 |
| atcctgcaag ggttgatga tggcgagat ctgaaggatg ctgatttcta taagcagcaa   | 360 |
| gctaaacttc ttttcaagaa cttgtcaaaa gggcatcatg aagcttcacg gatgtmaatt | 420 |
| gagacagggc cctactatct ccactacatt attgarggca gagtatgtta tctgactatg | 480 |
| tgtgamcgt cttatccgaa gaaacttgca ttccagtacc tagaagatct gaaaaatgaa  | 540 |
| tttgagag                                                          |     |

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Thr Ser His Leu Leu Phe Thr Phe Pro Pro Val Cys Leu Leu     |  |
| 1 5 10 15                                                       |  |
| Ser Leu Ser Arg Ser Phe Phe Pro Pro Ala Thr Ala Gly Arg Ala Ala |  |
| 20 25 30                                                        |  |
| Ala Ser Arg Ala Leu Arg Arg Arg Arg Ala Ser Thr Cys Ala Ala Pro |  |
| 35 40 45                                                        |  |
| His Leu Pro Leu Leu Pro Leu Leu Ala Leu Gly Thr Gln Ala Thr Ala |  |
| 50 55 60                                                        |  |
| Ala Ala Ala Leu Arg Ile Gly Leu Ser Pro Thr Gly Ser Gly Phe Ser |  |
| 65 70 75 80                                                     |  |
| Ala Arg Leu Ser Pro Leu Ala Ser Arg Pro Arg Leu Arg Ser Ser Ala |  |
| 85 90 95                                                        |  |
| His Arg Pro Ala Ile Leu Gln Gly Leu Asp Asp Gly Arg Asp Leu Lys |  |
| 100 105 110                                                     |  |
| Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys Leu Leu Phe Lys Asn Leu |  |
| 115 120 125                                                     |  |
| Ser Lys Gly His His Glu Ala Ser Arg Met Xaa Ile Glu Thr Gly Pro |  |
| 130 135 140                                                     |  |
| Tyr Tyr Phe His Tyr Ile Ile Xaa Gly Arg Val Cys Tyr Leu Thr Met |  |
| 145 150 155 160                                                 |  |
| Cys Xaa Arg Ser Tyr Pro Lys Lys Leu Ala Phe Gln Tyr Leu Glu Asp |  |
| 165 170 175                                                     |  |

Leu Lys Asn Glu Phe Glu  
180

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1500917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | His | Pro | Thr | Ile | Cys | Cys | Ser | Pro | Ser | Leu | Pro | Phe | Ala | Ser | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Cys | Leu | Val | Ala | Ser | Phe | Leu | Arg | Arg | Arg | Leu | Gly | Glu | Arg | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Val | Gly | Pro | Phe | Val | Gly | Asp | Glu | His | Pro | Pro | Ala | Arg | Arg | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Phe | Arg | Ser | Phe | Pro | Tyr | Ser | Arg | Ser | Ala | His | Arg | Arg | Arg | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Arg | Arg | Ser | Gly | Ser | Gly | Tyr | His | Arg | Arg | Gly | Pro | Ala | Ser | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Pro | Ala | Ser | Arg | His | Ser | Pro | Arg | Ala | Leu | Ala | Ser | Gly | Pro | Pro | His |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Thr | Gly | Arg | Arg | Ser | Cys | Lys | Gly | Trp | Met | Met | Gly | Glu | Ile |     |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..790

(D) OTHER INFORMATION: / Ceres Seq. ID 1500926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atgctctacc  | ggagtagcgc | aactccgcaa | gcaaatcctc | ctatctccaa | gcctccaatc | 60  |
| tgtgaacggt  | gaaccccaat | cgaatgacgc | cgacggsagc | ctcctcctcc | cggctcccc  | 120 |
| attcgtctct  | atctccgatg | tgcgccgcct | ccagctcccc | ccgcgcggcg | gccacgggcc | 180 |
| tcgcccctgc  | tggaagggt  | tggagtgcgg | ctccgtacag | acgcgggatg | tctcttcttt | 240 |
| cgttgggagc  | agaacacgcc | gcagaaacgt | tatatgtgct | tccctgttcg | gagttggagc | 300 |
| tcccgaagca  | ctggtcattg | gagtagtcgc | cttgttggtg | ttcggcccca | agggcttagc | 360 |
| agaggtagcc  | aggaatttgg | ggaagacttt | gcgtgctttc | caaccaacca | ttagagagat | 420 |
| acaggatgta  | tcaaggaggt | tcaggagcac | tcttgaacga | gaaatcggaa | ttgatgaggt | 480 |
| ttcccagtcg  | acgaattata | caccacgac  | catgaataac | aaccaacaac | ctgctgccga | 540 |
| ctcaaatatc  | aagcctgcac | ctgcacctta | caccagcgat | gaacttgtga | aagtaactga | 600 |
| agaacaaatt  | gctgcatcag | ctgctgcaga | gagttatcgt | cagttggtgc | ggtgtgtccg | 660 |
| cttaaaacttt | atgtgtggtt | ggttggtact | tttgtggttg | ttattttttt | ggacctcgtg | 720 |
| atagtcggtc  | ggttcaatgt | tatcgcggct | actggcaaac | cttaagtgat | acggtattct | 780 |
| tcttttcggt  |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1500927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Thr | Gly | Val | Ala | Gln | Leu | Arg | Lys | Gln | Ile | Leu | Leu | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Gln | Ser | Val | Asn | Gly | Glu | Pro | Gln | Ser | Asn | Asp | Ala | Asp | Xaa |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Leu | Leu | Pro | Ala | Pro | Pro | Phe | Val | Ser | Ile | Ser | Asp | Val | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Arg | Leu | Gln | Leu | Pro | Pro | Arg | Gly | Gly | His | Arg | Pro | Arg | Pro | Cys | Trp |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Gly | Leu | Glu | Cys | Gly | Ser | Val | Gln | Thr | Arg | Met | Val | Ser | Ser | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Gly | Ser | Arg | Thr | Arg | Arg | Arg | Asn | Val | Ile | Cys | Ala | Ser | Leu | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Val | Gly | Ala | Pro | Glu | Ala | Leu | Val | Ile | Gly | Val | Val | Ala | Leu | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Phe | Gly | Pro | Lys | Gly | Leu | Ala | Glu | Val | Ala | Arg | Asn | Leu | Gly | Lys |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | Leu | Arg | Ala | Phe | Gln | Pro | Thr | Ile | Arg | Glu | Ile | Gln | Asp | Val | Ser |
|     |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Arg | Glu | Phe | Arg | Ser | Thr | Leu | Glu | Arg | Glu | Ile | Gly | Ile | Asp | Glu | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gln | Ser | Thr | Asn | Tyr | Thr | Pro | Thr | Thr | Met | Asn | Asn | Asn | Gln | Gln |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Ala | Ala | Asp | Ser | Asn | Ile | Lys | Pro | Ala | Pro | Ala | Pro | Tyr | Thr | Ser |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Glu | Leu | Val | Lys | Val | Thr | Glu | Gln | Ile | Ala | Ala | Ser | Ala | Ala |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Glu | Ser | Tyr | Arg | Gln | Leu | Val | Arg | Cys | Val | Arg | Leu | Asn | Phe | Ile |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Cys | Gly | Trp | Leu | Val | Leu | Leu | Trp | Trp | Leu | Phe | Phe | Trp | Thr | Ser |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Ser | Phe | Val | Gly | Ser | Arg | Thr | Arg | Arg | Asn | Val | Ile |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Cys | Ala | Ser | Leu | Phe | Gly | Val | Gly | Ala | Pro | Glu | Ala | Leu | Val | Ile | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Ala | Leu | Leu | Val | Phe | Gly | Pro | Lys | Gly | Leu | Ala | Glu | Val | Ala |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Asn | Leu | Gly | Lys | Thr | Leu | Arg | Ala | Phe | Gln | Pro | Thr | Ile | Arg | Glu |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Gln | Asp | Val | Ser | Arg | Glu | Phe | Arg | Ser | Thr | Leu | Glu | Arg | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ile | Asp | Glu | Val | Ser | Gln | Ser | Thr | Asn | Tyr | Thr | Pro | Thr | Thr | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Asn | Asn | Gln | Gln | Pro | Ala | Ala | Asp | Ser | Asn | Ile | Lys | Pro | Ala | Pro |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |

Ala Pro Tyr Thr Ser Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile  
115 120 125  
Ala Ala Ser Ala Ala Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val  
130 135 140  
Arg Leu Asn Phe Ile Cys Gly Trp Leu Val Leu Leu Trp Trp Leu Phe  
145 150 155 160  
Phe Trp Thr Ser

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1500929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

|             |            |            |             |             |             |     |
|-------------|------------|------------|-------------|-------------|-------------|-----|
| aaggattttt  | gcaccgtgcc | tctgcctcca | ggattgtcgt  | gccgcgcctc  | caccattttc  | 60  |
| gccgccgcgc  | ccccgacacc | acctccaagg | atccttgccc  | ccgcccctgt  | actcctcgcg  | 120 |
| tccgcattctc | ccgctccatt | tccgctgccc | gcgatgcgct  | cgcacgtgtc  | gccgcctcgc  | 180 |
| gcccgcgggc  | cgcgattacm | cccctcccca | tcaccacctc  | gctgtggtgt  | acccccgtcc  | 240 |
| ttggcgccgc  | caccccgcac | ccgctccgag | attggctctt  | ccaccgctcc  | ccctggagat  | 300 |
| gagcgctcgc  | ttagggttag | gcgtccaacg | gttgtaccct  | ccaccacaag  | cgagaggaga  | 360 |
| tcgctggaag  | aggggggctg | ggagacgaac | aggaacacgg  | tccacatctg  | ggtgcmctcg  | 420 |
| cmtccacttc  | tctcgaatcc | tgamgcccac | acagcgccctc | cgcmtctcgtg | agaccgcgcac | 480 |

gc

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Phe | Cys | Thr | Val | Pro | Leu | Pro | Pro | Gly | Leu | Ser | Cys | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ser | Thr | Ile | Phe | Ala | Ala | Ala | Pro | Thr | Pro | Pro | Pro | Pro | Arg | Ile | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ala | Pro | Ala | Pro | Val | Leu | Leu | Ala | Ser | Ala | Ser | Pro | Ala | Pro | Phe | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Pro | Ala | Met | Arg | Ser | His | Val | Ser | Pro | Pro | Ser | Ala | Arg | Gly | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Xaa | Pro | Ser | Pro | Ser | Pro | Pro | Arg | Cys | Gly | Val | Pro | Pro | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Ala | Pro | Pro | Pro | Arg | Thr | Pro | Ser | Glu | Ile | Gly | Ser | Ser | Thr | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Gly | Asp | Glu | Arg | Ser | Leu | Arg | Val | Arg | Arg | Pro | Thr | Val | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Ser | Thr | Thr | Ser | Glu | Arg | Arg | Ser | Leu | Glu | Glu | Gly | Gly | Trp | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Arg | Asn | Thr | Val | His | Ile | Trp | Val | Xaa | Ser | Xaa | Pro | Thr | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Asn | Pro | Xaa | Ala | His | Thr | Ala | Pro | Pro | Xaa | Ser |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Ile | Phe | Ala | Pro | Cys | Leu | Cys | Leu | Gln | Asp | Cys | Arg | Ala | Ala | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Pro | Pro | Phe | Ser | Pro | Pro | Arg | Pro | Arg | His | His | Leu | Gln | Gly | Ser | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Pro | Pro | Leu | Tyr | Ser | Ser | Arg | Pro | His | Leu | Pro | Leu | His | Phe | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Cys | Pro | Arg | Cys | Ala | Arg | Thr | Cys | Arg | Arg | Pro | Arg | Pro | Ala | Gly | Arg |  |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Tyr | Xaa | Pro | Pro | His | His | Leu | Ala | Val | Val | Tyr | Pro | Arg | Pro |     |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Trp | Arg | Arg | His | Pro | Ala | Pro | Arg | Pro | Arg | Leu | Ala | Leu | Pro | Pro | Leu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Pro | Leu | Glu | Met | Ser | Ala | Arg | Leu | Gly | Leu | Gly | Val | Gln | Arg | Leu | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Pro | Pro | Gln | Ala | Arg | Gly | Asp | Arg | Trp | Lys | Arg | Gly | Ala | Gly | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg | Thr | Gly | Thr | Arg | Ser | Thr | Ser | Gly | Cys | Xaa | Arg | Xaa | Pro | Leu | Ser |  |
| 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Arg | Ile | Leu | Xaa | Pro | Thr | Gln | Arg | Leu | Arg | Xaa | Arg | Glu | Thr | Ala | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1500932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Ser | His | Val | Ser | Pro | Pro | Ser | Ala | Arg | Gly | Pro | Arg | Leu | Xaa |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Ser | Pro | Ser | Pro | Pro | Arg | Cys | Gly | Val | Pro | Pro | Ser | Leu | Ala | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Pro | Arg | Thr | Pro | Ser | Glu | Ile | Gly | Ser | Ser | Thr | Ala | Pro | Pro | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Glu | Arg | Ser | Leu | Arg | Val | Arg | Arg | Pro | Thr | Val | Val | Pro | Ser | Thr |  |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Ser | Glu | Arg | Arg | Ser | Leu | Glu | Glu | Gly | Gly | Trp | Glu | Thr | Asn | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asn | Thr | Val | His | Ile | Trp | Val | Xaa | Ser | Xaa | Pro | Thr | Leu | Ser | Asn | Pro |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Xaa | Ala | His | Thr | Ala | Pro | Pro | Xaa | Ser |     |     |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1716:



(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 463 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..463  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500945  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:  
aatcaacaca ccaccaccac cagcagcaca tcaatttagc tagttccagg aacacgcgag 60  
gaaaccgcag catggccaac aaccgcacatc tcgacgagta caaccccgcc gtcgaatgga 120  
gccgctccga cgaggcggac gccgtccgga tctcgctccc agggttcaag agggaggaca 180  
tacgcgtgct ggtggacagc caccggccacc tgcggacgcg cggcgagcgg cacatcgccg 240  
gcaacagggtg gagccgcttc cagacggacg tcgacctccc cgccaactgc aacgccgacg 300  
gcatccgcgc caagttcgag aacgacaggc tcaccatcac gctccccaag agcacctcct 360  
cggcgcccat tccggcgccg ccgcagaggc cgcacgtgaa ggcgcgctcg acgtcgtcgg 420  
cgaggcttcc gccggtgact gctaggccag tggcgaggcc tgc

(2) INFORMATION FOR SEQ ID NO:1717:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 153 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..153  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500946  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:  
Ser Thr His His His His Gln Gln His Ile Asn Leu Ala Ser Ser Arg  
1                  5                  10                  15  
Asn Thr Arg Gly Asn Arg Ser Met Ala Asn Asn Arg Ile Phe Asp Glu  
                  20                  25                  30  
Tyr Asn Pro Ala Val Glu Trp Ser Arg Ser Asp Glu Ala Asp Ala Val  
                  35                  40                  45  
Arg Ile Ser Leu Pro Gly Phe Lys Arg Glu Asp Ile Arg Val Leu Val  
                  50                  55                  60  
Asp Ser His Gly His Leu Arg Thr Arg Gly Glu Arg His Ile Ala Gly  
65                  70                  75                  80  
Asn Arg Trp Ser Arg Phe Gln Thr Asp Val Asp Leu Pro Ala Asn Cys  
                  85                  90                  95  
Asn Ala Asp Gly Ile Arg Ala Lys Phe Glu Asn Asp Arg Leu Thr Ile  
                  100                 105                 110  
Thr Leu Pro Lys Ser Thr Ser Ser Ala Pro Ile Pro Ala Pro Pro Gln  
                 115                 120                 125  
Arg Pro His Val Lys Ala Pro Ser Thr Ser Ser Ala Arg Leu Pro Pro  
130                 135                 140  
Val Thr Ala Arg Pro Val Ala Arg Pro  
145                 150

(2) INFORMATION FOR SEQ ID NO:1718:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 130 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

```
Met Ala Asn Asn Arg Ile Phe Asp Glu Tyr Asn Pro Ala Val Glu Trp
1 5 10 15
Ser Arg Ser Asp Glu Ala Asp Ala Val Arg Ile Ser Leu Pro Gly Phe
 20 25 30
Lys Arg Glu Asp Ile Arg Val Leu Val Asp Ser His Gly His Leu Arg
 35 40 45
Thr Arg Gly Glu Arg His Ile Ala Gly Asn Arg Trp Ser Arg Phe Gln
 50 55 60
Thr Asp Val Asp Leu Pro Ala Asn Cys Asn Ala Asp Gly Ile Arg Ala
65 70 75 80
Lys Phe Glu Asn Asp Arg Leu Thr Ile Thr Leu Pro Lys Ser Thr Ser
 85 90 95
Ser Ala Pro Ile Pro Ala Pro Pro Gln Arg Pro His Val Lys Ala Pro
 100 105 110
Ser Thr Ser Ser Ala Arg Leu Pro Pro Val Thr Ala Arg Pro Val Ala
 115 120 125
Arg Pro
130
```

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1500948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

```
Met Glu Pro Leu Arg Arg Gly Gly Arg Arg Pro Asp Leu Ala Pro Arg
1 5 10 15
Val Gln Glu Gly Gly His Thr Arg Ala Gly Gly Gln Pro Arg Pro Pro
 20 25 30
Ala Asp Ala Arg Arg Ala Ala His Arg Arg Gln Gln Val Glu Pro Leu
 35 40 45
Pro Asp Gly Arg Arg Pro Pro Arg Gln Leu Gln Arg Arg Arg His Pro
 50 55 60
Arg Gln Val Arg Glu Arg Gln Ala His His His Ala Pro Gln Glu His
65 70 75 80
Leu Leu Gly Ala His Ser Gly Ala Ala Ala Glu Ala Ala Arg Glu Gly
 85 90 95
Ala Val Asp Val Val Gly Glu Ala Ser Ala Gly Asp Cys
 100 105
```

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1500953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

```
ctcgcagcca gcaggacacc actcatcttc ttctcccccg cctcgtttcc atcgccacca 60
ccctcttctc ctgcggtcct cccccgtccc actcccaccc ccctcgccctc cgcctccact 120
gcagctgccg ccatgcagag cctcctcctg cccaccgctg ccgtggcccc ggtggcgctt 180
```

```
ccgtgcggaa ggcggaatct cccgggacgc ctctccgtcc gcgcctccgc gacggtggta 240
gcggcaccgc ggcgggagac ggatcccaag aagcgggtgg tgatcacggg gatggggctg 300
gtctccggtt tcgggaacga tgtagacgct tactacgacc gcctgctagt cggggagagc 360
ggcatcgggc ccatcgaccg cttcgacgct tctaagttcc ccaccgctt tgccggtcag 420
atccggggct tctcctccga gggatacatc gacggaaaga acgaccgcmg cttgatgat 480
tgccctccgat actgcatcgt cagtggcaag aaggctctcg
```

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

```
Leu Ala Ala Ser Arg Thr Pro Leu Ile Phe Phe Ser Pro Ala Ser Phe
1 5 10 15
Pro Ser Pro Pro Ser Ser Pro Ala Val Leu Pro Arg Pro Thr Pro
20 25 30
Thr Pro Leu Ala Ser Ala Ser Thr Ala Ala Ala Ala Met Gln Ser Leu
35 40 45
Leu Leu Pro Thr Ala Ala Val Ala Pro Val Ala Pro Pro Cys Gly Arg
50 55 60
Arg Asn Leu Pro Gly Arg Leu Ser Val Arg Ala Ser Ala Thr Val Val
65 70 75 80
Ala Ala Pro Arg Arg Glu Thr Asp Pro Lys Lys Arg Val Val Ile Thr
85 90 95
Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val Asp Ala Tyr Tyr
100 105 110
Asp Arg Leu Leu Val Gly Glu Ser Gly Ile Gly Pro Ile Asp Arg Phe
115 120 125
Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln Ile Arg Gly Phe
130 135 140
Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Asp Arg Xaa Leu Asp Asp
145 150 155 160
Cys Leu Arg Tyr Cys Ile Val Ser Gly Lys Lys Ala Leu
165 170
```

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

```
Arg Ser Gln Gln Asp Thr Thr His Leu Leu Leu Pro Arg Leu Val Ser
1 5 10 15
Ile Ala Thr Thr Leu Phe Ser Cys Gly Pro Pro Pro Ser His Ser His
20 25 30
Pro Pro Arg Leu Arg Leu His Cys Ser Cys Arg His Ala Glu Pro Pro
35 40 45
Pro Ala His Arg Cys Arg Gly Pro Gly Gly Ala Ser Val Arg Lys Ala
50 55 60
Glu Ser Pro Gly Thr Pro Leu Arg Pro Arg Leu Arg Asp Gly Gly Ser
```

(2) INFORMATION FOR SEQ ID NO:1723:

(A) LENGTH: 129 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(1X) FEATURE.  
(A) NAM

(B) LOCATION: 1..129

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1723:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:11:10  
Gln Ser Leu Leu Leu Pro Thr Ala Ala Val Al

(2) INFORMATION FOR SEQ ID NO:1724:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1500963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 94 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..94  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500964  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:  
Met Lys Leu Leu Gly Trp Met His Arg Lys Leu Arg Gln Asn Ser Asn  
1                  5                  10                  15  
Asp Val Phe Lys Glu Phe Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys  
                  20                  25                  30  
Ile Thr Gly Leu Ala Ala Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala  
                  35                  40                  45  
Asn Glu Tyr Phe Ala Ala Asp Asn Asp Phe Thr Asn Asn His Pro Ser  
50                  55                  60  
Ser Pro Ala Ala Asp Leu Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr  
65                  70                  75                  80  
Ile Gly Thr Leu Gly Ile Ala Pro Ser Arg Val Cys Arg Cys  
                  85                  90  
(2) INFORMATION FOR SEQ ID NO:1726:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 88 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..88  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500965  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:  
Met His Arg Lys Leu Arg Gln Asn Ser Asn Asp Val Phe Lys Glu Phe  
1                  5                  10                  15  
Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys Ile Thr Gly Leu Ala Ala  
                  20                  25                  30  
Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala Asn Glu Tyr Phe Ala Ala  
                  35                  40                  45  
Asp Asn Asp Phe Thr Asn Asn His Pro Ser Ser Pro Ala Ala Asp Leu  
50                  55                  60  
Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr Ile Gly Thr Leu Gly Ile  
65                  70                  75                  80  
Ala Pro Ser Arg Val Cys Arg Cys  
                  85  
(2) INFORMATION FOR SEQ ID NO:1727:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 68 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..68  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500966  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:  
Met Met Cys Ser Lys Ser Ser Thr Thr Leu Glu Val Gly Arg Ala Thr  
1                  5                  10                  15

Ala Ser Pro Gly Trp Pro Arg Arg Thr Arg Pro Leu Ser Ser Pro Pro  
20 25 30  
Pro Thr Asn Thr Ser Pro Pro Thr Thr Ser Pro Thr Ile Ile His  
35 40 45  
Arg Arg Arg Pro Pro Thr Ser Ser Pro Leu Val Ala Ala Ala Ser Ser  
50 55 60  
Pro Leu Ala Arg  
65

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| tccgttccgy tccttcctcc ccctatctag ctagccttcc cgttctctgca tcgcggcgga   | 60  |
| gatggggcgcc tccaccacgc cgctcgcgtc ggcggcgggcg ctgcttctgca tgctgctcgc | 120 |
| gccgctcgcc gcggcgggcg acagcatgtc gatcgtctcc tacggcgagc ggasmgmsn     | 180 |
| aggaggcgcg gcggatgtac gccgagtggc tggcgggcgca cggccggacc tacaacgccg   | 240 |
| tcggsaggag gagcgcaggt tcgaggtgtt cagggacaac ctccgctacg tcgacgcca     | 300 |
| caacgccgcc gccgamggcg gcgtccactc cttccgcctc gggctcaacc gcttcgcca     | 360 |
| cctcaccaac gacgagtacc gcrccamcta cctcggcgctc aggagcaggc              |     |

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Arg Ser Xaa Pro Ser Ser Pro Tyr Leu Ala Ser Leu Pro Val Pro Ala |  |
| 1 5 10 15                                                       |  |
| Ser Arg Arg Arg Trp Ala Pro Pro Pro Arg Arg Ser Arg Arg Arg Arg |  |
| 20 25 30                                                        |  |
| Arg Cys Phe Cys Cys Cys Ser Arg Arg Ser Pro Arg Arg Arg Thr Ala |  |
| 35 40 45                                                        |  |
| Cys Arg Ser Ser Pro Thr Ala Ser Gly Xaa Xaa Xaa Glu Ala Arg Arg |  |
| 50 55 60                                                        |  |
| Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Asn Ala Val |  |
| 65 70 75 80                                                     |  |
| Xaa Arg Arg Ser Ala Gly Ser Arg Cys Ser Gly Thr Thr Ser Ala Thr |  |
| 85 90 95                                                        |  |
| Ser Thr Pro Thr Thr Pro Pro Pro Xaa Arg Ala Ser Thr Pro Ser Ala |  |
| 100 105 110                                                     |  |
| Ser Gly Ser Thr Ala Ser Pro Thr Ser Pro Thr Thr Ser Thr Xaa Pro |  |
| 115 120 125                                                     |  |
| Xaa Thr Ser Ala Ser Gly Ala Gly                                 |  |
| 130 135                                                         |  |

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500976  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:  
Met Gly Ala Ser Thr Thr Pro Leu Ala Ser Ala Ala Ala Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ala Pro Leu Ala Ala Ala Asp Ser Met Ser Ile Val  
20 25 30  
Ser Tyr Gly Glu Arg Xaa Xaa Xaa Gly Gly Ala Ala Asp Val Arg Arg  
35 40 45  
Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg Arg Xaa Glu Glu  
50 55 60  
Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr Val Asp Ala His  
65 70 75 80  
Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg Leu Gly Leu Asn  
85 90 95  
Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa Xaa Tyr Leu Gly  
100 105 110  
Val Arg Ser Arg  
115

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..88  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

Met Ser Ile Val Ser Tyr Gly Glu Arg Xaa Xaa Gly Gly Ala Ala  
1 5 10 15  
Asp Val Arg Arg Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg  
20 25 30  
Arg Xaa Glu Glu Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr  
35 40 45  
Val Asp Ala His Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg  
50 55 60  
Leu Gly Leu Asn Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa  
65 70 75 80  
Xaa Tyr Leu Gly Val Arg Ser Arg  
85

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..485  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

agcacatcga tcagtcgcgt gtctaggttt cctctctcac catagcgccc gctctgtgcg

```
ccttcgttca cctctccttc ctctcctccc tgcctgccag ggagagggga agtcagagggc 120
acggagtggc gcagagcaga cgcacgtgaa ccatnngtag ctgtccctgt cgtcgtcgtc 180
gtcgtcaacg aatccacaca aggaaaggat ggagaagaag ccgaccatcc tcatgaacag 240
gtacgagctc gggcgcacgc tcgggcaggg cacccttcgcc aagggtgtacc acggccggaa 300
cctcgcgtcc ggcgaaagcg tggccatcaa ggatcatcgac aaggagaagg tgatgcgcgt 360
cggcatgata gaccagatca agcgcgagat ctccgtcatg cgcctcgtcc gccaccccaa 420
cgtcgtgcag ctgcacgagg gtgatggcca gcaagagcaa gatatacttc gccatggagt 480
acgtc
```

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

```
Ala His Arg Ser Val Ala Cys Leu Gly Phe Leu Ser His His Ser Ala
1 5 10 15
Arg Ser Val Ala Leu Arg Ser Pro Leu Leu Pro Leu Leu Pro Ala Cys
20 25 30
Gln Gly Glu Gly Lys Ser Glu Ala Arg Ser Gly Ala Glu Gln Thr His
35 40 45
Val Asn His Xaa
50
```

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

```
Met Glu Lys Lys Pro Thr Ile Leu Met Asn Arg Tyr Glu Leu Gly Arg
1 5 10 15
Thr Leu Gly Gln Gly Thr Phe Ala Lys Val Tyr His Gly Arg Asn Leu
20 25 30
Ala Ser Gly Glu Ser Val Ala Ile Lys Val Ile Asp Lys Glu Lys Val
35 40 45
Met Arg Val Gly Met Ile Asp Gln Ile Lys Arg Glu Ile Ser Val Met
50 55 60
Arg Leu Val Arg His Pro Asn Val Val Gln Leu His Glu Gly Asp Gly
65 70 75 80
Gln Gln Glu Gln Asp Ile Leu Arg His Gly Val Arg
85 90
```

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide



(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1500988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

```
Met Asn Arg Tyr Glu Leu Gly Arg Thr Leu Gly Gln Gly Thr Phe Ala
1 5 10 15
Lys Val Tyr His Gly Arg Asn Leu Ala Ser Gly Glu Ser Val Ala Ile
20 25 30
Lys Val Ile Asp Lys Glu Lys Val Met Arg Val Gly Met Ile Asp Gln
35 40 45
Ile Lys Arg Glu Ile Ser Val Met Arg Leu Val Arg His Pro Asn Val
50 55 60
Val Gln Leu His Glu Gly Asp Gly Gln Gln Glu Gln Asp Ile Leu Arg
65 70 75 80
His Gly Val Arg
```

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1500992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

```
aacatctcct cacttcacac cactcccgcc attgtcctgc gcctttctgc accgccacac 60
acacccccgt ccaatccaat ggcgccctgc caagccgtcc tcgcggtcgt ggtcctcgcc 120
gcgctgctcc cgctcgccct ctctcgcggg ctgcggcttg gccaccaccg cccagccgca 180
cccgaggccg caccggtcacg caccgctcgg aggtggcgcg tggctctcgg cccacgccac 240
cttctacggc ggcgggcgacg cgctccggcac catggggcgga cgtgtgggta cggcaacctt 300
tacagccagg ggtacggcac caacacggcg gcgctgagca cggcgctctt caacaacggc 360
ctcagctgcg gcgcctgctt cgaggtgcgg tgcgamgcgg cggggggcgcg cggccgctcg 420
trcmtgcmgg gctccgtcgt ggtgacggcc accaacttct gc
```

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

```
Asn Ile Ser Ser Leu His Thr Thr Pro Ala Ile Val Leu Arg Leu Ser
1 5 10 15
Ala Pro Pro His Thr Pro Arg Ser Asn Pro Met Ala Pro Arg Gln Ala
20 25 30
Val Leu Ala Val Val Val Leu Ala Ala Leu Leu Pro Leu Ala Leu Ser
35 40 45
Arg Gly Leu Arg Leu Gly His His Arg Pro Ala Ala Pro Glu Ala Ala
50 55 60
Arg Ser Arg Thr Ala Arg Arg Trp Arg Val Val Leu Gly Pro Arg His
65 70 75 80
Leu Leu Arg Arg Arg Arg Arg Val Arg His His Gly Arg Thr Cys Gly
85 90 95
Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn Thr Ala Ala Leu
100 105 110
```

Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe Glu  
115 120 125  
Val Arg Cys Xaa Ala Ala Gly Gly Gly Arg Ser Xaa Xaa Xaa Gly  
130 135 140  
Ser Val Val Val Thr Ala Thr Asn Phe Cys  
145 150

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1500994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

His Leu Leu Thr Ser His His Ser Arg His Cys Pro Ala Pro Phe Cys  
1 5 10 15  
Thr Ala Thr His Thr Pro Leu Gln Ser Asn Gly Ala Ser Pro Ser Arg  
20 25 30  
Pro Arg Gly Arg Gly Pro Arg Arg Ala Ala Pro Ala Arg Pro Leu Ser  
35 40 45  
Arg Ala Ala Ala Trp Pro Pro Pro Pro Ser Arg Thr Arg Gly Arg Thr  
50 55 60  
Val Thr His Arg Ser Glu Val Ala Arg Gly Pro Arg Pro Thr Pro Pro  
65 70 75 80  
Ser Thr Ala Ala Ala Thr Arg Pro Ala Pro Trp Ala Asp Val Trp Val  
85 90 95  
Arg Gln Pro Leu Gln Pro Gly Val Arg His Gln His Gly Gly Ala Glu  
100 105 110  
His Gly Ala Leu Gln Gln Arg Pro Gln Leu Arg Arg Leu Leu Arg Gly  
115 120 125  
Ala Val Arg Xaa Gly Gly Gly Arg Arg Pro Leu Xaa Xaa Xaa Gly Leu  
130 135 140  
Arg Arg Gly Asp Gly His Gln Leu Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1500995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

Met Ala Pro Arg Gln Ala Val Leu Ala Val Val Val Leu Ala Ala Leu  
1 5 10 15  
Leu Pro Leu Ala Leu Ser Arg Gly Leu Arg Leu Gly His His Arg Pro  
20 25 30  
Ala Ala Pro Glu Ala Ala Arg Ser Arg Thr Ala Arg Arg Trp Arg Val  
35 40 45  
Val Leu Gly Pro Arg His Leu Leu Arg Arg Arg Arg Arg Val Arg His  
50 55 60  
His Gly Arg Thr Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly  
65 70 75 80  
Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser

(2) INFORMATION FOR SEQ ID NO:1740:

(A) LENGTH: 436 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..436

(D) OTHER INFORMATION: / Ceres Seq. ID 1501005

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO:1 |            |            |            |            |            |  |     |
|----------------------------------------|------------|------------|------------|------------|------------|--|-----|
| ggctatccaag                            | gctccagtcg | tcccgcgatt | agttgtactg | tacattgttc | ctgcgaagac |  | 60  |
| actgggctcg                             | ccgggtcaat | cggcagcttg | aacaagccat | ggcggcgcac | cggccgaacg |  | 120 |
| ccgcggcgcc                             | gctgctcgcc | aagctcgacg | ccaccgccac | gccgccggcg | aasgcacaca |  | 180 |
| agtacccctt                             | cttctgcgcc | gtgctcgcat | ccatgacctc | cgtgtctatg | ggctacaacg |  | 240 |
| tcgcggtgac                             | gagcggcgcg | cagatcttca | tggcggagga | cctcgggatg | agcgacgcgc |  | 300 |
| agatcgaggt                             | gctctcgggg | gtcatcaaca | tatactcgct | cgtcggcgcg | ctgctggcag |  | 360 |
| ctcggacctc                             | cgaccgtctc | ggcggcgccc | tcaccatcgt | cctcgccaac | gccttcttcc |  | 420 |
| tcctcggccc                             | gctcgc     |            |            |            |            |  |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1501006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1501007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742:

Met Ala Ala His Arg Pro Asn Ala Ala Ala Pro Leu Leu Ala Lys Leu  
1 5 10 15  
Asp Ala Thr Ala Thr Pro Pro Ala Xaa Ala Xaa Lys Tyr Pro Phe Phe  
20 25 30  
Cys Ala Val Leu Ala Ser Met Thr Ser Val Leu Met Gly Tyr Asn Val  
35 40 45  
Ala Val Thr Ser Gly Ala Gln Ile Phe Met Ala Glu Asp Leu Gly Met  
50 55 60  
Ser Asp Ala Gln Ile Glu Val Leu Ser Gly Val Ile Asn Ile Tyr Ser  
65 70 75 80  
Leu Val Gly Ala Leu Leu Ala Gly Trp Thr Ser Asp Arg Leu Gly Arg  
85 90 95  
Arg Leu Thr Ile Val Leu Ala Asn Ala Phe Phe Leu Val Gly Pro Leu  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1501008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

Met Thr Ser Val Leu Met Gly Tyr Asn Val Ala Val Thr Ser Gly Ala  
1 5 10 15  
Gln Ile Phe Met Ala Glu Asp Leu Gly Met Ser Asp Ala Gln Ile Glu  
20 25 30  
Val Leu Ser Gly Val Ile Asn Ile Tyr Ser Leu Val Gly Ala Leu Leu  
35 40 45  
Ala Gly Trp Thr Ser Asp Arg Leu Gly Arg Arg Leu Thr Ile Val Leu  
50 55 60  
Ala Asn Ala Phe Phe Leu Val Gly Pro Leu  
65 70

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..528

(D) OTHER INFORMATION: / Ceres Seq. ID 1501016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

aagacttcgt cgtcaccaaa aaaataaagc agaaaaaac agagagtagt agactacgac 60  
agcgtccgtc gaaccggagg gtcggaggcg gaggcgaaga tgaggaagaa gctcggcacc 120  
cggttccccg cggctcgaat caaaaagata atgcaagcag atgaggatgt tggaaagatt 180  
gcattagcag tgcctgtttt agtctcgagg gctcttgaat tgtttttaca agatttaatt 240  
gaccggactt atgaaattac tcttcaaagt ggagcaaaga cactgaattc cttccacctg 300  
aagcaatgtg tgaagaggta cagttctttt gatttcctaa ctgaagttgt cagcaaggta 360  
ccagatcttg gtggtgctga ttcattgtgga gatgaaagag tgttacctag aagaagaaag 420  
tcaaattggc gtgaccaga gaatgatgaa tcaagatcta gtaaatggc tataaganat 480  
gcaaatacca ncnccagagg gacgtdggar gggctcgaggc agagggcg

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..143  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501017  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:  
Met Arg Lys Lys Leu Gly Thr Arg Phe Pro Ala Ala Arg Ile Lys Lys  
1                  5                  10                  15  
Ile Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro  
                  20                  25                  30  
Val Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp  
                  35                  40                  45  
Arg Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser  
                  50                  55                  60  
Phe His Leu Lys Gln Cys Val Lys Arg Tyr Ser Phe Asp Phe Leu  
65                  70                  75                  80  
Thr Glu Val Val Ser Lys Val Pro Asp Leu Gly Gly Ala Asp Ser Cys  
                  85                  90                  95  
Gly Asp Glu Arg Val Leu Pro Arg Arg Arg Lys Ser Asn Gly Ser Asp  
                  100                 105                 110  
Pro Glu Asn Asp Glu Ser Arg Ser Ser Lys Met Ala Ile Arg Xaa Ala  
                 115                 120                 125  
Asn Thr Xaa Xaa Arg Gly Thr Xaa Xaa Gly Ser Arg Gln Arg Ala  
130                 135                 140  
(2) INFORMATION FOR SEQ ID NO:1746:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 126 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..126  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1501018  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:  
Met Gln Ala Asp Glu Asp Val Gly Lys Ile Ala Leu Ala Val Pro Val  
1                  5                  10                  15  
Leu Val Ser Arg Ala Leu Glu Leu Phe Leu Gln Asp Leu Ile Asp Arg  
                  20                  25                  30  
Thr Tyr Glu Ile Thr Leu Gln Ser Gly Ala Lys Thr Leu Asn Ser Phe  
                  35                  40                  45  
His Leu Lys Gln Cys Val Lys Arg Tyr Ser Ser Phe Asp Phe Leu Thr  
                  50                  55                  60  
Glu Val Val Ser Lys Val Pro Asp Leu Gly Gly Ala Asp Ser Cys Gly  
65                  70                  75                  80  
Asp Glu Arg Val Leu Pro Arg Arg Arg Lys Ser Asn Gly Ser Asp Pro  
                  85                  90                  95  
Glu Asn Asp Glu Ser Arg Ser Ser Lys Met Ala Ile Arg Xaa Ala Asn  
                 100                 105                 110  
Thr Xaa Xaa Arg Gly Thr Xaa Xaa Gly Ser Arg Gln Arg Ala  
                 115                 120                 125  
(2) INFORMATION FOR SEQ ID NO:1747:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 538 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..538  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atccgcctcc | gaacccacga | ggccacgacc | cactactaca | tcagtccacc | gccaccgcgc | 60  |
| accgcgagtc | cgcgacagac | atccgcgccc | cggcctcact | ctcactcccc | agtccccacc | 120 |
| gtgcccgcac | aagcgacgcg | acgcagccac | gcagggagag | ggaaatggcc | acggccgcga | 180 |
| ctgccacggc | ggggagtaga | gcagccgtgc | tgctgctgct | ctcgctggcg | ctggcgctgg | 240 |
| cgtcgcgccc | ctccgacgcc | ggcgcgggcg | gcgactgcc  | cttcccggcc | gtgttcaact | 300 |
| tcggcgactc | caactcggac | acggggcgcc | tgtcatcgct | cttcggcgcc | gcaccgccgc | 360 |
| ccaacggcag | gaccttcttc | ggcatgccc  | cmggccgcta | ctgcgatggt | cgcctcgtca | 420 |
| tcgacttcat | cgtgaaacc  | tggggctgac | tcacctcagt | gcgtacctga | actcgatcgg | 480 |
| aagcaacttc | acacagggag | ccaactttgc | aacagctggt | tcatcgatca | gaagacag   |     |

(2) INFORMATION FOR SEQ ID NO:1748:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 179 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..179  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Arg | Leu | Arg | Thr | His | Glu | Ala | Thr | His | Tyr | Tyr | Ile | Ser | Pro |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Pro | Pro | Arg | Thr | Ala | Ser | Pro | Arg | Gln | Thr | Ser | Ala | Pro | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ser | His | Ser | Pro | Val | Pro | Thr | Val | Pro | Pro | Gln | Ala | Thr | Arg | Arg |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | His | Ala | Gly | Arg | Gly | Lys | Trp | Pro | Arg | Pro | Arg | Leu | Pro | Arg | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Gly | Val | Glu | Gln | Pro | Cys | Cys | Cys | Ser | Arg | Trp | Arg | Trp | Arg | Trp |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Arg | Cys | Gly | Pro | Pro | Thr | Pro | Ala | Arg | Ala | Ala | Thr | Ala | Thr | Ser | Arg |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Cys | Ser | Thr | Ser | Ala | Thr | Pro | Thr | Arg | Thr | Arg | Ala | Ala | Cys | His |
|     |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |
| Arg | Ser | Ser | Ala | Pro | His | Arg | Arg | Pro | Thr | Ala | Gly | Pro | Ser | Ser | Ala |
|     |     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |
| Cys | Pro | Xaa | Ala | Ala | Thr | Ala | Met | Val | Ala | Ser | Ser | Ser | Thr | Ser | Ser |
|     |     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |
| Leu | Lys | Pro | Gly | Ala | Asp | Ser | Pro | Gln | Cys | Val | Pro | Glu | Leu | Asp | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Lys | Gln | Leu | His | Thr | Gly | Ser | Gln | Leu | Cys | Asn | Ser | Trp | Phe | Ile | Asp |
|     |     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Lys | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1749:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 148 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

```
Pro Pro Pro Asn Pro Arg Gly His Asp Pro Leu Leu His Gln Ser Thr
1 5 10 15
Ala Thr Ala His Arg Glu Ser Ala Thr Asp Ile Arg Ala Pro Ala Ser
 20 25 30
Leu Ser Leu Pro Ser Pro His Arg Ala Ala Thr Ser Asp Ala Thr Gln
 35 40 45
Pro Arg Arg Glu Arg Glu Met Ala Thr Ala Ala Thr Ala Thr Ala Gly
 50 55 60
Ser Arg Ala Ala Val Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala
 65 70 75 80
Leu Arg Pro Ser Asp Ala Gly Ala Gly Gly Asp Cys His Phe Pro Ala
 85 90 95
Val Phe Asn Phe Gly Asp Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser
 100 105 110
Leu Phe Gly Ala Ala Pro Pro Pro Asn Gly Arg Thr Phe Phe Gly Met
 115 120 125
Pro Xaa Gly Arg Tyr Cys Asp Gly Arg Leu Val Ile Asp Phe Ile Ala
 130 135 140
Glu Thr Trp Gly
145
```

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

```
Met Ala Thr Ala Ala Thr Ala Thr Ala Gly Ser Arg Ala Ala Val Leu
1 5 10 15
Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala Leu Arg Pro Ser Asp Ala
 20 25 30
Gly Ala Gly Gly Asp Cys His Phe Pro Ala Val Phe Asn Phe Gly Asp
 35 40 45
Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser Leu Phe Gly Ala Ala Pro
 50 55 60
Pro Pro Asn Gly Arg Thr Phe Phe Gly Met Pro Xaa Gly Arg Tyr Cys
 65 70 75 80
Asp Gly Arg Leu Val Ile Asp Phe Ile Ala Glu Thr Trp Gly
 85 90
```

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1501027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

```
accctctccag tcaggccgtc ccgcgccgac gtcaacggag acgtgtcaac ggcggcggtg
agaagacca taaccttcta gatttttttc cgctgcctca atggatctct gggagagggc
```

60  
120

```
ccggggccttc gccggcgagg cggcgaacgg tcgcaggaac tctccgcgga ggcggccaag 180
cgctcgtcgg cgctggtctc ggagacggcg aagaagtcca aggagatctt ctccgaaacc 240
gcctccaagt cgcgggagat cgccgctgag gccaccaagc aggccgacct cctcgccggc 300
cagatcaagc acctcgctc cgacctccct gtgccttcga tcccgcctat ccccgcgatc 360
ccgcctatcc ccgcccgtgc ctcgtcggtg cccgacgcgg ccgagcttga gtgctacggc 420
atcaccgacg acctccgcga gttcgtcaag ggcattgacca taaacacctt ccgcgacttc 480
ccactgc
```

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1501028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

```
Pro Ser Ser Gln Ala Val Pro Arg Arg Arg Gln Arg Arg Val Asn
1 5 10 15
Gly Gly Gly Glu Lys Thr His Asn Leu Leu Asp Phe Phe Pro Leu Pro
20 25 30
Gln Trp Ile Ser Gly Arg Gly Pro Gly Pro Ser Pro Ala Arg Arg Arg
35 40 45
Thr Val Ala Gly Thr Leu Arg Gly Gly Gly Gln Ala Leu Val Gly Ala
50 55 60
Gly Leu Gly Asp Gly Glu Val Gln Gly Asp Leu Leu Arg Asn Arg
65 70 75 80
Leu Gln Val Ala Gly Asp Arg Arg
85
```

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1501029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

```
Met Asp Leu Trp Glu Arg Ala Arg Ala Phe Ala Gly Glu Ala Asn
1 5 10 15
Gly Arg Arg Asn Ser Pro Arg Arg Arg Pro Ser Ala Arg Arg Trp
20 25 30
Ser Arg Arg Arg Arg Arg Ser Pro Arg Arg Ser Ser Pro Lys Pro Pro
35 40 45
Pro Ser Arg Gly Arg Ser Pro Leu Arg Pro Pro Ser Arg Pro Thr Ser
50 55 60
Ser Pro Ala Arg Ser Ser Thr Ser Pro Pro Thr Ser Leu Cys Leu Arg
65 70 75 80
Ser Arg Pro Ser Pro Arg Ser Arg Leu Ser Pro Pro Leu Pro Arg Arg
85 90 95
Cys Pro Thr Arg Pro Ser Leu Ser Ala Thr Ala Ser Pro Thr Thr Ser
100 105 110
Ala Ser Ser Ser Arg Ala
115
```

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501037

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| gtgctgccgc | cagatctaac | caaaccccgc  | gccctcctca  | cgcctccggcg | agctacggac  | 60  |
| tcagcagatc | accgtcgctc | gagttgtacc  | tgaaggcggtg | cccgtggaac  | cggccgcgag  | 120 |
| ataagggcgg | cgggaaggcg | ggcgacgatg  | ccggtggcag  | cgtcggccat  | ctacttcctc  | 180 |
| aaccttcgcg | gggacgtcct | catcaaccgc  | ctctaccgtg  | atgatgttgg  | gggaaatatg  | 240 |
| gttgatgcgt | tcagaatgca | tatcatgcaa  | acaaaagaac  | ttggcacatg  | ccctgttcgt  | 300 |
| caaataggag | gctgctcctt | cctttatatg  | aggatcagta  | atgtttacat  | tgtgatcgta  | 360 |
| gtagcagca  | atgctaagt  | tgcattgtrct | ttcaaatttg  | ttgtcgaggc  | ggtaggctctc | 420 |
| ttcaagtcct | acttcgggtg | agcttttgat  | gaagacgcta  | tcaggaataa  | ctttgttttg  | 480 |
| atatatgaac | ttcttgatga | gatcatggat  | ttt         |             |             |     |

- (2) INFORMATION FOR SEQ ID NO:1755:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501038

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Val | Ala | Ala | Ser | Ala | Ile | Tyr | Phe | Leu | Asn | Leu | Arg | Gly | Asp |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Leu | Ile | Asn | Arg | Leu | Tyr | Arg | Asp | Asp | Val | Gly | Gly | Asn | Met | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Ala | Phe | Arg | Met | His | Ile | Met | Gln | Thr | Lys | Glu | Leu | Gly | Thr | Cys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Pro | Val | Arg | Gln | Ile | Gly | Gly | Cys | Ser | Phe | Leu | Tyr | Met | Arg | Ile | Ser |  |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Asn | Val | Tyr | Ile | Val | Ile | Val | Val | Ser | Ser | Asn | Ala | Asn | Val | Ala | Cys |  |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Xaa | Phe | Lys | Phe | Val | Val | Glu | Ala | Val | Ala | Leu | Phe | Lys | Ser | Tyr | Phe |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gly | Gly | Ala | Phe | Asp | Glu | Asp | Ala | Ile | Arg | Asn | Asn | Phe | Val | Leu | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Tyr | Glu | Leu | Leu | Asp | Glu | Ile | Met | Asp | Phe |     |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |  |

- (2) INFORMATION FOR SEQ ID NO:1756:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501039

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Asp | Ala | Phe | Arg | Met | His | Ile | Met | Gln | Thr | Lys | Glu | Leu | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |

Thr Cys Pro Val Arg Gln Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg  
20 25 30  
Ile Ser Asn Val Tyr Ile Val Ile Val Val Ser Ser Asn Ala Asn Val  
35 40 45  
Ala Cys Xaa Phe Lys Phe Val Val Glu Ala Val Ala Leu Phe Lys Ser  
50 55 60  
Tyr Phe Gly Gly Ala Phe Asp Glu Asp Ala Ile Arg Asn Asn Phe Val  
65 70 75 80  
Leu Ile Tyr Glu Leu Leu Asp Glu Ile Met Asp Phe  
85 90

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

Met His Ile Met Gln Thr Lys Glu Leu Gly Thr Cys Pro Val Arg Gln  
1 5 10 15  
Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg Ile Ser Asn Val Tyr Ile  
20 25 30  
Val Ile Val Val Ser Ser Asn Ala Asn Val Ala Cys Xaa Phe Lys Phe  
35 40 45  
Val Val Glu Ala Val Ala Leu Phe Lys Ser Tyr Phe Gly Gly Ala Phe  
50 55 60  
Asp Glu Asp Ala Ile Arg Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu  
65 70 75 80  
Asp Glu Ile Met Asp Phe  
85

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| accagtcccc  | tttacatcca | cacacaacgc | gcaccacacc | acaccacacc | acccgacgcc  | 60  |
| aacgtccgag  | accaaactcc | gatccccact | atgccggcgg | acggggaggg | gctggcgccg  | 120 |
| gccgtccact  | tctggggcga | gcacccggcc | acggaggcgg | agttctactc | ggcgcacggc  | 180 |
| acggagggcg  | agccctccta | cttcaccacg | cccgaacggg | gcgcccggcg | gctcttcacg  | 240 |
| cgcgcggtga  | ggccccgcgc | gcccgaacgg | cccagggcgc | tcgtgttcat | ggtccacggc  | 300 |
| tacggcaatg  | acatcagctg | gacgttccag | tccacggcgg | tcttcctcgc | gcgggtccggg | 360 |
| ttcgccctgct | tcgcggccga | cctcccgggc | cacggccgct | ccac       |             |     |

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Pro | Leu | Tyr | Ile | His | Thr | Gln | Arg | Ala | Pro | His | His | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Asp | Ala | Asn | Val | Arg | Asp | Gln | Thr | Pro | Ile | Pro | Thr | Met | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Asp | Gly | Glu | Ala | Leu | Ala | Pro | Ala | Val | His | Phe | Trp | Gly | Glu | His |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Pro | Ala | Thr | Glu | Ala | Glu | Phe | Tyr | Ser | Ala | His | Gly | Thr | Glu | Gly | Glu |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Tyr | Phe | Thr | Thr | Pro | Asp | Ala | Gly | Ala | Arg | Arg | Leu | Phe | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ala | Trp | Arg | Pro | Arg | Ala | Pro | Xaa | Arg | Pro | Arg | Ala | Leu | Val | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Val | His | Gly | Tyr | Gly | Asn | Asp | Ile | Ser | Trp | Thr | Phe | Gln | Ser | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Val | Phe | Leu | Ala | Arg | Ser | Gly | Phe | Ala | Cys | Phe | Ala | Ala | Asp | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gly | His | Gly | Arg | Ser | His |     |     |     |     |     |     |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Pro | Phe | Thr | Ser | Thr | His | Asn | Ala | His | His | Thr | Thr | Pro | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Pro | Thr | Pro | Thr | Ser | Glu | Thr | Lys | Leu | Arg | Ser | Pro | Leu | Cys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Thr | Gly | Arg | Arg | Trp | Arg | Arg | Pro | Ser | Thr | Ser | Gly | Ala | Ser | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Pro | Arg | Arg | Arg | Ser | Ser | Thr | Arg | Arg | Thr | Ala | Arg | Arg | Ala | Ser |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Pro | Pro | Thr | Ser | Pro | Arg | Pro | Thr | Arg | Ala | Pro | Gly | Gly | Ser | Ser | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Arg | Gly | Gly | Pro | Ala | Arg | Pro | Xaa | Gly | Pro | Gly | Arg | Ser | Cys | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Ser | Thr | Ala | Thr | Ala | Met | Thr | Ser | Ala | Gly | Arg | Ser | Ser | Pro | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Ser | Ser | Arg | Gly | Pro | Gly | Ser | Pro | Ala | Ser | Arg | Pro | Thr | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Ala | Thr | Ala | Ala | Pro |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1501061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

```
Met Pro Ala Asp Gly Glu Ala Leu Ala Pro Ala Val His Phe Trp Gly
1 5 10 15
Glu His Pro Ala Thr Glu Ala Glu Phe Tyr Ser Ala His Gly Thr Glu
 20 25 30
Gly Glu Pro Ser Tyr Phe Thr Thr Pro Asp Ala Gly Ala Arg Arg Leu
 35 40 45
Phe Thr Arg Ala Trp Arg Pro Arg Ala Pro Xaa Arg Pro Arg Ala Leu
 50 55 60
Val Phe Met Val His Gly Tyr Gly Asn Asp Ile Ser Trp Thr Phe Gln
65 70 75 80
Ser Thr Ala Val Phe Leu Ala Arg Ser Gly Phe Ala Cys Phe Ala Ala
 85 90 95
Asp Leu Pro Gly His Gly Arg Ser His
 100 105
```

(2) INFORMATION FOR SEQ ID NO:1762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..503

(D) OTHER INFORMATION: / Ceres Seq. ID 1501090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

```
aacttcaacg agtcccattt tggcaaggct tcggagtacc aaactggcga attgcgacgt 60
tggcggaatt gtaatggcaa taattccttc ctccttcgtt ccccatctct cctctttcta 120
ggtttctacc cctcatcggt cctcgtctcca cggccatggt gaggatgaag caggtaaaga 180
tctcggtaaa gaaggacgtg gattcgtaca caatccgcgg cactaacaag gtcgtccatg 240
tgggcgactg cgtgctgatg cgggcgtcgg actcggacaa gcagccgtat gtrgcgcggg 300
tggaagaagat ggargccgac ggacgcggca gstgncgggt rcaggtrcgc tgggtactacc 360
gccctgagga atccaagggc ggtcgccggc agttccacgg cgccaaggag cttttccttt 420
ccgatcattt cgacctacag arcgccaca ccacgaggg gaaatgtgtt gtccactctt 480
tcaagaacta caccaagctt gat
```

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

```
Met Val Arg Met Lys Gln Val Lys Ile Ser Val Lys Lys Asp Val Asp
1 5 10 15
Ser Tyr Thr Ile Arg Gly Thr Asn Lys Val Val His Val Gly Asp Cys
 20 25 30
Val Leu Met Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg
 35 40 45
Val Glu Lys Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa
 50 55 60
Arg Trp Tyr Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe
65 70 75 80
His Gly Ala Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | His | Thr | Ile | Glu | Gly | Lys | Cys | Val | Val | His | Ser | Phe | Lys | Asn | Tyr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Lys | Leu | Asp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1501092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gln | Val | Lys | Ile | Ser | Val | Lys | Lys | Asp | Val | Asp | Ser | Tyr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Arg | Gly | Thr | Asn | Lys | Val | Val | His | Val | Gly | Asp | Cys | Val | Leu | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Ala | Ser | Asp | Ser | Asp | Lys | Gln | Pro | Tyr | Xaa | Ala | Arg | Val | Glu | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Xaa | Ala | Asp | Gly | Arg | Gly | Xaa | Xaa | Arg | Xaa | Gln | Xaa | Arg | Trp | Tyr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Arg | Pro | Glu | Glu | Ser | Lys | Gly | Gly | Arg | Arg | Gln | Phe | His | Gly | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Glu | Leu | Phe | Leu | Ser | Asp | His | Phe | Asp | Leu | Gln | Xaa | Ala | His | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Glu | Gly | Lys | Cys | Val | Val | His | Ser | Phe | Lys | Asn | Tyr | Thr | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |

Asp

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1501093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ala | Ser | Asp | Ser | Asp | Lys | Gln | Pro | Tyr | Xaa | Ala | Arg | Val | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Met | Xaa | Ala | Asp | Gly | Arg | Gly | Xaa | Xaa | Arg | Xaa | Gln | Xaa | Arg | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Tyr | Tyr | Arg | Pro | Glu | Glu | Ser | Lys | Gly | Gly | Arg | Arg | Gln | Phe | His | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Glu | Leu | Phe | Leu | Ser | Asp | His | Phe | Asp | Leu | Gln | Xaa | Ala | His |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ile | Glu | Gly | Lys | Cys | Val | Val | His | Ser | Phe | Lys | Asn | Tyr | Thr | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

Leu Asp

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..547
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| acgccaccgc | cacctccacc  | tcctcgaaac | cgccgcgacc  | gacgcagcga | abwnccttc  | 60  |
| ccgcgccgac | gccgaaaccc  | tagctcctct | tacgccatgg  | ccaccgtgtc | gctcactccg | 120 |
| caggcggctc | tctccaccga  | gtccggcggc | gccctggctt  | ctgccaccat | cctccgcttc | 180 |
| ccgccaaact | tcgtacgcca  | gctcagcacc | aaggcacgac  | gcaactgcag | caacatcggc | 240 |
| gtcgcgcaga | tcgtcgccgc  | cgctgggtcc | gactgcctcg  | ctgctcgccg | cctccgcggs | 300 |
| gcggnatgtc | agcgcaattc  | ctaacgctaa | ggttgcgcas  | cgtccgcoct | cgtattggcc | 360 |
| gagcgtaacc | tgctcggctc  | cgacgccagc | ctcgccgtcc  | acgcggggga | raggctkgga | 420 |
| agaaggatag | ccacggatgc  | tatcaccacg | ccggtagtga  | acacgtcggc | ctactggttc | 480 |
| aacaactcgc | aagagctaata | cgactttaan | gagggggargc | atgctagctt | cgagtatggg | 540 |

aggtatk

(2) INFORMATION FOR SEQ ID NO:1767:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..107
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Pro | Pro | Pro | Pro | Pro | Pro | Pro | Arg | Asn | Arg | Arg | Asp | Arg | Ser | Ser |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Xaa | Xaa | Phe | Pro | Arg | Arg | Arg | Arg | Asn | Pro | Ser | Ser | Ser | Tyr | Ala |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Met | Ala | Thr | Val | Ser | Leu | Thr | Pro | Gln | Ala | Val | Phe | Ser | Thr | Glu | Ser |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Gly | Gly | Ala | Leu | Ala | Ser | Ala | Thr | Ile | Leu | Arg | Phe | Pro | Pro | Asn | Phe |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     | 60  |     |     |     |     |  |
| Val | Arg | Gln | Leu | Ser | Thr | Lys | Ala | Arg | Arg | Asn | Cys | Ser | Asn | Ile | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Val | Ala | Gln | Ile | Val | Ala | Ala | Ala | Trp | Ser | Asp | Cys | Leu | Ala | Ala | Arg |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Leu | Arg | Xaa | Ala | Xaa | Cys | Gln | Arg | Asn | Ser |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1768:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 142 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..142
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | His | Arg | His | Leu | His | Leu | Leu | Glu | Thr | Ala | Ala | Thr | Asp | Arg | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Xaa | Xaa | Pro | Ser | Arg | Ala | Asp | Ala | Glu | Thr | Leu | Ala | Pro | Leu | Thr | Pro |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Trp | Pro | Pro | Cys | Arg | Ser | Leu | Arg | Arg | Arg | Ser | Ser | Pro | Pro | Ser | Pro |  |

35 40 45  
Ala Ala Pro Trp Leu Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser  
50 55 60  
Tyr Ala Ser Ser Ala Pro Arg His Asp Ala Thr Ala Ala Thr Ser Ala  
65 70 75 80  
Ser Arg Arg Ser Ser Pro Pro Arg Gly Pro Thr Ala Ser Leu Leu Ala  
85 90 95  
Ala Ser Ala Xaa Arg Xaa Val Ser Ala Ile Pro Asn Ala Lys Val Ala  
100 105 110  
Xaa Arg Pro Pro Ser Tyr Trp Pro Ser Val Thr Cys Ser Ala Pro Thr  
115 120 125  
Pro Ala Ser Pro Ser Thr Arg Gly Xaa Gly Xaa Glu Glu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser  
1 5 10 15  
Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe  
20 25 30  
Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly  
35 40 45  
Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg  
50 55 60  
Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..921
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

artagcttcr cwcrrrctc crggggctcc gcrgtctccg tagtccgctc cggcgccacg 60  
gcccggctcg gaggggcgtt tcggggaggc cgaacgganc gccagcggtt ccgtttgggt 120  
ggcgtggagg cgaactgctg ctggagcgt acccggttt cctccgttca ctacgctcg 180  
cgatctgatg atcgttggct agttgctctg ccagartccc agccagcgct cctccgccat 240  
gatccargcg gtgatggtga tcagcaccca ggccaagccc cgcttctca agttctacag 300  
tttccagcca cccgagaagc atcaggacct cgtccgctgt gtcttccaat tactctctgc 360  
aaggccccag agcgcgagca attttgtcaa ggtggactcc atctttggcc cggaacaaa 420  
aatggtctac aagcatttgg gccacactat actttgtttt tgtctttgat agctctgaga 480  
acgagcttgc catgctcgac ctctgacaag tgtttgttga aacattggac agatgcttca 540  
agaatgtatg cgagcttgac atcgtattta acttcaacaa gctgcacacc attttggatg 600  
agatgatatc ggggggacag gtgatcgaaa caagttcaga acagataatg aaatctgtgg 660  
aagagattga aaggctggag aaacaatcga gcacaaccag cttcataccc aagtcgatta 720  
cagagcggtt taccggttga gcttccactc gtttccagaa caatgtgaca ttttaaggtgt 780  
gaacagaact gagatatact attcagtctc atttttagttc tccgataaga ctttgtatgc 840

ccccgcccc cggtgtatt ctgtaagcct gtaacctgga tatgaatgcg gcatctgcag 900  
tccaataata ctgcctgcgt t

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Xaa | Ala | Val | Met | Val | Ile | Ser | Thr | Gln | Ala | Lys | Pro | Arg | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Lys | Phe | Tyr | Ser | Phe | Gln | Pro | Pro | Glu | Lys | His | Gln | Asp | Leu | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Arg | Cys | Val | Phe | Gln | Leu | Leu | Ser | Ala | Arg | Pro | Glu | Ser | Ala | Ser | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Val | Lys | Val | Asp | Ser | Ile | Phe | Gly | Pro | Gly | Thr | Lys | Met | Val | Tyr |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | His | Leu | Gly | His | Thr | Ile | Leu | Cys | Phe | Cys | Leu |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ile | Ser | Thr | Gln | Ala | Lys | Pro | Arg | Leu | Leu | Lys | Phe | Tyr | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gln | Pro | Pro | Glu | Lys | His | Gln | Asp | Leu | Val | Arg | Cys | Val | Phe | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Ser | Ala | Arg | Pro | Glu | Ser | Ala | Ser | Asn | Phe | Val | Lys | Val | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Ile | Phe | Gly | Pro | Gly | Thr | Lys | Met | Val | Tyr | Lys | His | Leu | Gly | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ile | Leu | Cys | Phe | Cys | Leu |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asp | Leu | Val | Gln | Val | Phe | Val | Glu | Thr | Leu | Asp | Arg | Cys | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Asn | Val | Cys | Glu | Leu | Asp | Ile | Val | Phe | Asn | Phe | Asn | Lys | Leu | His |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Thr | Ile | Leu | Asp | Glu | Met | Ile | Ser | Gly | Gly | Gln | Val | Ile | Glu | Thr | Ser |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Glu | Gln | Ile | Met | Lys | Ser | Val | Glu | Glu | Ile | Glu | Arg | Leu | Glu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ser | Ser | Thr | Thr | Ser | Phe | Ile | Pro | Lys | Ser | Ile | Thr | Glu | Arg | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| acagagggat | cgatcatccgc | cccacccaca | actgctccag | atccaggcac | ggcacggcac | 60  |
| ggcagccggg | ccaacccaag  | ccggtcttct | cttctctctc | gtccgtccct | cactcgccgc | 120 |
| gacgtgacaa | gacaacgcga  | cgcgcgcgca | satnancgtc | gtccaaggca | cgcaggggcc | 180 |
| agccaaccaa | tcgctccgt   | ccgggtctgg | tggtggccgg | aatgggcctc | ctcgatcagc | 240 |
| tctgggacga | gacggtggcc  | ggcccgcgac | cggactccgg | cctcggcaag | ctccgcaagt | 300 |
| actctctctt | ctccccctcc  | tcctctctgt | cgctgtccat | cctgggtccc | gc         |     |

(2) INFORMATION FOR SEQ ID NO:1775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Glu | Gly | Ser | Ser | Ser | Ala | Pro | Pro | Thr | Thr | Ala | Pro | Asp | Pro | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ala | Arg | His | Gly | Ser | Arg | Ala | Asn | Pro | Ser | Pro | Ser | Ser | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Arg | Pro | Ser | Leu | Thr | Arg | Arg | Asp | Val | Thr | Arg | Gln | Arg | Asp | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Arg | Ala | Xaa | Xaa | Arg | Arg | Pro | Arg | His | Ala | Gly | Ala | Ser | Gln | Pro | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ser | Val | Arg | Val | Trp | Trp | Trp | Pro | Glu | Trp | Ala | Ser | Ser | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Thr | Arg | Arg | Trp | Pro | Ala | Arg | Asp | Arg | Thr | Pro | Ala | Ser | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ser | Ala | Ser | Thr | Pro | Pro | Ser | Pro | Pro | Pro | Pro | Pro | Arg | Arg | Arg |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Ser | Trp | Leu | Pro |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..116  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501125  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:  
Arg Gly Ile Val Ile Arg Pro Thr His Asn Cys Ser Arg Ser Arg His  
1                    5                    10                    15  
Gly Thr Ala Arg Gln Pro Gly Gln Pro Lys Pro Val Phe Ser Ser Leu  
            20                    25                    30  
Ser Ser Val Pro His Ser Pro Arg Asp Lys Thr Thr Arg Arg Ala  
            35                    40                    45  
Arg Xaa Xaa Xaa Ser Ser Lys Ala Arg Arg Gly Gln Pro Thr Asn Arg  
            50                    55                    60  
Val Arg Pro Gly Leu Val Val Ala Gly Met Gly Leu Leu Asp Gln Leu  
65                    70                    75                    80  
Trp Asp Glu Thr Val Ala Gly Pro Arg Pro Asp Ser Gly Leu Gly Lys  
            85                    90                    95  
Leu Arg Lys Tyr Ser Ser Phe Ser Pro Ser Ser Ser Ser Ser Ser  
            100                    105                    110  
Ile Leu Ala Pro  
            115

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| acaaacgaac aaggcattaa tctcctccaa tcctccagt atccccgggta accaaatcaa | 60  |
| atcagccctt tcttttgcta cggttttgta tttcatcgt tcgcccaga aaatcgaagg   | 120 |
| aacgcgccgc caccggccgc aacaaagcaa agcaggcctc cggctccctg aactgacttc | 180 |
| agaagtcacc aacgcaccca gcacagacag aagaccctcg ccggacgctc gctctcgccg | 240 |
| gggacaactc aatcccagag ccaggatggc ccgctacgat cgcgcgatca ccgtgttctc | 300 |
| acccgacggc cacctcttcc aggtcgagta cgccctcgag gccgtccgca agggcaacgc | 360 |
| cgtgtcggc gtccgcggcg tcgacaccgt cgtcctcggc gtcgagaaga agtccacccc  | 420 |
| caagctccag gactccaggt ccgtrcgcaa gatcgtkagc ctggacaccc acatcgc    |     |

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

Gln Thr Asn Lys Ala Leu Ile Ser Ser Asn Pro Pro Val Ile Pro Gly  
1                    5                    10                    15  
Asn Gln Ile Lys Ser Ala Leu Ser Phe Ala Thr Val Leu Tyr Phe Ile  
            20                    25                    30  
Val Ser Pro Lys Lys Ile Glu Gly Thr Arg Arg His Arg Pro Gln Gln  
            35                    40                    45  
Ser Lys Ala Gly Leu Arg Leu Pro Glu Leu Thr Ser Glu Val Thr Asn

50 55 60  
Ala Pro Ser Thr Asp Arg Arg Pro Ser Pro Asp Ala Arg Ser Arg Arg  
65 70 75 80  
Gly Gln Leu Asn Pro Glu Ala Arg Met Ala Arg Tyr Asp Arg Ala Ile  
85 90 95  
Thr Val Phe Ser Pro Asp Gly His Leu Phe Gln Val Glu Tyr Ala Leu  
100 105 110  
Glu Ala Val Arg Lys Gly Asn Ala Ala Val Gly Val Arg Gly Val Asp  
115 120 125  
Thr Val Val Leu Gly Val Glu Lys Lys Ser Thr Pro Lys Leu Gln Asp  
130 135 140  
Ser Arg Ser Xaa Arg Lys Ile Xaa Ser Leu Asp Thr His Ile  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

atcatgcatt cttcatggcg acggtgacca gtttgagctt ctcaggcagc tgcagacacg 60  
ggccacgcta tactgcccgg ccggcgccag ttctcgtagt agtcagctac ttaatgatca 120  
gctagctaga gcatcgcgna gattacaagt ngcgcgggc atggcggtgg cggcggtccc 180  
ttcctgcggc gccttcgccc ctccctgcct agtgagtaca aggagagcct tctcctcggt 240  
ggtggccatg gcttccgcag ccccggtgag agctcccagc aggaagccct tcgcccctcc 300  
tcgcgaggtta caccgccccg tggcgcactc gctgcccccg cagaagcggg agatcttoga 360  
gtcgctcgar tcgtgggcgg cggacaacat cctggtgctc ctcaagccccg tggagaggtc 420  
ctggcagccg cagactacct gc

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

Ser Cys Ile Leu His Gly Asp Gly Asp Gln Phe Glu Leu Leu Arg Gln  
1 5 10 15  
Leu Gln Thr Arg Ala Thr Leu Tyr Cys Pro Ala Gly Gly Ser Ser Arg  
20 25 30  
Ser Ser Gln Leu Leu Asn Asp Gln Leu Ala Arg Ala Ser Xaa Arg Leu  
35 40 45  
Gln Xaa Ala Ala Gly Met Ala Val Ala Ala Phe Pro Ser Cys Gly Ala  
50 55 60  
Phe Ala Pro Pro Cys Leu Val Ser Thr Arg Arg Ala Phe Ser Ser Val  
65 70 75 80  
Val Ala Met Ala Ser Ala Ala Pro Val Arg Ala Pro Ser Arg Lys Pro  
85 90 95  
Phe Ala Pro Pro Arg Glu Val His Arg Pro Val Ala His Ser Leu Pro  
100 105 110  
Pro Gln Lys Arg Glu Ile Phe Glu Ser Leu Xaa Ser Trp Ala Ala Asp  
115 120 125

Asn Ile Leu Val Leu Leu Lys Pro Val Glu Arg Ser Trp Gln Pro Gln  
130 135 140  
Thr Thr Cys  
145

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Val | Ala | Ala | Phe | Pro | Ser | Cys | Gly | Ala | Phe | Ala | Pro | Pro | Cys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Leu | Val | Ser | Thr | Arg | Arg | Ala | Phe | Ser | Ser | Val | Val | Ala | Met | Ala | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Ala | Pro | Val | Arg | Ala | Pro | Ser | Arg | Lys | Pro | Phe | Ala | Pro | Pro | Arg |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Glu | Val | His | Arg | Pro | Val | Ala | His | Ser | Leu | Pro | Pro | Gln | Lys | Arg | Glu |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Phe | Glu | Ser | Leu | Xaa | Ser | Trp | Ala | Ala | Asp | Asn | Ile | Leu | Val | Leu |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |  |
| Leu | Lys | Pro | Val | Glu | Arg | Ser | Trp | Gln | Pro | Gln | Thr | Thr | Cys |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

|            |            |             |            |            |             |     |
|------------|------------|-------------|------------|------------|-------------|-----|
| atcgcccgcn | gtcctctcct | ctcctccccg  | gccccttcac | tccaccaacg | aacccccacgc | 60  |
| aggcagcagc | acgcgcaasc | gcaaggaagg  | cacaaacact | annngccggg | catggcgacg  | 120 |
| cgggcgagac | tggagaaggg | cgggcccggc  | aggaaggagc | ccggcaaggt | gccgtcgccg  | 180 |
| ctgtaccgcg | agcacgargg | ggagcgggag  | tnggtgccct | ggctcgtccc | cgatcatctt  | 240 |
| gtcgccagca | tcaccgtctt | cgctcgtcacc | atgtacgcc  | acaactgcmc | cgcgcgcgac  | 300 |
| accaacaagt | gcgtcgcccc | cttctctcgm  | cgcttctcct | tccagccgct | gcgacagaac  | 360 |
| ccgctcttcg | ggccctcctc | cgccacgctc  | accaagatgg | gggccctggt | gtgggagaag  | 420 |
| gtggtgcacc | gccaccaggg | ctggcgccct  | ctctccagca | tgtk       |             |     |

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

Ile Ala Arg Xaa Pro Leu Leu Ser Ser Pro Ala Pro Ser Leu His Gln

|     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |
| Arg | Thr | Pro | Arg | Gln | Gln | His |
|     |     | 20  |     | 25  |     | 30  |
| His | Xaa | Xaa | Pro | Gly | Met | Ala |
|     |     | 35  |     | 40  |     | 45  |
| Pro | Ala | Arg | Lys | Glu | Pro | Gly |
|     |     | 50  |     | 55  |     | 60  |
| His | Xaa | Gly | Glu | Arg | Glu | Xaa |
| 65  |     |     |     | 70  |     | 75  |
| Val | Ala | Ser | Ile | Thr | Val | Phe |
|     |     | 85  |     | 90  |     | 95  |
| Xaa | Ala | Arg | Asp | Thr | Asn | Lys |
|     |     | 100 |     | 105 |     | 110 |
| Ser | Phe | Gln | Pro | Leu | Arg | Gln |
|     |     | 115 |     | 120 |     | 125 |
| Thr | Leu | Thr | Lys | Met | Gly | Ala |
|     |     | 130 |     | 135 |     | 140 |
| His | Gln | Gly | Trp | Arg | Leu | Leu |
| 145 |     |     |     | 150 |     |     |

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Pro | Xaa | Val | Leu | Ser | Ser | Pro | Pro | Arg | Pro | Leu | His | Ser | Thr | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Glu | Pro | His | Ala | Gly | Ser | Ser | Thr | Arg | Xaa | Arg | Lys | Glu | Gly | Thr | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Xaa | Xaa | Arg | Ala | Trp | Arg | Arg | Gly | Arg | Thr | Trp | Arg | Arg | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Arg | Arg | Gly | Arg | Ser | Pro | Ala | Arg | Cys | Arg | Arg | Arg | Cys | Thr | Arg | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Xaa | Gly | Ser | Gly | Ser | Xaa | Cys | Pro | Gly | Ser | Ser | Pro | Ser | Ser | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Pro | Ala | Ser | Pro | Ser | Ser | Ser | Ser | Pro | Cys | Thr | Pro | Thr | Thr | Xaa |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Arg | Ala | Thr | Pro | Thr | Ser | Ala | Ser | Pro | Ala | Ser | Ser | Xaa | Ala | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Ser | Ser | Arg | Cys | Asp | Arg | Thr | Arg | Ser | Ser | Gly | Pro | Pro | Pro | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Arg | Ser | Pro | Arg | Trp | Gly | Pro | Trp | Cys | Gly | Arg | Arg | Trp | Cys | Thr | Ala |
|     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Thr | Arg | Ala | Gly | Ala | Ser | Ser | Pro | Ala | Cys |     |     |     |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Arg Pro Xaa Ser Ser Pro Leu Leu Pro Gly Pro Phe Thr Pro Pro Thr  
1 5 10 15  
Asn Pro Thr Gln Ala Ala Ala Arg Ala Xaa Ala Arg Lys Ala Gln Thr  
20 25 30  
Leu Xaa Ala Gly His Gly Asp Ala Gly Gly Arg Gly Glu Gly Arg Ala  
35 40 45  
Gly Glu Glu Gly Ala Arg Gln Gly Ala Val Ala Val Pro Ala Ala  
50 55 60  
Arg Xaa Gly Ala Gly Xaa Gly Ala Leu Ala Arg Pro Arg His Leu Arg  
65 70 75 80  
Arg Gln His His Arg Leu Arg Arg His His Val Arg Gln Gln Leu Xaa  
85 90 95  
Arg Ala Arg His Gln Gln Val Arg Arg Pro Leu Pro Arg Xaa Leu Leu  
100 105 110  
Leu Pro Ala Ala Ala Thr Glu Pro Ala Leu Arg Ala Leu Leu Arg His  
115 120 125  
Ala His Gln Asp Gly Gly Pro Gly Val Gly Glu Gly Gly Ala Pro Pro  
130 135 140  
Pro Gly Leu Ala Pro Pro Leu Gln His  
145 150

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ttctcgccct accatcgccct gaccgacgcg cccgttttct cctgaaaaca gaaggctccg | 60  |
| gcctccggca tccgccaaaa aggggaaaaa aggagagata acacacacac acacaaaccc  | 120 |
| caatcccctg cggcgccgat ggaccgcgtc tcggcgggct ccggcgggcaa ctccctccc  | 180 |
| tccgtcggcc cgcagcgggc gaagcggcgc gtgtgctact tctacgaccc ggatgtgggc  | 240 |
| aactactact acgggcaggg ccattccgat aagccgcacc gcatccggat gacgcactcg  | 300 |
| ctgctggcgc gctacggcct cctcaaccag atgcaggtgt accgccccaa cccggcccgc  | 360 |
| gaccgcgacc tctgccgctt ccacgccgac gactacatca acttcctgcg ctccgtcacg  | 420 |
| ccggaaacgc agcaggacca gatccgcctg ctcaagcgct tcaacgctcg cgaggactgc  | 480 |

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met Asp Pro Ser Ser Ala Gly Ser Gly Asn Ser Leu Pro Ser Val  
1 5 10 15  
Gly Pro Asp Gly Gln Lys Arg Arg Val Cys Tyr Phe Tyr Asp Pro Asp  
20 25 30  
Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His Arg  
35 40 45

Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln  
50 55 60  
Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg  
65 70 75 80  
Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu  
85 90 95  
Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu  
100 105 110  
Asp Cys

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1501165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

Met Lys Pro His Arg Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr  
1 5 10 15  
Gly Leu Leu Asn Gln Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp  
20 25 30  
Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg  
35 40 45  
Ser Val Thr Pro Glu Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg  
50 55 60  
Phe Asn Val Gly Glu Asp Cys  
65 70

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1501166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln Met Gln  
1 5 10 15  
Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg Phe His  
20 25 30  
Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu Thr Gln  
35 40 45  
Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu Asp Cys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1501167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atctcacttt | ctttctcgct | gcgtccgcca | tgctctcgct | ttccttctct | ctgctttgct | 60  |
| tttgtgtcgt | cgatgtcgaa | aactccttcc | agaccaagct | tcgtctgctg | tcggcttgca | 120 |
| ccagtcctca | cggccacgt  | cgagggagac | gaagggatag | gaggcggagg | cggagggttc | 180 |
| aaaaaatggt | cgggagcatg | caggcgggtg | acccagcggg | cgggataagc | gcgttgctcg | 240 |
| cattgcgcca | stcctcgcca | tgctctagcc | gctggccctg | ctccgccctt | tcattggcgc | 300 |
| gcgtggccgg | ggcgtccgat | gttgcggcct | ccgcgttggg | gctagcggga | aaaggggaag | 360 |
| gcggcgcgct | cagtrgttct | acgggtgccg | gccgtctcgc | ccatggtcgc | cacacgaagg | 420 |
| aagatagcca | cgcgccggac | gcaggaggcc | ggggcgggtg | tacgagctga | ccccaggtg  | 480 |
| gtgaacatgt | tccatctctt | gcctattctg | ttcctctctg |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1501168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Phe | Phe | Leu | Ala | Ala | Ser | Ala | Met | Leu | Ser | Leu | Ser | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Cys | Phe | Cys | Val | Val | Asp | Val | Glu | Asn | Ser | Phe | Gln | Thr | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Leu | Ser | Ala | Cys | Thr | Ser | Pro | His | Gly | Pro | Arg | Arg | Gly |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Arg | Arg | Arg | Asp | Arg | Arg | Arg | Arg | Arg | Arg | Leu | Gln | Lys | Met | Val | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ser | Met | Gln | Ala | Val | Asp | Pro | Ala | Gly | Arg | Ile | Ser | Ala | Leu | Leu | Ala |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Leu | Arg | Xaa | Ser | Ser | Pro | Cys | Ser | Ser | Arg | Trp | Pro | Cys | Ser | Ala | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Leu | Ala | Arg | Val | Ala | Gly | Ala | Ser | Asp | Val | Ala | Ala | Ser | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Leu | Ala | Gly | Lys | Gly | Glu | Gly | Gly | Gly | Val | Ser | Xaa | Ser | Thr | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Gly | Arg | Leu | Ala | His | Gly | Arg | His | Thr | Lys | Glu | Asp | Ser | His | Ala |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| Pro | Asp | Ala | Gly | Gly | Arg | Gly | Gly | Cys | Thr | Ser |     |     |     |     |     |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1501169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Leu | Ser | Phe | Ser | Leu | Leu | Cys | Phe | Cys | Val | Val | Asp | Val |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Glu | Asn | Ser | Phe | Gln | Thr | Lys | Leu | Arg | Leu | Leu | Ser | Ala | Cys | Thr | Ser |



```

 20 25 30
Pro His Gly Pro Arg Arg Gly Arg Arg Asp Arg Arg Arg Arg
 35 40 45
Arg Leu Gln Lys Met Val Gly Ser Met Gln Ala Val Asp Pro Ala Gly
 50 55 60
Arg Ile Ser Ala Leu Leu Ala Leu Arg Xaa Ser Ser Pro Cys Ser Ser
 65 70 75 80
Arg Trp Pro Cys Ser Ala Leu Ser Leu Ala Arg Val Ala Gly Ala Ser
 85 90 95
Asp Val Ala Ala Ser Ala Leu Gly Leu Ala Gly Lys Gly Glu Gly Gly
 100 105 110
Gly Val Ser Xaa Ser Thr Gly Ala Gly Arg Leu Ala His Gly Arg His
 115 120 125
Thr Lys Glu Asp Ser His Ala Pro Asp Ala Gly Gly Arg Gly Gly Cys
 130 135 140
Thr Ser
145
```

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

```

Met Val Gly Ser Met Gln Ala Val Asp Pro Ala Gly Arg Ile Ser Ala
1 5 10 15
Leu Leu Ala Leu Arg Xaa Ser Ser Pro Cys Ser Ser Arg Trp Pro Cys
 20 25 30
Ser Ala Leu Ser Leu Ala Arg Val Ala Gly Ala Ser Asp Val Ala Ala
 35 40 45
Ser Ala Leu Gly Leu Ala Gly Lys Gly Glu Gly Gly Val Ser Xaa
 50 55 60
Ser Thr Gly Ala Gly Arg Leu Ala His Gly Arg His Thr Lys Glu Asp
 65 70 75 80
Ser His Ala Pro Asp Ala Gly Gly Arg Gly Gly Cys Thr Ser
 85 90
```

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1501203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

```

arctgcagcc agagccaccc accttatcgt catcctcgct cgctcctcat cgccagcgcc 60
tctctctctt cctccttctt cccaccgct gccgacatgg ctgcgcaaga agagaagacc 120
gctggtgttg ttgctgctgc tgccgatgtc gcgacagagg agcctacgcc ggcggsgagc 180
agcaacctca gccggctggg gcggcgcgca gggcaggacc atcggcgccc ggcggggctc 240
cgccaacccc ttcgacttct ccaccatgat gaaccttctc aatgacccta gcatcaagga 300
gatggcagag cagatcgcca aggaccgggc gttcacggag atggcggsa gctgcagaag 360
acgggtggtg ccccgcgga gcaacagcag cagcaggcgc ggcagcagca gcagcagctg 420
gacccgcaga agtacgtggc gacgatgcag cagctgatgc ag
```

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Cys | Ser | Gln | Ser | His | Pro | Pro | Tyr | Arg | His | Pro | Arg | Ser | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Ala | Ser | Ala | Ser | Ser | Ser | Ser | Ser | Phe | Phe | Pro | Thr | Ala | Ala | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Met | Ala | Ala | Gln | Glu | Glu | Lys | Thr | Ala | Val | Val | Val | Ala | Ala | Ala | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Val | Ala | Thr | Glu | Glu | Pro | Thr | Pro | Ala | Xaa | Ser | Ser | Asn | Leu | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Leu | Gly | Arg | Arg | Ala | Gly | Gln | Asp | His | Arg | Arg | Pro | Ala | Gly | Leu |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Arg | Gln | Pro | Leu | Arg | Leu | Leu | His | His | Asp | Glu | Pro | Ser | Gln |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Ala | Ala | Arg | Ala | Thr | His | Leu | Ile | Val | Ile | Leu | Ala | Arg | Ser | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ser | Pro | Ala | Pro | Pro | Pro | Pro | Pro | Pro | Ser | Ser | Pro | Pro | Leu | Pro | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Trp | Leu | Arg | Lys | Lys | Arg | Arg | Pro | Leu | Leu | Leu | Leu | Leu | Leu | Leu | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Ser | Arg | Gln | Arg | Ser | Leu | Arg | Arg | Arg | Xaa | Ala | Ala | Thr | Ser | Ala |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Gly | Trp | Gly | Gly | Ala | Gln | Gly | Arg | Thr | Ile | Gly | Ala | Arg | Arg | Gly | Ser |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Asn | Pro | Phe | Asp | Phe | Ser | Thr | Met | Met | Asn | Leu | Leu | Asn | Asp | Pro |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Ile | Lys | Glu | Met | Ala | Glu | Gln | Ile | Ala | Lys | Asp | Pro | Ala | Phe | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Met | Ala | Xaa | Ser | Cys | Arg | Arg | Arg | Trp | Cys | Pro | Arg | Gly | Ser | Asn |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Ser | Ser | Ser | Arg | Arg | Gly | Ser | Ser | Ser | Ser | Trp | Thr | Arg | Arg | Ser |     |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |
| Thr | Trp | Arg | Arg | Cys | Ser | Ser |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..103  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501206  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:  
Met Ser Arg Gln Arg Ser Leu Arg Arg Arg Xaa Ala Ala Thr Ser Ala  
1                    5                    10                    15  
Gly Trp Gly Gly Ala Gln Gly Arg Thr Ile Gly Ala Arg Arg Gly Ser  
                    20                    25                    30  
Ala Asn Pro Phe Asp Phe Ser Thr Met Met Asn Leu Leu Asn Asp Pro  
                    35                    40                    45  
Ser Ile Lys Glu Met Ala Glu Gln Ile Ala Lys Asp Pro Ala Phe Thr  
                    50                    55                    60  
Glu Met Ala Xaa Ser Cys Arg Arg Arg Trp Cys Pro Arg Gly Ser Asn  
65                    70                    75                    80  
Ser Ser Ser Arg Arg Gly Ser Ser Ser Ser Ser Trp Thr Arg Arg Ser  
                    85                    90                    95  
Thr Trp Arg Arg Cys Ser Ser  
                    100

(2) INFORMATION FOR SEQ ID NO:1798:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 509 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..509  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aataaatcgc | ggaattccca | acgccgcacc | ttcaccgccg | ggctccccag | tccaatccaa | 60  |
| cccaacccca | gtccggcgac | ggttcgggc  | agcgcgcgat | cggatcgctg | cgggttcggc | 120 |
| ttctcgctga | acggcgcgga | ttcctgcccc | cgatcggagg | gcgtyggctg | cggcgsctcg | 180 |
| gcgtctgata | tgctgcggtc | ggcttcttct | tgggararga | gtgggatgga | cggggaagcg | 240 |
| atccggatgg | gtggcggcaa | cttggcgccc | gcctacctct | ccggcgccgc | caccgcmacc | 300 |
| gccatcacca | tcgaggatcc | gaaccagaac | cagaaccaga | accagaacca | gaaccaaagc | 360 |
| cagttcctgt | tcagcgccaa | ctccacggcg | ctgcagctgt | tcggaagcrc | cgcggtcccc | 420 |
| acggttggtc | ctgctggtta | tataavttac | actgggaaac | accacacctc | ctgttatgaa | 480 |
| ccaagcaagt | acttcaaaca | tcggcgcatg |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1799:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 169 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..169  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

|                                                                    |  |
|--------------------------------------------------------------------|--|
| Asn Lys Ser Arg Asn Ser Gln Arg Arg Thr Phe Thr Ala Gly Leu Pro    |  |
| 1                    5                    10                    15 |  |
| Ser Pro Ile Gln Pro Asn Pro Ser Pro Ala Thr Val Pro Gly Ser Ala    |  |
| 20                    25                    30                     |  |
| Arg Ser Asp Arg Arg Gly Phe Gly Phe Ser Ser Asn Gly Ala Asp Ser    |  |
| 35                    40                    45                     |  |
| Cys Pro Arg Ser Glu Gly Xaa Gly Cys Gly Xaa Ser Ala Ser Asp Leu    |  |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Leu Arg Ser Ala Ser Ser Trp Xaa Xaa Ser Gly Met Asp Gly Glu Ala |     |     |
| 65                                                              | 70  | 75  |
| Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala Tyr Leu Ser Gly Ala |     | 80  |
|                                                                 | 85  | 90  |
| Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro Asn Gln Asn Gln Asn |     | 95  |
|                                                                 | 100 | 105 |
| Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu Phe Ser Ala Asn Ser |     | 110 |
|                                                                 | 115 | 120 |
| Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val Pro Thr Val Gly Pro |     | 125 |
|                                                                 | 130 | 135 |
| Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro Pro Ser Cys Tyr Glu |     | 140 |
| 145                                                             | 150 | 155 |
| Pro Ser Lys Tyr Phe Lys His Arg Arg                             |     | 160 |
|                                                                 | 165 |     |

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Ile Asn Arg Gly Ile Pro Asn Ala Ala Pro Ser Pro Pro Gly Ser Pro |     |     |
| 1                                                               | 5   | 10  |
| Val Gln Ser Asn Pro Thr Pro Val Arg Arg Phe Arg Ala Ala Arg     |     | 15  |
|                                                                 | 20  | 25  |
| Asp Arg Ile Val Ala Gly Ser Ala Ser Arg Arg Thr Ala Arg Ile Pro |     | 30  |
|                                                                 | 35  | 40  |
| Ala Pro Asp Arg Arg Ala Xaa Ala Ala Ala Xaa Arg Arg Leu Ile Cys |     | 45  |
|                                                                 | 50  | 55  |
| Cys Gly Arg Leu Leu Leu Gly Xaa Xaa Val Gly Trp Thr Gly Lys Arg |     | 60  |
| 65                                                              | 70  | 75  |
| Ser Gly Trp Val Ala Ala Thr Trp Arg Pro Pro Thr Ser Pro Ala Pro |     | 80  |
|                                                                 | 85  | 90  |
| Pro Pro Xaa Pro Pro Ser Pro Cys Arg Ile Arg Thr Arg Thr Arg Thr |     | 95  |
|                                                                 | 100 | 105 |
| Arg Thr Arg Thr Arg Thr Lys Ala Ser Ser Cys Ser Ala Pro Thr Pro |     | 110 |
|                                                                 | 115 | 120 |
| Arg Arg Cys Ser Cys Ser Glu Xaa Pro Arg Ser Pro Arg Leu Val Leu |     | 125 |
|                                                                 | 130 | 135 |
|                                                                 |     | 140 |
| Leu Val Ile                                                     |     |     |
| 145                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

|                                                                 |   |    |
|-----------------------------------------------------------------|---|----|
| Met Asp Gly Glu Ala Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala |   |    |
| 1                                                               | 5 | 10 |
|                                                                 |   | 15 |

Tyr Leu Ser Gly Ala Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro  
20 25 30  
Asn Gln Asn Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu  
35 40 45  
Phe Ser Ala Asn Ser Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val  
50 55 60  
Pro Thr Val Gly Pro Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro  
65 70 75 80  
Pro Ser Cys Tyr Glu Pro Ser Lys Tyr Phe Lys His Arg Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aacggaactt agctgccgag cgcccaaagc cccaccgccg ctcccatcaa gcggcgctaa | 60  |
| aggtttcctc gcccgcaacg cgatgccgaa gaacaaggga aaggaggga agaaccggaa  | 120 |
| gcggggcaag aacgargcgg acgacgagaa gcgggagctg gntgttcaag gaggacgggc | 180 |
| aggagtacgc gcaggtgacg cggatgctgg gcaacggccg ctgcgaggcg ccgtcttcct | 240 |
| gaacacccgt tccgatcttt gcccagaagg tctacttggg catcaataag aaactcttct | 300 |
| ccctcaaact gattgtgggt ccacccctct ctgtctggaa aatgttgtca ccaaactacc | 360 |
| ctatttcctg ttccagtttg gcatggaagt ataagttgtg tacttctatt ctcaagttgt | 420 |
| tgtctttgta ttatgaaatg tttccaataa tcagcagttt ttgatgtatg gtcgtg     |     |

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Glu Leu Ser Cys Arg Ala Pro Lys Ala Pro Pro Pro Leu Pro Ser |  |
| 1 5 10 15                                                       |  |
| Ser Gly Ala Lys Gly Phe Leu Ala Arg Asn Ala Met Pro Lys Asn Lys |  |
| 20 25 30                                                        |  |
| Gly Lys Gly Gly Lys Asn Arg Lys Arg Gly Lys Asn Xaa Ala Asp Asp |  |
| 35 40 45                                                        |  |
| Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg Ala Gly Val Arg Ala |  |
| 50 55 60                                                        |  |
| Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg Gly Ala Val Phe Leu |  |
| 65 70 75 80                                                     |  |
| Asn Thr Arg Ser Asp Leu Cys Pro Glu Gly Leu Leu Gly His Gln     |  |
| 85 90 95                                                        |  |

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1501261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

```
Arg Asn Leu Ala Ala Glu Arg Pro Lys Pro His Arg Arg Ser His Gln
1 5 10 15
Ala Ala Leu Lys Val Ser Ser Pro Ala Thr Arg Cys Arg Arg Thr Arg
20 25 30
Glu Arg Glu Ala Arg Thr Gly Ser Gly Ala Arg Thr Xaa Arg Thr Thr
35 40 45
Arg Ser Gly Ser Trp Xaa Phe Lys Glu Asp Gly Gln Glu Tyr Ala Gln
50 55 60
Val Thr Arg Met Leu Gly Asn Gly Arg Cys Glu Ala Pro Ser Ser
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1501262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

```
Met Pro Lys Asn Lys Gly Lys Gly Lys Asn Arg Lys Arg Gly Lys
1 5 10 15
Asn Xaa Ala Asp Asp Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg
20 25 30
Ala Gly Val Arg Ala Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg
35 40 45
Gly Ala Val Phe Leu Asn Thr Arg Ser Asp Leu Cys Pro Glu Gly Leu
50 55 60
Leu Gly His Gln
65
```

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1501268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

```
acgatccac tctccccgt cactcaagg agtcaaggtg caaagctaag cttagctcat 60
tgctcaagct tccgtctctt tctctctgcg agactgcaca ctgccaccac gcgcaatggc 120
ggcattccac catttggtgc cggccttgct ccttctactc ctgctccctt ccacccttga 180
ggcgacgtcc tcggcgctgc ttggcatcag ctacggtcgc gttggcaaca acctccctgc 240
agctacatca gtgccgcaga ttgtggcttc cctgggcgtc ggccgcgtcc gactctacga 300
tgctgacagc accaccattc ggccttcgc caacacgggc gtcgagctcg tcgtcggcgt 360
ccctgacgag tgcctcgcca ctgtctccac cccgacgggc gcmgcctcct gggtccgctc 420
caacatttcc cctgcgctc ccggccacaa agatcgctt cctcacagtc ggcaacgag
```

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..159
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501269
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Thr | Leu | Pro | Ala | His | Leu | Lys | Glu | Ser | Arg | Cys | Lys | Ala | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Ser | Leu | Leu | Lys | Leu | Pro | Ser | Leu | Ser | Leu | Cys | Glu | Thr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| His | Cys | His | His | Ala | Gln | Trp | Arg | His | Ser | Thr | Ile | Cys | Cys | Arg | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Ser | Phe | Tyr | Ser | Cys | Ser | Leu | Pro | Pro | Leu | Arg | Arg | Arg | Pro | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Cys | Leu | Ala | Ser | Ala | Thr | Val | Ala | Leu | Ala | Thr | Thr | Ser | Leu | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | His | Gln | Cys | Arg | Arg | Leu | Trp | Leu | Pro | Trp | Ala | Ser | Ala | Ala | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Ser | Thr | Met | Leu | Thr | Ala | Pro | Pro | Phe | Ala | Pro | Ser | Pro | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ser | Ser | Ser | Ser | Ser | Ala | Ser | Leu | Thr | Ser | Ala | Ser | Pro | Leu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Pro | Arg | Arg | Ala | Xaa | Pro | Pro | Gly | Ser | Ala | Pro | Thr | Phe | Pro | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Ala | Leu | Pro | Ala | Thr | Lys | Ile | Ala | Phe | Leu | Thr | Val | Gly | Asn | Glu |     |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1808:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..121
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Phe | His | His | Leu | Leu | Pro | Ala | Leu | Leu | Leu | Leu | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Pro | Ser | Thr | Pro | Glu | Ala | Thr | Ser | Ser | Ala | Leu | Leu | Gly | Ile | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Arg | Val | Gly | Asn | Asn | Leu | Pro | Ala | Ala | Thr | Ser | Val | Pro | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Ala | Ser | Leu | Gly | Val | Gly | Arg | Val | Arg | Leu | Tyr | Asp | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Thr | Thr | Ile | Arg | Ala | Phe | Ala | Asn | Thr | Gly | Val | Glu | Leu | Val | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Val | Pro | Asp | Glu | Cys | Leu | Ala | Thr | Val | Ser | Thr | Pro | Thr | Gly | Xaa |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Ser | Trp | Val | Arg | Ser | Asn | Ile | Ser | Pro | Cys | Ala | Pro | Gly | His | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asp | Arg | Leu | Pro | His | Ser | Arg | Gln | Arg |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1809:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 422 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..422  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

|            |            |            |             |            |             |     |
|------------|------------|------------|-------------|------------|-------------|-----|
| aaggagagag | agagaggcag | agggagagat | tggagggagg  | cccctgcccc | aggcaagaga  | 60  |
| aaccgcggcg | cgcggagaga | gggtgagggt | gagttctcag  | aagcccgtga | ggacttggct  | 120 |
| gctcttgaga | aggactatga | ggaagtcggg | gcagaggggt  | ccgatgacga | gggtgacgag  | 180 |
| ggagacgact | attgagtagc | tggctaataa | gtagttctct  | ggtgggtaat | ggttggggtta | 240 |
| ttttgagtat | atactctatg | gttccactcc | attggatact  | gctgctgtgt | gtgtttccat  | 300 |
| tttgtagtat | gtagtaaatt | gttcgtagcc | ccctattggc  | catgattgtt | catatcatcc  | 360 |
| ttctttgggt | tgaacgcta  | ttcgtccaat | ttcgggtgtat | atgctataat | gctattatgt  | 420 |

tg

(2) INFORMATION FOR SEQ ID NO:1810:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 64 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..64  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Glu | Arg | Glu | Arg | Gly | Arg | Gly | Arg | Asp | Trp | Arg | Glu | Ala | Pro | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gln | Gly | Lys | Arg | Asn | Arg | Gly | Ala | Arg | Glu | Gly | Glu | Gly | Glu | Phe |     |  |
|     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |  |
| Ser | Glu | Ala | Arg | Glu | Asp | Leu | Ala | Ala | Leu | Glu | Lys | Asp | Tyr | Glu | Glu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Val | Gly | Ala | Glu | Gly | Ala | Asp | Asp | Glu | Gly | Asp | Glu | Gly | Asp | Asp | Tyr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..65  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Arg | Glu | Arg | Glu | Ala | Glu | Gly | Glu | Ile | Gly | Gly | Arg | Pro | Leu | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Ala | Arg | Glu | Thr | Ala | Ala | Arg | Gly | Glu | Arg | Val | Arg | Val | Ser | Ser |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Gln | Lys | Pro | Val | Arg | Thr | Trp | Leu | Leu | Leu | Arg | Arg | Thr | Met | Arg | Lys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Ser | Val | Gln | Arg | Val | Pro | Met | Thr | Arg | Val | Thr | Arg | Glu | Thr | Thr | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

Glu  
65

(2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..570
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| ataaagcacc | ctctccttgc | gccaattcgg  | acacggccac | cacacatccc  | ttcctctctt  | 60  |
| tctcctcgag | gctcgagcat | tctgtctgct  | cggacccac  | cgccacaggc  | tcggcgggcc  | 120 |
| ggcgatctcg | ctcaccggcg | ggaacatgac  | tacttcaagg | cgccttgctg  | acaggaagac  | 180 |
| cgcaaagtgc | cagaagaaca | tcaccaggag  | gggttctgtg | cctgaaacca  | ctgtcaagaa  | 240 |
| gggaaatgac | tacctgttg  | gccctctagt  | gcttgggttc | ttcatctttg  | tcgtcattgg  | 300 |
| atcatcgttg | tttcagatca | tcaggacggc  | aaccagcggc | ggggtggctt  | gagagccggc  | 360 |
| ccacatctaa | tccccagtat | agagagttgc  | ttgttataca | tgcattccagc | taggattggg  | 420 |
| tagcagctaa | aatgttaaac | gtgacaagac  | tgccctgcat | tccgttcatt  | tggtgggcct  | 480 |
| tgaatctgga | actgaaccat | aaggcagaat  | catgtacctt | atataaagtg  | ttaaattgggt | 540 |
| aactggatct | cagtgtttca | tttaattcttc |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1813:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..56
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | His | Pro | Leu | Leu | Ala | Arg | Ile | Arg | Thr | Arg | Pro | Pro | His | Ile |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Ser | Ser | Leu | Ser | Pro | Arg | Gly | Ser | Ser | Ile | Arg | Ala | Ala | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Pro | Gln | Ala | Arg | Arg | Ser | Gly | Asp | Leu | Ala | His | Arg | Arg | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Asp | Tyr | Phe | Lys | Ala | Pro | Cys |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1814:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..48
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Pro | Ser | Pro | Cys | Ala | Asn | Ser | Asp | Thr | Ala | Thr | Thr | His | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Leu | Ser | Phe | Ser | Ser | Arg | Leu | Glu | His | Ser | Cys | Cys | Ser | Asp | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Thr | Gly | Ser | Ala | Val | Arg | Arg | Ser | Arg | Ser | Pro | Ala | Gly | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..68  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501309  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:  
Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Thr Ala Lys Phe Gln  
1                  5                  10                  15  
Lys Asn Ile Thr Arg Arg Gly Ser Val Pro Glu Thr Thr Val Lys Lys  
                  20                  25                  30  
Gly Asn Asp Tyr Pro Val Gly Pro Leu Val Leu Gly Phe Phe Ile Phe  
                  35                  40                  45  
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser  
50                  55                  60  
Gly Gly Val Ala  
65

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1036 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1036  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501310  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:  
aacccaagag cgaaaatgga tccgcaccag ttcgccccct cccagcagtc ggcgctgacc 60  
atggaatcgg cggagatcac ggccgcgcgc gccgcgcgc gcgcacccaa cggcgctgcc 120  
cgggctatcg tcgaggacga cgacgaggac gacgacgtcc ccgaggtggc cgccctgcata 180  
tcgacgatgc tcgaccgcgg gggtagcgtg gagagccacc gcctcttcct ggcgcgcgc 240  
accgcgctgg agatgctccg cgaccgcgtt acgccgttcc ggaggaagag ctgcgccgga 300  
ccctccccga gttccgcgcc tgggtgggaat acaggccaga rctcgaacgc ctgccttct 360  
ccactaccct cgcctccgac ccgtccagca aggtgaaagt tgtgttctgt ccacctggac 420  
ctgtcaaaat cgcagctatc cggctgatat ataccgaagt caaagatgag aacttgtcca 480  
gactgattct gatactgcag ggcaaaataa tgtctacaac cagagaatcc atcaaggagw 540  
tctttcgatt taaagttgac acattccaga tcacggaatt actggtgaac atcactaagc 600  
atgtcctcaa gcccaagcat gaagtgttga ctgcagaggg gaaagctaag ctctgaagg 660  
agtacaatgt ggtggattca cagttgcctc gcatgctgga gaatgatgct gttgctcgt 720  
attacgggct aggcaaggga actggtgtta aggttatata cgacagcgag cttaccggga 780  
accatgtgac gtaccgatgc attacctgag gggcccatgt gtttcggtgg atgaagtgtc 840  
gtaagcagtc tgtaaaaaat tacctctaag aggggcaggt gacactgttc tgctaggcct 900  
ttgtaagcac ccaattatgc aggatgaagc tcgctgtaag ctattggtaa aatcatcttg 960  
cgccattgcc gtaccttaag tgcttggtgt taatcttgga aacagtgaga caactaatcc 1020  
tgtagtgagt tatctc

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 131 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1501311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

```
Asn Pro Arg Ala Lys Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln
1 5 10 15
Ser Ala Leu Thr Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala
20 25 30
Ala Arg Ala Pro Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp
35 40 45
Glu Asp Asp Asp Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu
50 55 60
Asp Arg Gly Gly Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg
65 70 75 80
Thr Ala Leu Glu Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys
85 90 95
Ser Ser Pro Gly Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly
100 105 110
Gln Xaa Ser Asn Ala Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg
115 120 125
Pro Ala Arg
130
```

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1501312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

```
Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln Ser Ala Leu Thr Met
1 5 10 15
Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Arg Ala Pro Asn
20 25 30
Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Val
35 40 45
Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly Ser
50 55 60
Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu Met
65 70 75 80
Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly Pro
85 90 95
Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn Ala
100 105 110
Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg
115 120 125
```

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1501313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Arg Ala Pro

1 5 10 15  
Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Asp  
20 25 30  
Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly  
35 40 45  
Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu  
50 55 60  
Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly  
65 70 75 80  
Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn  
85 90 95  
Ala Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| atagagacav | ggagggggag | tgggccgagg  | tcaataggat | ataactccag | gactcctctc | 60  |
| catcagaatc | agagacgagt | cgagtggagg  | ggcagaggcc | acaaaacaga | gagtacccaa | 120 |
| acgatcgatc | tgtgcatctc | cccgtccgctc | ccgcaaccat | ctaattcaga | agcagacatc | 180 |
| aatggcgagc | hacggctgca | acggcaacgg  | caacggcaac | ggcaacggca | agggcggtcc | 240 |
| ggcgggtgtg | gtggtaccgg | agatcaagtt  | caccaagctc | ttcatcaacg | gcgagttcgt | 300 |
| cgacgcgcgc | tccggcaaga | cattcgatac  | cagggaccga | ggtaccaggg | ctacacgctc | 360 |
| aaggagccta | tggcgctcgt | gggcgtcatc  | atcccctgga | acttccccac | catgatgttc | 420 |
| ttcctcaagg | tcagcccggc | gctcgccrcg  | ggctgcac   |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

Met Ala Ser Xaa Gly Cys Asn Gly Asn Gly Asn Gly Asn Gly  
1 5 10 15  
Lys Ala Ala Pro Ala Gly Val Val Val Pro Glu Ile Lys Phe Thr Lys  
20 25 30  
Leu Phe Ile Asn Gly Glu Phe Val Asp Ala Ala Ser Gly Lys Thr Phe  
35 40 45  
Asp Thr Arg Asp Pro Gly Thr Arg Ala Thr Arg Ser Arg Ser Leu Ser  
50 55 60  
Ala Ser Trp Ala Ser Ser Pro Gly Thr Ser Pro Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1501324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| gcctcgcgca | ctcgcaactta | acctagccgc | cagccctcga  | cgaccgacgc | gacgtcgct  | 60  |
| tcgcccctgc | tccaacccct  | gcccccttcg | tcgctccggc  | ctcggcagga | agatcctcca | 120 |
| tcgacggtcc | tgtegatgcc  | tctgctgtca | tcgttctgag  | gagagcctca | gtggtcggat | 180 |
| ccttgatgtg | ttgggccccg  | tcgaggcgat | tgtcaccact  | tcacacaggg | gcaaagtgcg | 240 |
| gtcggtcctc | ccccctctgga | tcctccaccg | ccaatgctcg  | atgcctgcat | cgacaaagct | 300 |
| cccgtccgaa | gtctccccct  | ttcggatcct | tcccctgccc  | gtgcttgctt | cctcgtcctg | 360 |
| ggatactcgc | ccggccccct  | catcgtccag | agaacctggc  | atgagacacg | ccaccagagc | 420 |
| ttgtttacag | ttcagcccag  | ttggccatta | ctttgctagt  | gcttcacatg | acaggactgc | 480 |
| tagaatttgg | tcaattgata  | aaatccagcc | tttgcggaata | atggctgggc | atctttctga | 540 |
| tgt        |             |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1501325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Ala | Leu | Ala | Leu | Asn | Leu | Ala | Ala | Ser | Pro | Arg | Arg | Pro | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Arg | Leu | Arg | Pro | Cys | Ser | Asn | Pro | Cys | Pro | Leu | Arg | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Leu | Gly | Arg | Lys | Ile | Leu | His | Arg | Arg | Ser | Cys | Arg | Cys | Leu | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Cys | His | Arg | Ser | Glu | Glu | Ser | Leu | Ser | Gly | Arg | Ile | Leu | Asp | Val | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Pro | Val | Glu | Ala | Ile | Val | Thr | Thr | Ser | His | Arg | Gly | Lys | Val | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Val | Leu | Pro | Leu | Trp | Ile | Leu | His | Arg | Gln | Cys | Ser | Met | Pro | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Thr | Lys | Leu | Pro | Ser | Glu | Val | Ser | Pro | Phe | Arg | Ile | Leu | Pro | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Val | Leu | Ala | Ser | Ser | Ser | Trp | Asp | Thr | Pro | Pro | Ala | Pro | Ser | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Arg | Glu | Pro | Gly | Met | Arg | His | Ala | Thr | Arg | Ala | Cys | Leu | Gln | Phe |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ser | Pro | Val | Gly | His | Tyr | Phe | Ala | Ser | Ala | Ser | His | Asp | Arg | Thr | Ala |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Ile | Trp | Ser | Ile | Asp | Lys | Ile | Gln | Pro | Leu | Arg | Ile | Met | Ala | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| His | Leu | Ser | Asp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 536 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..536

(D) OTHER INFORMATION: / Ceres Seq. ID 1501326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| aatcaccttc | ttcgtttcat | cctctgattc | wccccctgcw  | ggtctgctct | gctcccatcc | 60  |
| catggagccc | gacgcgccc  | aaaaccctag | ccccagcccc  | gtccccccgc | ccatctccgc | 120 |
| ctactaccag | acgcgcgccg | aacaccacgc | cgctcgtaact | agcgactggc | tcgcccacgc | 180 |
| cgccgcgcga | gccgcagcct | tccccggcgc | cgataccgcc  | gatgcmgcmc | cgcccccgtc | 240 |
| ccccgggggc | ggcggcgtga | tcgaggagtt | caacttctgg  | cgccgcaagc | ccgaggccgc | 300 |
| cgaggcggtg | gccgccatca | tggtctctgc | cgcmgtcatc  | cgctccagca | gggccaccac | 360 |
| catgatggag | ctcgagatcg | agctcaagaa | ggcatctgac  | aagctcaagt | cctgggatgc | 420 |
| tacatccatt | tctctttctg | ctgcttgtga | tttgttcatg  | cggtttgtaa | cgaggacctc | 480 |
| acatctggag | catgagaagt | ttgatgcagc | aaaatcgcg   | ctaattgagc | gaggag     |     |

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1501327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Thr | Phe | Phe | Val | Ser | Ser | Ser | Asp | Xaa | Pro | Pro | Xaa | Gly | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Cys | Ser | His | Pro | Met | Glu | Pro | Asp | Ala | Ala | Gln | Asn | Pro | Ser | Pro | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Val | Pro | Pro | Pro | Ile | Ser | Ala | Tyr | Tyr | Gln | Thr | Arg | Ala | Glu | His |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| His | Ala | Val | Val | Thr | Ser | Asp | Trp | Leu | Ala | His | Ala | Ala | Ala | Ala | Ala |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Ala | Ala | Phe | Pro | Gly | Ala | Asp | Thr | Ala | Asp | Xaa | Xaa | Pro | Pro | Pro | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Pro | Gly | Gly | Gly | Gly | Val | Ile | Glu | Glu | Phe | Asn | Phe | Trp | Arg | Arg | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Pro | Glu | Ala | Ala | Glu | Ala | Val | Ala | Ala | Ile | Met | Ala | Leu | Ala | Xaa | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Arg | Ser | Ser | Arg | Ala | Thr | Thr | Met | Met | Glu | Leu | Glu | Ile | Glu | Leu |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Lys | Lys | Ala | Ser | Asp | Lys | Leu | Lys | Ser | Trp | Asp | Ala | Thr | Ser | Ile | Ser |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |  |
| Leu | Ser | Ala | Ala | Cys | Asp | Leu | Phe | Met | Arg | Phe | Val | Thr | Arg | Thr | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| His | Leu | Glu | His | Glu | Lys | Phe | Asp | Ala | Ala | Lys | Ser | Arg | Leu | Ile | Glu |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Arg | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1501328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

Met Glu Pro Asp Ala Ala Gln Asn Pro Ser Pro Ser Pro Val Pro Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Ile | Ser | Ala | Tyr | Tyr | Gln | Thr | Arg | Ala | Glu | His | His | Ala | Val | Val |
|     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Thr | Ser | Asp | Trp | Leu | Ala | His | Ala | Ala | Ala | Ala | Ala | Ala | Phe | Pro |     |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ala | Asp | Thr | Ala | Asp | Xaa | Xaa | Pro | Pro | Pro | Ser | Pro | Gly | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Val | Ile | Glu | Glu | Phe | Asn | Phe | Trp | Arg | Arg | Lys | Pro | Glu | Ala | Ala |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ala | Val | Ala | Ala | Ile | Met | Ala | Leu | Ala | Xaa | Val | Ile | Arg | Ser | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Ala | Thr | Thr | Met | Met | Glu | Leu | Glu | Ile | Glu | Leu | Lys | Lys | Ala | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Lys | Leu | Lys | Ser | Trp | Asp | Ala | Thr | Ser | Ile | Ser | Leu | Ser | Ala | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Cys | Asp | Leu | Phe | Met | Arg | Phe | Val | Thr | Arg | Thr | Ser | His | Leu | Glu | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Glu | Lys | Phe | Asp | Ala | Ala | Lys | Ser | Arg | Leu | Ile | Glu | Arg | Gly |     |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..492
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| acactcgctc | tcgccactgt | cgtccaccga | tccgtcatgg | cgactgctgc  | gccattgttg | 60  |
| ctcttccacg | gtctcctcct | cctcctctcc | ctggcgctcg | gcccattggcg | tgaacgtgaa | 120 |
| gcccggggag | caccacatcc | tcaacaggca | gagcttcccc | ccgggggttcg | tcttcggcac | 180 |
| ggcgtcttcg | gcgtagcagg | tggaggggaa | cacgcacagg | tacggggcgcg | ggccctgcat | 240 |
| ctgggacacc | ttcctcaagt | atccaggcac | tactcctgat | aacgcgaccg  | cggacgtgac | 300 |
| agtcgacgag | tacaatcgct | acatggatga | tgtggacaat | atggtcgggg  | ttggcttcga | 360 |
| cgcgtaccgc | ttctcgatct | catggtcgcg | tattttcccc | agtgggattg  | ggagggttaa | 420 |
| caaggatggt | gtggactatt | accacaggct | catcaactac | ttgctggcga  | accatattac | 480 |
| tccttacgtg | gt         |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Ala | Leu | Ala | Thr | Val | Val | His | Arg | Ser | Val | Met | Ala | Thr | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Leu | Leu | Leu | Phe | His | Gly | Leu | Leu | Leu | Leu | Ser | Leu | Ala |     |
|     | 20  |     |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Gly | Pro | Trp | Arg | Glu | Arg | Glu | Ala | Arg | Gly | Ala | Pro | His | Pro | Gln |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Ala | Glu | Leu | Pro | Pro | Gly | Val | Arg | Leu | Arg | His | Gly | Val | Phe | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Pro | Gly | Gly | Gly | Glu | His | Ala | Gln | Val | Arg | Ala | Arg | Ala | Leu | His |

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(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

(2) INFORMATION FOR SEQ ID NO:1830:

- (xi) SEQUENCE DESCRIPTION: SEO ID NO:1830:

(2) INFORMATION FOR SEQ ID NO:1831:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:



- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..136  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501340  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

```
Val Glu Ser Arg Thr Phe Leu Pro Arg Ser Arg Xaa Gln Ser Ala Thr
1 5 10 15
Thr His Thr Pro Thr Asn Thr Met Asp Ala Ala Ala Lys Glu Ala
20 25 30
Leu Ile Leu Asp Leu His Ala Val Glu Ala Val Lys Leu Gly Thr Phe
35 40 45
Val Leu Lys Ser Gly Ile Thr Ser Pro Ile Tyr Leu Asp Leu Arg Val
50 55 60
Leu Val Ser His Pro Arg Leu Leu Ala Ser Val Ala Ser Leu Leu Gly
65 70 75 80
Ala Leu Pro Ala Thr Arg Pro Tyr Asp Leu Leu Cys Gly Val Pro Xaa
85 90 95
Thr Ala Leu Pro Phe Ala Ala Ala Leu Ser Val Ala Xaa Ser Val Pro
100 105 110
Met Leu Leu Ser Arg Tyr Asp Thr Lys Arg Val Glu Gly Ala Phe Arg
115 120 125
Xaa Ala Gln Xaa Val Leu Ile Val
130 135
```

(2) INFORMATION FOR SEQ ID NO:1832:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 135 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..135  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

```
Arg Val Lys Asn Phe Ser Pro Pro Phe Ala Xaa Thr Val Gly His Tyr
1 5 10 15
Thr His Ala Ala His Gln His His Gly Arg Arg Arg Glu Gly Gly Ala
20 25 30
Asp Pro Gly Pro Ala Arg Gly Gly Gly Arg Glu Ala Gly His Leu Arg
35 40 45
Ala Gln Val Arg Asp His Leu Pro Asp Leu Pro Gly Pro Ala Arg Ala
50 55 60
Arg Leu Pro Pro Ala Pro Ala Arg Leu Arg Arg Val Pro Pro Arg Arg
65 70 75 80
Ala Pro Gly His Ala Pro Leu Arg Pro Ser Leu Arg Arg Ala Leu Xaa
85 90 95
Ser Ala Ala Leu Arg Gly Arg Ala Leu Arg Arg Xaa Leu Arg Ala His
100 105 110
Ala Ala Gln Pro Leu Arg His Gln Ala Arg Arg Gly Arg Leu Pro Xaa
115 120 125
Arg Pro Xaa Arg Ala His Arg
130 135
```

(2) INFORMATION FOR SEQ ID NO:1833:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 112 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1501342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ala | Ala | Ala | Lys | Glu | Ala | Leu | Ile | Leu | Asp | Leu | His | Ala | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Ala | Val | Lys | Leu | Gly | Thr | Phe | Val | Leu | Lys | Ser | Gly | Ile | Thr | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Ile | Tyr | Leu | Asp | Leu | Arg | Val | Leu | Val | Ser | His | Pro | Arg | Leu | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ser | Val | Ala | Ser | Leu | Leu | Gly | Ala | Leu | Pro | Ala | Thr | Arg | Pro | Tyr |
|     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |
| Asp | Leu | Leu | Cys | Gly | Val | Pro | Xaa | Thr | Ala | Leu | Pro | Phe | Ala | Ala | Ala |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Leu | Ser | Val | Ala | Xaa | Ser | Val | Pro | Met | Leu | Leu | Ser | Arg | Tyr | Asp | Thr |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Lys | Arg | Val | Glu | Gly | Ala | Phe | Arg | Xaa | Ala | Gln | Xaa | Val | Leu | Ile | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..539

(D) OTHER INFORMATION: / Ceres Seq. ID 1501345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| agcagcccat | ccccagcagc | actgcctcgt | cgtctcgc   | attggcggtg | gcataccgct | 60  |
| cggcattgtg | cccattacca | tgccgcgct  | gcccgcggcc | gacgatttac | tcattctcga | 120 |
| gttcacgcg  | agcaaccgcc | gtatcccca  | cgccgtgttc | aactccttca | tcgcctccca | 180 |
| atccccacc  | tccgccttct | ccgcacctc  | acagcgctc  | cgaaaagccc | tagtgctccg | 240 |
| cgccctcgac | gccgccctct | acaccgtggg | cgccctctgc | tcctccagcc | tcctcctcca | 300 |
| caaggcgaga | aaggtcctcg | ccgacccga  | cgagccgcc  | tgcttcccc  | accagattcc | 360 |
| ttttacagaa | aatgaagaaa | acgatgaggc | tagggctgcy | gtggccgata | tcaagcgctt | 420 |
| cctcgacctt | gagtgggcca | acctccgcm  | ctccacgctc | gagctcgtmg | ccggggacgg | 480 |
| gtcccaccag | actggtgcmg | ctgccgacca | caccatgcgt | acaaagcttc | gcctgttcg  |     |

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Pro | Ser | Pro | Ala | Ala | Leu | Pro | Arg | Arg | Leu | Ala | Tyr | Trp | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Trp | His | His | Arg | Arg | His | Cys | Ala | His | Tyr | His | Ala | Ala | Ala | Ala | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Arg | Arg | Phe | Thr | His | Ser | Arg | Val | His | Arg | Glu | Gln | Pro | Pro | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

Pro Pro Arg Arg Val Gln Leu Leu His Arg Leu Pro Ile Pro Thr Leu  
50 55 60  
Arg Leu Leu Pro His Leu Thr Ala Pro Pro Lys Ser Pro Ser Ala Pro  
65 70 75 80  
Arg Pro Arg Arg Arg Pro Leu His Arg Gly Arg Leu Leu Leu Leu Gln  
85 90 95  
Pro Pro Pro Pro Gln Gly Ala Lys Gly Pro Arg Arg Pro Arg Arg Ser  
100 105 110  
Arg Leu Leu Pro Pro Pro Asp Ser Phe Tyr Arg Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1501347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

Ala Ala His Pro Gln Gln His Cys Leu Val Val Ser His Ile Gly Val  
1 5 10 15  
Gly Ile Thr Val Gly Ile Val Pro Ile Thr Met Pro Pro Leu Pro Ala  
20 25 30  
Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile Ala Ser Asn Arg Arg Ile  
35 40 45  
Pro His Ala Val Phe Asn Ser Phe Ile Ala Ser Gln Ser Pro Pro Ser  
50 55 60  
Ala Phe Ser Arg Thr Ser Gln Arg Leu Arg Lys Ala Leu Val Leu Arg  
65 70 75 80  
Ala Leu Asp Ala Ala Leu Tyr Thr Val Gly Ala Ser Cys Ser Ser Ser  
85 90 95  
Leu Leu Leu His Lys Ala Arg Lys Val Leu Ala Asp Pro Asp Ala Ala  
100 105 110  
Ala Cys Phe Pro His Gln Ile Pro Phe Thr Glu Asn Glu Glu Asn Asp  
115 120 125  
Glu Ala Arg Ala Ala Val Ala Asp Leu Lys Arg Leu Leu Asp Leu Glu  
130 135 140  
Trp Ala Asn Leu Pro Xaa Ser Thr Leu Glu Leu Xaa Ala Gly Asp Gly  
145 150 155 160  
Ser His Gln Thr Gly Xaa Ala Ala Asp His Thr Met Arg Thr Lys Leu  
165 170 175  
Arg Leu Phe

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

Met Pro Pro Leu Pro Ala Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile  
1 5 10 15  
Ala Ser Asn Arg Arg Ile Pro His Ala Val Phe Asn Ser Phe Ile Ala

```

 20 25 30
Ser Gln Ser Pro Pro Ser Ala Phe Ser Arg Thr Ser Gln Arg Leu Arg
 35 40 45
Lys Ala Leu Val Leu Arg Ala Leu Asp Ala Ala Leu Tyr Thr Val Gly
 50 55 60
Ala Ser Cys Ser Ser Ser Leu Leu Leu His Lys Ala Arg Lys Val Leu
 65 70 75 80
Ala Asp Pro Asp Ala Ala Ala Cys Phe Pro His Gln Ile Pro Phe Thr
 85 90 95
Glu Asn Glu Glu Asn Asp Glu Ala Arg Ala Ala Val Ala Asp Leu Lys
 100 105 110
Arg Leu Leu Asp Leu Glu Trp Ala Asn Leu Pro Xaa Ser Thr Leu Glu
 115 120 125
Leu Xaa Ala Gly Asp Gly Ser His Gln Thr Gly Xaa Ala Ala Asp His
 130 135 140
Thr Met Arg Thr Lys Leu Arg Leu Phe
 145 150
```

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

```

agccttccaa tctctaggag aaacgtcttg ccctccactc caacatcgac acgactactc 60
gtccgactag aaccaaactt ttcaatccat cgttcgcagt tcagttcaca cttcacaggc 120
gagcgcgacc atggataccc aagcacgtcc ggttccccgc gtcaagctcg gcacccaggg 180
attcgagggtg tccaagctgg ggttcgggtg catggggctg acgggcgcat acaactcccc 240
gctggacgac gaggccggca tcgcgcgtcat cgcgcacgct ttcagccgcg gagtcacctt 300
gttcgacacc tccgacgtat acggggccct caccaacgaa atcctcctcg gcaaggcgct 360
gaagcagctg ccgcgggagc aggtgcaggt ggccaccaag ttcgggatam ggcgtgacga 420
gagcggcacs ggnaccgtgt gcggccggcc ggagtacgtt cgtrcctgct gcgaggccag 480
cctgcgccgc ctcggcacgc actgcatcga c
```

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

```

Ser Leu Pro Ile Ser Arg Arg Asn Val Leu Pro Ser Thr Pro Thr Ser
1 5 10 15
Thr Arg Leu Leu Val Arg Leu Glu Pro Asn Phe Ser Ile His Arg Ser
 20 25 30
Gln Phe Ser Ser His Phe Thr Gly Glu Arg Asp His Gly Tyr Pro Ser
 35 40 45
Thr Ser Gly Ser Pro Arg Gln Ala Arg His Pro Gly Ile Arg Gly Val
 50 55 60
Gln Ala Gly Val Arg Val His Gly Ala Asp Gly Arg Ile Gln Leu Pro
 65 70 75 80
Ala Gly Arg Arg Gly Arg His Arg Arg His Arg Ala Arg Phe Gln Pro
```

(2) INFORMATION FOR SEQ ID NO:1840:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1501366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1501367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atctataaca gccgccacct tcccccttat actcgccgga ggcaaccagt actcgtgcca  | 60  |
| cgactgccac ccttcctctt ccttgatgc tccgaatacc catctcagat tccaagggcc   | 120 |
| gcgcggtgta atccccggt ctccccaccc accatatatc tagtatcgc gcctcaaadc    | 180 |
| cctcgcgaaa cgccccgccg taagcagttg ttgtctgccg tgatttgagc cggggcgagc  | 240 |
| gattgatccc gggacgaggt gtctcagctc ttgatcttga tcctgatcct gggaggcggt  | 300 |
| cctggtttat tgggtgggagc gaagaagcca tgataccttc cgtgaggctc tctcctggtc | 360 |
| ctgcagcctt ctcaggtccc agcctacgct caaaattacc gtcaattcca tccatctcca  | 420 |
| gtctcaaacc ctccaaatat gtggtctcct cgctgaaacc actctaccta gcaccgctag  | 480 |
| atggtccgcg cactgccgag cttaagtctc ggagac                            |     |

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Tyr Asn Ser Arg His Leu Pro Pro Tyr Thr Arg Arg Arg Gln Pro |  |
| 1 5 10 15                                                       |  |
| Val Leu Val Pro Arg Leu Pro Pro Leu Leu Phe Leu Val Ile Ser Glu |  |
| 20 25 30                                                        |  |
| Tyr Pro Ser Gln Ile Pro Arg Ala Ala Pro Cys Asn Pro Arg Leu Ser |  |
| 35 40 45                                                        |  |
| Pro Pro Thr Ile Tyr Leu Val Ser Ala Pro Gln Ile Pro Arg Glu Thr |  |
| 50 55 60                                                        |  |
| Pro Arg Arg Lys Gln Leu Leu Ser Ala Val Ile                     |  |
| 65 70 75                                                        |  |

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ile Pro Ser Val Arg Leu Ser Pro Gly Pro Ala Ala Phe Ser Gly |  |
| 1 5 10 15                                                       |  |
| Ser Ser Leu Arg Ser Lys Leu Pro Ser Ile Pro Ser Ile Ser Ser Leu |  |
| 20 25 30                                                        |  |
| Lys Pro Ser Lys Tyr Val Val Ser Ser Leu Lys Pro Leu Tyr Leu Ala |  |
| 35 40 45                                                        |  |

Pro Leu Asp Gly Pro Arg Thr Ala Glu Leu Lys Ser Arg Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aattctgcaa agcaggarcc cggttcgttc tgcacctttc gtctcgctct cgcccgcmcg  | 60  |
| accccgcgga scctagccta gccttgcccc cgaccgcgga ttccccctcg gccgcgcgcg  | 120 |
| gcccgcaccc gcaccgcga tgatgaactg cgccggaggg nangaccccg tggaggactt   | 180 |
| cctgatctcc ggcgcgctcg acgacgaaga tctagccatc ttctgcgacg gaggacttgg  | 240 |
| gattgarggt gtcaatggag atgcttgtgg atttgagcag tctaatttgg gcaaaaggag  | 300 |
| tagagatgaa ccatgttcat ctggtctaaa atccaaagct tgtcgtgaaa aaatgaggag  | 360 |
| ggacaagctg aatgacaggt tcctggaatt aarttcggtt atgaatcctg gaaaacaagc  | 420 |
| aaagttggat aaagccaata tcttgarcga mgcagcccgat atggtggcac aacttagagg | 480 |
| tgaggcagaa aagcttaaag aatcaaatga gaagctgcgg grgaatatc              |     |

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Met Asn Cys Ala Gly Gly Xaa Asp Pro Val Glu Asp Phe Leu Ile |  |
| 1 5 10 15                                                       |  |
| Ser Gly Ala Val Asp Asp Glu Asp Leu Ala Ile Phe Cys Asp Gly Gly |  |
| 20 25 30                                                        |  |
| Leu Gly Ile Xaa Gly Val Asn Gly Asp Ala Cys Gly Phe Glu Gln Ser |  |
| 35 40 45                                                        |  |
| Asn Leu Gly Lys Arg Ser Arg Asp Glu Pro Cys Ser Ser Gly Leu Lys |  |
| 50 55 60                                                        |  |
| Ser Lys Ala Cys Arg Glu Lys Met Arg Arg Asp Lys Leu Asn Asp Arg |  |
| 65 70 75 80                                                     |  |
| Phe Leu Glu Leu Xaa Ser Val Met Asn Pro Gly Lys Gln Ala Lys Leu |  |
| 85 90 95                                                        |  |
| Asp Lys Ala Asn Ile Leu Xaa Xaa Ala Ala Arg Met Val Ala Gln Leu |  |
| 100 105 110                                                     |  |
| Arg Gly Glu Ala Glu Lys Leu Lys Glu Ser Asn Glu Lys Leu Arg Xaa |  |
| 115 120 125                                                     |  |
| Asn Ile                                                         |  |
| 130                                                             |  |

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501418  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:  
Met Asn Cys Ala Gly Gly Xaa Asp Pro Val Glu Asp Phe Leu Ile Ser  
1 5 10 15  
Gly Ala Val Asp Asp Glu Asp Leu Ala Ile Phe Cys Asp Gly Gly Leu  
20 25 30  
Gly Ile Xaa Gly Val Asn Gly Asp Ala Cys Gly Phe Glu Gln Ser Asn  
35 40 45  
Leu Gly Lys Arg Ser Arg Asp Glu Pro Cys Ser Ser Gly Leu Lys Ser  
50 55 60  
Lys Ala Cys Arg Glu Lys Met Arg Arg Asp Lys Leu Asn Asp Arg Phe  
65 70 75 80  
Leu Glu Leu Xaa Ser Val Met Asn Pro Gly Lys Gln Ala Lys Leu Asp  
85 90 95  
Lys Ala Asn Ile Leu Xaa Xaa Ala Ala Arg Met Val Ala Gln Leu Arg  
100 105 110  
Gly Glu Ala Glu Lys Leu Lys Glu Ser Asn Glu Lys Leu Arg Xaa Asn  
115 120 125  
Ile

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..546  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

gaggcgatcg catcgagac tcggagccgg caaaacccta aggggaaggt ttctgcaagg 60  
aggagggaga tgcagggcgc cagcacatgc tcctggagga gcccttccgc ctgcctccg 120  
tcctctccc cgccaagcct aaagtattcc catcactcac caagatagtt gggacgctcg 180  
ggcccaattc acactcgggt gagattattc aggaatgcct cactgctgga atgtcagttg 240  
cacgatttga tttctcatgg atggatgctg cgtatcacca ggagaccctt gataatttga 300  
ggaaagcggc acagaatgtg aagaagttgt gccctgtaat gttggatact cttggtccag 360  
aaattcaggt tcacaattcc actggtgagc caattgagtt gaaagctggg aatcatgtta 420  
tcataactcc agatatttct aaagctctct ctgctgagat cctaccaatt aagtttggtg 480  
atctggcaaa agctgtgaag aaggkgkata ctctttttat gggccaatat ctcttcacag 540  
gaagtg

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Met Leu Leu Glu Glu Pro Phe Arg Leu Ala Ser Val Leu Ser Pro Ala  
1 5 10 15  
Lys Pro Lys Val Phe Pro Ser Leu Thr Lys Ile Val Gly Thr Leu Gly  
20 25 30  
Pro Asn Ser His Ser Val Glu Ile Ile Gln Glu Cys Leu Thr Ala Gly



35 40 45  
Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His  
50 55 60  
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys  
65 70 75 80  
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His  
85 90 95  
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile  
100 105 110  
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile  
115 120 125  
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe  
130 135 140  
Met Gly Gln Tyr Leu Phe Thr Gly Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1501441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His  
1 5 10 15  
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys  
20 25 30  
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His  
35 40 45  
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile  
50 55 60  
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile  
65 70 75 80  
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe  
85 90 95  
Met Gly Gln Tyr Leu Phe Thr Gly Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1501442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

Met Asp Ala Ala Tyr His Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala  
1 5 10 15  
Ala Gln Asn Val Lys Lys Leu Cys Pro Val Met Leu Asp Thr Leu Gly  
20 25 30  
Pro Glu Ile Gln Val His Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys  
35 40 45  
Ala Gly Asn His Val Ile Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 552 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..552

(D) OTHER INFORMATION: / Ceres Seq. ID 1501471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| tcgcatacgg | gagcttgcc  | ttctaaatcc  | tgagctaaca  | ataatcttga  | caaaggaaga  | 60  |
| agggcacaca | gttcaacgca | acgaatattg  | ttatgctgg   | ggccttggtg  | aatatgttaa  | 120 |
| atggttgaat | actgacaaga | aacccctgca  | tgacccgatt  | gcgttcagaa  | aggagttgga  | 180 |
| tggtataaca | gtggatgtct | cccttcaatg  | gtcctctgat  | tcctactctg  | atacagtgtc  | 240 |
| aggatacgc  | aacagtatcc | gcactattga  | tggtgggtact | catattgatg  | gtctaaaggc  | 300 |
| ttcattgacg | agaaccatta | ataaccttgc  | aaagaagtgc  | aagmtattaa  | ggataaggat  | 360 |
| attaccttga | gtggggagca | tgtaagagaa  | ggaatgacat  | gcattcatttc | agtgaagggtc | 420 |
| cctagtccag | agtttgaggg | tcaaacaaaag | acaaggttgg  | gaaatccaga  | agtacggaga  | 480 |
| atagttgacg | agtctgttca | agaaaactta  | acagagtact  | tagagcttca  | tccagatggt  | 540 |
| ctggattcaa | tc         |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1501472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Arg | Glu | Leu | Ala | Phe | Leu | Asn | Pro | Glu | Leu | Thr | Ile | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Lys | Glu | Glu | Gly | His | Thr | Val | Gln | Arg | Asn | Glu | Tyr | Cys | Tyr | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Gly | Leu | Val | Glu | Tyr | Val | Lys | Trp | Leu | Asn | Thr | Asp | Lys | Lys | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | His | Asp | Pro | Ile | Ala | Phe | Arg | Lys | Glu | Leu | Asp | Gly | Ile | Thr | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Val | Ser | Leu | Gln | Trp | Ser | Ser | Asp | Ser | Tyr | Ser | Asp | Thr | Val | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Tyr | Ala | Asn | Ser | Ile | Arg | Thr | Ile | Asp | Gly | Gly | Thr | His | Ile | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Leu | Lys | Ala | Ser | Leu | Thr | Arg | Thr | Ile | Asn | Asn | Leu | Ala | Lys | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Lys | Xaa | Leu | Arg | Ile | Arg | Ile | Leu | Pro |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| actaccgag  | tctacttcac | actcgtgcac  | ccatccgggt | cactgggtca | ctgacaccgc | 60  |
| gccccaatca | cgcgcgcgcc | acccgcgatg  | atggcggcgg | cggcgatctc | cggctccagc | 120 |
| ggccacctcg | tcgtctcttc | cccccgcttc  | aggcagccgc | tcacgctccc | ttctcgcagc | 180 |
| ggtcgcccaa | tcgcgcgcgc | cgcctcggcc  | gtggcccgcg | gcggggtcgc | ggtcgcccgc | 240 |
| gtgtccagcc | ccgctgtgtc | ggccgtcgcg  | gggaaggatg | ccaaacaggc | tcctaaggat | 300 |
| ttccttcata | tcaatgattt | tgacaaggat  | acaataatga | atatacctta | tcgagcgatc | 360 |
| gaggttaagg | cagcgataaa | gtctggagac  | aggagcttcc | aaccattcaa | tgggaaatca | 420 |
| atggcgatga | tttttgccaa | gccatcaatg  | aggacccgtg | tttcatttga | ggcgggattc | 480 |
| ttcttacttg | gtgggcatgc | tatttatattg | gggcc      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1501486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Tyr | Pro | Ser | Ser | Leu | His | Thr | Arg | Ala | Pro | Ile | Arg | Val | Thr | Gly | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Thr | Pro | Arg | Pro | Asn | His | Ala | Arg | Ala | Thr | Arg | Asp | Asp | Gly | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Gly | Asp | Leu | Arg | Leu | Gln | Arg | Pro | Pro | Arg | Arg | Leu | Leu | Pro | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Gln | Ala | Ala | Ala | His | Ala | Pro | Phe | Ser | Gln | Arg | Ser | Pro | Asn | Arg |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Arg | Arg | Leu | Gly | Arg | Gly | Pro | Arg | Arg | Gly | Arg | Gly | Arg | Arg | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Val | Gln | Pro | Arg | Cys | Val | Gly | Arg | Arg | Gly | Glu | Gly | Cys | Gln | Thr | Gly |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Met | Ala | Ala | Ala | Ala | Ile | Ser | Gly | Ser | Ser | Gly | His | Leu | Val | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Ser | Pro | Arg | Phe | Arg | Gln | Pro | Leu | Thr | Leu | Pro | Ser | Arg | Ser | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Pro | Ile | Ala | Ala | Ala | Ala | Ser | Ala | Val | Ala | Arg | Gly | Gly | Val | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Ala | Ala | Val | Ser | Ser | Pro | Ala | Val | Ser | Ala | Val | Ala | Gly | Lys | Asp |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Ala | Lys | Gln | Ala | Pro | Lys | Asp | Phe | Leu | His | Ile | Asn | Asp | Phe | Asp | Lys |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |
| Asp | Thr | Ile | Met | Asn | Ile | Leu | Asn | Arg | Ala | Ile | Glu | Val | Lys | Ala | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Lys | Ser | Gly | Asp | Arg | Ser | Phe | Gln | Pro | Phe | Asn | Gly | Lys | Ser | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Met | Ile | Phe | Ala | Lys | Pro | Ser | Met | Arg | Thr | Arg | Val | Ser | Phe | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Gly | Phe | Phe | Leu | Leu | Gly | Gly | His | Ala | Ile | Tyr | Leu | Gly |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1501488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Ile | Ser | Gly | Ser | Ser | Gly | His | Leu | Val | Val | Ser |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Arg | Phe | Arg | Gln | Pro | Leu | Thr | Leu | Pro | Ser | Arg | Ser | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ile | Ala | Ala | Ala | Ala | Ser | Ala | Val | Ala | Arg | Gly | Gly | Val | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Val | Ser | Ser | Pro | Ala | Val | Ser | Ala | Val | Ala | Gly | Lys | Asp | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Gln | Ala | Pro | Lys | Asp | Phe | Leu | His | Ile | Asn | Asp | Phe | Asp | Lys | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Ile | Met | Asn | Ile | Leu | Asn | Arg | Ala | Ile | Glu | Val | Lys | Ala | Ala | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Ser | Gly | Asp | Arg | Ser | Phe | Gln | Pro | Phe | Asn | Gly | Lys | Ser | Met | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Met | Ile | Phe | Ala | Lys | Pro | Ser | Met | Arg | Thr | Arg | Val | Ser | Phe | Glu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Phe | Phe | Leu | Leu | Gly | Gly | His | Ala | Ile | Tyr | Leu | Gly |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..577

(D) OTHER INFORMATION: / Ceres Seq. ID 1501489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| aaccctcctg | ctcctcctcc | cacggtcccg  | ccatttcgtc | ccccgctcac | caactcaaac | 60  |
| cccctccgct | ctcaaaccct | aaccctagcc  | ctagcccgtc | cccggcggac | cgacgatgcc | 120 |
| gaagaggctg | gcggggcggc | ggacgaagag  | gagttccgcg | ccgaggtgga | ggagcgcctc | 180 |
| atcaacgagg | agtacaagat | ctggaagaag  | aacacaccct | tcctctacga | cctcgtcatc | 240 |
| accacgcgc  | tcgaatggcc | ctcccttacc  | gtgcagtggc | tccccgaccg | caccgagccg | 300 |
| ccggggaagg | accactccgt | ccagaagatg  | atccttggca | cgcacacctc | tgacaacgag | 360 |
| cccaactacc | tcattgctcg | gcaggtccag  | ctgcccctcg | acgacgccga | ggccgacgcc | 420 |
| cgcyactacg | acgatgacca | cgccgacatc  | ggtgggtttg | gcgcmgsctc | cgggaargtg | 480 |
| caaattgttc | agcagataaa | tcattgatgga | gaggtcaatc | gagctcgcta | tatgccccaa | 540 |
| aattcattta | taattgctac | taagacagtt  | agcgacag   |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1501490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Pro | Ala | Pro | Pro | Pro | Thr | Val | Pro | Pro | Phe | Arg | Pro | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Asn | Ser | Asn | Pro | Leu | Arg | Ser | Gln | Thr | Leu | Thr | Leu | Ala | Leu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | Arg | Arg | Thr | Asp | Asp | Ala | Glu | Glu | Val | Gly | Gly | Ala | Ala | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Glu | Glu | Glu | Phe | Arg | Ala | Glu | Val | Glu | Glu | Arg | Leu | Ile | Asn | Glu | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Lys | Ile | Trp | Lys | Lys | Asn | Thr | Pro | Phe | Leu | Tyr | Asp | Leu | Val | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | His | Ala | Leu | Glu | Trp | Pro | Ser | Leu | Thr | Val | Gln | Trp | Leu | Pro | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Thr | Glu | Pro | Pro | Gly | Lys | Asp | His | Ser | Val | Gln | Lys | Met | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | His | Thr | Ser | Asp | Asn | Glu | Pro | Asn | Tyr | Leu | Met | Leu | Ala | Gln |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Gln | Leu | Pro | Leu | Asp | Asp | Ala | Glu | Ala | Asp | Ala | Arg | Xaa | Tyr | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Asp | His | Ala | Asp | Ile | Gly | Gly | Phe | Gly | Xaa | Xaa | Ser | Xaa | Xaa | Val |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Ile | Val | Gln | Gln | Ile | Asn | His | Asp | Gly | Glu | Val | Asn | Arg | Ala | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Met | Pro | Gln | Asn | Ser | Phe | Ile | Ile | Ala | Thr | Lys | Thr | Val | Ser | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Cys | Ser | Ser | Ser | His | Gly | Pro | Ala | Ile | Ser | Ser | Pro | Ala | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Leu | Lys | Pro | Pro | Pro | Leu | Ser | Asn | Pro | Asn | Pro | Ser | Pro | Ser | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Pro | Ala | Asp | Arg | Arg | Cys | Arg | Arg | Gly | Arg | Arg | Gly | Gly | Gly | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Arg | Gly | Val | Pro | Arg | Arg | Gly | Gly | Gly | Ala | Pro | His | Gln | Arg | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Asp | Leu | Glu | Glu | Glu | His | Thr | Leu | Pro | Leu | Arg | Pro | Arg | His | His |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Arg | Ala | Arg | Met | Ala | Leu | Pro | Tyr | Arg | Ala | Val | Ala | Pro | Arg | Pro |

85 90 95  
His Arg Ala Ala Gly Glu Gly Pro Leu Arg Pro Glu Asp Asp Pro Trp  
100 105 110  
His Ala His Leu  
115

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

```
aaaaaactct ctgtctctct aggttttttg attttagccg ccgccgctgc tcatctcaca 60
tccctcgaga agacgcctgc tcctcgccga tcgatacgat ggccgtcttc tccgacctcc 120
acaccgccga cggcctcaag tccctcgagg ctcacctgcg cggcaaaacc tatgtgtctg 180
gtgactccat tactaaggat gacattaagg tcttcgccgc ggtgccgtcg aagcctggcg 240
ctgagtttcc taatgccgcc cgctggtagc agaccgtctc tgcggctgta gcctcaagat 300
tccctggtaa ggctgttggg gtaaatctgc ctgcccggatc agctcctgcg gcagctgctc 360
ctgcccgtga ggctgaggat gatgatgacc ttgatctttt tggatgatgaa actgaggagg 420
acaagaaggc agctgatgag cgtgccgccg ctgccaaggc ctcttctaaa aagaaagaaa 480
gtggtaaata ctccgtcctt atggatgtca aaccatggga cgatgagact gatatgaaga 540
agctggaggga ggctgtccgc agtgtccaga tggaggggtc gacttgggga gcatacaagc 600
ttgtgcctgt tggatacggc atcaagaaga tgactatcat gttgacaatt gtcgacgac 660
ttgtgtccat cgacactcta attgaggacc accttacgca agagcccatc aatgagtacg 720
tccagagttg cgacattgtg gctttcaaca agatctagag ttcagtttct gagattgggc 780
aacggcagcg gctcagctcg tcaagtttgt gctgggatgc cagtttatcc cttctagtct 840
attacagaaa tgttggtcgg agctgagtc attataaaca tcttggtctg agtttattgt 900
tgagtggtag cagttttttt caatatacat ttatcttaaa aacagcggta ctgatgtttt 960
tttgtct
```

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

```
Lys Thr Leu Cys Leu Ser Arg Phe Phe Asp Phe Ser Arg Arg Arg Cys
1 5 10 15
Ser Ser His Ile Pro Arg Glu Asp Ala Cys Ser Ser Pro Ile Asp Thr
20 25 30
Met Ala Val Phe Ser Asp Leu His Thr Ala Asp Gly Leu Lys Ser Leu
35 40 45
Glu Ala His Leu Ala Gly Lys Thr Tyr Val Ser Gly Asp Ser Ile Thr
50 55 60
Lys Asp Asp Ile Lys Val Phe Ala Ala Val Pro Ser Lys Pro Gly Ala
65 70 75 80
Glu Phe Pro Asn Ala Ala Arg Trp Tyr Glu Thr Val Ser Ala Ala Val
85 90 95
Ala Ser Arg Phe Pro Gly Lys Ala Val Gly Val Asn Leu Pro Ala Gly
100 105 110
Ser Ala Pro Ala Ala Ala Pro Ala Asp Glu Ala Glu Asp Asp Asp
```

|                         |                     |                         |
|-------------------------|---------------------|-------------------------|
| 115                     | 120                 | 125                     |
| Asp Leu Asp Leu Phe Gly | Asp Glu Thr Glu Glu | Asp Lys Lys Ala Ala     |
| 130                     | 135                 | 140                     |
| Asp Glu Arg Ala Ala Ala | Lys Ala Ser Ser     | Lys Lys Lys Glu Ser     |
| 145                     | 150                 | 155                     |
| Gly Lys Ser Ser Val Leu | Met Asp Val Lys     | Pro Trp Asp Asp Glu Thr |
| 165                     | 170                 | 175                     |
| Asp Met Lys Lys Leu Glu | Glu Ala Val Arg     | Ser Val Gln Met Glu Gly |
| 180                     | 185                 | 190                     |
| Leu Thr Trp Gly Ala Ser | Lys Leu Val Pro     | Val Gly Tyr Gly Ile Lys |
| 195                     | 200                 | 205                     |
| Lys Met Thr Ile Met Leu | Thr Ile Val Asp     | Asp Leu Val Ser Ile Asp |
| 210                     | 215                 | 220                     |
| Thr Leu Ile Glu Asp His | Leu Thr Gln Glu     | Pro Ile Asn Glu Tyr Val |
| 225                     | 230                 | 235                     |
| Gln Ser Cys Asp Ile Val | Ala Phe Asn Lys     | Ile                     |
| 245                     | 250                 |                         |

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1501517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Ala Val Phe Ser Asp Leu His Thr Ala Asp Gly Leu Lys Ser Leu |             |
| 1                                                               | 5 10 15     |
| Glu Ala His Leu Ala Gly Lys Thr Tyr Val Ser Gly Asp Ser Ile Thr |             |
| 20                                                              | 25 30       |
| Lys Asp Asp Ile Lys Val Phe Ala Ala Val Pro Ser Lys Pro Gly Ala |             |
| 35                                                              | 40 45       |
| Glu Phe Pro Asn Ala Ala Arg Trp Tyr Glu Thr Val Ser Ala Ala Val |             |
| 50                                                              | 55 60       |
| Ala Ser Arg Phe Pro Gly Lys Ala Val Gly Val Asn Leu Pro Ala Gly |             |
| 65                                                              | 70 75 80    |
| Ser Ala Pro Ala Ala Ala Ala Pro Ala Asp Glu Ala Glu Asp Asp Asp |             |
| 85                                                              | 90 95       |
| Asp Leu Asp Leu Phe Gly Asp Glu Thr Glu Glu Asp Lys Lys Ala Ala |             |
| 100                                                             | 105 110     |
| Asp Glu Arg Ala Ala Ala Ala Lys Ala Ser Ser Lys Lys Lys Glu Ser |             |
| 115                                                             | 120 125     |
| Gly Lys Ser Ser Val Leu Met Asp Val Lys Pro Trp Asp Asp Glu Thr |             |
| 130                                                             | 135 140     |
| Asp Met Lys Lys Leu Glu Ala Val Arg Ser Val Gln Met Glu Gly     |             |
| 145                                                             | 150 155 160 |
| Leu Thr Trp Gly Ala Ser Lys Leu Val Pro Val Gly Tyr Gly Ile Lys |             |
| 165                                                             | 170 175     |
| Lys Met Thr Ile Met Leu Thr Ile Val Asp Asp Leu Val Ser Ile Asp |             |
| 180                                                             | 185 190     |
| Thr Leu Ile Glu Asp His Leu Thr Gln Glu Pro Ile Asn Glu Tyr Val |             |
| 195                                                             | 200 205     |
| Gln Ser Cys Asp Ile Val Ala Phe Asn Lys Ile                     |             |
| 210                                                             | 215         |

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..584
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

|             |            |             |             |            |            |     |
|-------------|------------|-------------|-------------|------------|------------|-----|
| agctgacaac  | cagacgcgcc | agggtttcag  | gcttccacga  | atctccccgc | cgccctcaat | 60  |
| tccccctcggc | gccgcgcgct | cctccccctcg | cttcgggtcct | cggttagtta | accatccagg | 120 |
| ttctgtcaag  | atgtctgata | gccatgagac  | tgacaggaac  | attgagattt | ggaaaattaa | 180 |
| gaaactgata  | aaggcattgg | aatcagccag  | aggcaatggc  | acaagcatga | tctctcta   | 240 |
| catgcctcca  | cgtgatcagg | ttgctcgagt  | ggctaagatg  | ttaggtgatg | aatatggtag | 300 |
| tgcttcgaac  | atcaagagta | gagttaatcg  | tcaatctgtg  | ttggctgcca | tcacctcagc | 360 |
| tcagcagagg  | ttgaagctct | acaacaaagt  | gcctccta    | ggattggttc | tgtacactgg | 420 |
| aactattgtt  | actgaagacg | gaaaggaaaa  | gaaagttact  | attgattttg | agccattcaa | 480 |
| gcctatcaat  | gtgtcactct | acctttgtga  | caacaagttc  | cacactgagg | ctttaaata  | 540 |
| gctcttgga   | tctgatgaca | agtttgggtt  | cattgttatg  | gatg       |            |     |

(2) INFORMATION FOR SEQ ID NO:1865:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 194 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..194
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Asp | Asn | Gln | Thr | Arg | Gln | Gly | Phe | Arg | Leu | Pro | Arg | Ile | Ser | Pro |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Pro | Ser | Ile | Pro | Leu | Gly | Ala | Ala | Ala | Ser | Ser | Pro | Arg | Phe | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Arg | Leu | Val | Asn | His | Pro | Gly | Ser | Val | Lys | Met | Ser | Asp | Ser | His |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Thr | Asp | Arg | Asn | Ile | Glu | Ile | Trp | Lys | Ile | Lys | Lys | Leu | Ile | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Leu | Glu | Ser | Ala | Arg | Gly | Asn | Gly | Thr | Ser | Met | Ile | Ser | Leu | Ile |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Met | Pro | Pro | Arg | Asp | Gln | Val | Ala | Arg | Val | Ala | Lys | Met | Leu | Gly | Asp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Tyr | Gly | Thr | Ala | Ser | Asn | Ile | Lys | Ser | Arg | Val | Asn | Arg | Gln | Ser |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Leu | Ala | Ile | Thr | Ser | Ala | Gln | Gln | Arg | Leu | Lys | Lys | Leu | Tyr | Asn |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Lys | Val | Pro | Pro | Asn | Gly | Leu | Val | Leu | Tyr | Thr | Gly | Thr | Ile | Val | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Glu | Asp | Gly | Lys | Glu | Lys | Lys | Val | Thr | Ile | Asp | Phe | Glu | Pro | Phe | Lys |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Pro | Ile | Asn | Val | Ser | Leu | Tyr | Leu | Cys | Asp | Asn | Lys | Phe | His | Thr | Glu |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |
| Ala | Leu | Asn | Glu | Leu | Leu | Glu | Ser | Asp | Asp | Lys | Phe | Gly | Phe | Ile | Val |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Met | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1866:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 151 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..151
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Asp | Ser | His | Glu | Thr | Asp | Arg | Asn | Ile | Glu | Ile | Trp | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Leu | Ile | Lys | Ala | Leu | Glu | Ser | Ala | Arg | Gly | Asn | Gly | Thr | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ile | Ser | Leu | Ile | Met | Pro | Pro | Arg | Asp | Gln | Val | Ala | Arg | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Met | Leu | Gly | Asp | Glu | Tyr | Gly | Thr | Ala | Ser | Asn | Ile | Lys | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asn | Arg | Gln | Ser | Val | Leu | Ala | Ala | Ile | Thr | Ser | Ala | Gln | Gln | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Lys | Leu | Tyr | Asn | Lys | Val | Pro | Pro | Asn | Gly | Leu | Val | Leu | Tyr | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Thr | Ile | Val | Thr | Glu | Asp | Gly | Lys | Glu | Lys | Lys | Val | Thr | Ile | Asp |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Glu | Pro | Phe | Lys | Pro | Ile | Asn | Val | Ser | Leu | Tyr | Leu | Cys | Asp | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Phe | His | Thr | Glu | Ala | Leu | Asn | Glu | Leu | Leu | Glu | Ser | Asp | Asp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Gly | Phe | Ile | Val | Met | Asp |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1867:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..119
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ser | Leu | Ile | Met | Pro | Pro | Arg | Asp | Gln | Val | Ala | Arg | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Met | Leu | Gly | Asp | Glu | Tyr | Gly | Thr | Ala | Ser | Asn | Ile | Lys | Ser | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asn | Arg | Gln | Ser | Val | Leu | Ala | Ala | Ile | Thr | Ser | Ala | Gln | Gln | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Leu | Tyr | Asn | Lys | Val | Pro | Pro | Asn | Gly | Leu | Val | Leu | Tyr | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Thr | Ile | Val | Thr | Glu | Asp | Gly | Lys | Glu | Lys | Lys | Val | Thr | Ile | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Glu | Pro | Phe | Lys | Pro | Ile | Asn | Val | Ser | Leu | Tyr | Leu | Cys | Asp | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Phe | His | Thr | Glu | Ala | Leu | Asn | Glu | Leu | Leu | Glu | Ser | Asp | Asp | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Gly | Phe | Ile | Val | Met | Asp |     |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1868:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1030 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1030

(D) OTHER INFORMATION: / Ceres Seq. ID 1501547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

```
aaaaggaacc ctagccatga gcgccgcctc caagaagctc ttccaggccg ccagggtccct 60
cgctcctctcc gcttctaacc gctccgtcct cgccgcccag gccgcaccg ccgcgctcgc 120
cacgctcacc aactttggca ggaagaccct cccaccgcc tacttatcct accacaagca 180
gggatccac catgccgcgt cgggggtggg agccatcgcc gccgcagtcc cagctgmagt 240
ttacatgctc caggaccagg aggtcatgc tgcagagatg gagcgcacct tcattgccat 300
caagcctgat ggtgtccaaa gaggcctgat ttctgagatt atgagccgat ttgagagaaa 360
aggctataag cttgttgcca tcaagctgat tgttccatcc aaagaatttg ctgagaagca 420
ctaccatgat ctcaaggaaa ggcttttctt cagtgggttg tgtgattttc tcagctctgg 480
ccctgtgctt gcaatggttt gggaaggaga ggggtgtcatc aagtatggga gaaaactaat 540
tggtgccaca gaccacaga aatctgaacc aggaaccatc aggggtgatc ttgccattgt 600
tggtggaaga aacatcattc atggaagtga tggcccagag acagcgaagg atgagatcgc 660
tttatggttt gaacccaagg agctgggtctc ttacaccagc aatgcggaga agtggatcta 720
tggggtgaat taacgagaga gtcaatctgt tttttttcct tcttttgatc tcggttttca 780
cataattgcc gacagacctt ggcacaagga tgtaataaag tcgctaccgt cacttctgag 840
ttggattgtg accttcaggt gtagtaaggc acaaggaagg atggaaagga aaggaatata 900
ccgtgaaata tagagcgtgc actgagtagt cgcgatgttc aaatcaaaact atatatcacc 960
gtcactggag tcatgtaatc caagatgggt atgcagatgt ttctttggat ctatttctct 1020
agatatcccc
```

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1501548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

```
Lys Gly Thr Leu Ala Met Ser Ala Ala Ser Lys Lys Leu Phe Gln Ala
1 5 10 15
Ala Arg Ser Leu Val Leu Ser Ala Ser Asn Arg Ser Val Leu Ala Ala
20 25 30
Glu Gly Arg Thr Ala Ala Leu Ala Thr Leu Thr Asn Phe Gly Arg Lys
35 40 45
Thr Leu Pro Thr Ala Tyr Leu Ser Tyr His Lys Gln Gly Ser His His
50 55 60
Ala Ala Ser Gly Trp Gly Ala Ile Ala Ala Val Pro Ala Xaa Val
65 70 75 80
Tyr Met Leu Gln Asp Gln Glu Ala His Ala Ala Glu Met Glu Arg Thr
85 90 95
Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile Ser Glu
100 105 110
Ile Met Ser Arg Phe Glu Arg Lys Gly Tyr Lys Leu Val Ala Ile Lys
115 120 125
Leu Ile Val Pro Ser Lys Glu Phe Ala Glu Lys His Tyr His Asp Leu
130 135 140
Lys Glu Arg Pro Phe Phe Ser Gly Leu Cys Asp Phe Leu Ser Ser Gly
145 150 155 160
Pro Val Leu Ala Met Val Trp Glu Gly Glu Gly Val Ile Lys Tyr Gly
165 170 175
Arg Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser Glu Pro Gly Thr
180 185 190
Ile Arg Gly Asp Leu Ala Ile Val Val Gly Arg Asn Ile Ile His Gly
```

|                                         |                         |                     |
|-----------------------------------------|-------------------------|---------------------|
| 195                                     | 200                     | 205                 |
| Ser Asp Gly Pro Glu Thr                 | Ala Lys Asp Glu Ile     | Ala Leu Trp Phe Glu |
| 210                                     | 215                     | 220                 |
| Pro Lys Glu Leu Val Ser Tyr Thr Ser Asn | Ala Glu Lys Trp Ile Tyr |                     |
| 225                                     | 230                     | 235                 |
| Gly Val Asn                             |                         | 240                 |

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1501549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Ala | Ser | Lys | Lys | Leu | Phe | Gln | Ala | Ala | Arg | Ser | Leu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Ala | Ser | Asn | Arg | Ser | Val | Leu | Ala | Ala | Glu | Gly | Arg | Thr | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | Thr | Leu | Thr | Asn | Phe | Gly | Arg | Lys | Thr | Leu | Pro | Thr | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Leu | Ser | Tyr | His | Lys | Gln | Gly | Ser | His | His | Ala | Ala | Ser | Gly | Trp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Ala | Ile | Ala | Ala | Ala | Val | Pro | Ala | Xaa | Val | Tyr | Met | Leu | Gln | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Glu | Ala | His | Ala | Ala | Glu | Met | Glu | Arg | Thr | Phe | Ile | Ala | Ile | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asp | Gly | Val | Gln | Arg | Gly | Leu | Ile | Ser | Glu | Ile | Met | Ser | Arg | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Arg | Lys | Gly | Tyr | Lys | Leu | Val | Ala | Ile | Lys | Leu | Ile | Val | Pro | Ser |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Glu | Phe | Ala | Glu | Lys | His | Tyr | His | Asp | Leu | Lys | Glu | Arg | Pro | Phe |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Ser | Gly | Leu | Cys | Asp | Phe | Leu | Ser | Ser | Gly | Pro | Val | Leu | Ala | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Trp | Glu | Gly | Glu | Gly | Val | Ile | Lys | Tyr | Gly | Arg | Lys | Leu | Ile | Gly |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Thr | Asp | Pro | Gln | Lys | Ser | Glu | Pro | Gly | Thr | Ile | Arg | Gly | Asp | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Ile | Val | Val | Gly | Arg | Asn | Ile | Ile | His | Gly | Ser | Asp | Gly | Pro | Glu |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Thr | Ala | Lys | Asp | Glu | Ile | Ala | Leu | Trp | Phe | Glu | Pro | Lys | Glu | Leu | Val |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ser | Tyr | Thr | Ser | Asn | Ala | Glu | Lys | Trp | Ile | Tyr | Gly | Val | Asn |     |     |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1501550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

Met Leu Gln Asp Gln Glu Ala His Ala Ala Glu Met Glu Arg Thr Phe  
1 5 10 15  
Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile Ser Glu Ile  
20 25 30  
Met Ser Arg Phe Glu Arg Lys Gly Tyr Lys Leu Val Ala Ile Lys Leu  
35 40 45  
Ile Val Pro Ser Lys Glu Phe Ala Glu Lys His Tyr His Asp Leu Lys  
50 55 60  
Glu Arg Pro Phe Phe Ser Gly Leu Cys Asp Phe Leu Ser Ser Gly Pro  
65 70 75 80  
Val Leu Ala Met Val Trp Glu Gly Glu Gly Val Ile Lys Tyr Gly Arg  
85 90 95  
Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser Glu Pro Gly Thr Ile  
100 105 110  
Arg Gly Asp Leu Ala Ile Val Val Gly Arg Asn Ile Ile His Gly Ser  
115 120 125  
Asp Gly Pro Glu Thr Ala Lys Asp Glu Ile Ala Leu Trp Phe Glu Pro  
130 135 140  
Lys Glu Leu Val Ser Tyr Thr Ser Asn Ala Glu Lys Trp Ile Tyr Gly  
145 150 155 160  
Val Asn

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| attggcgac  | aaatcagcaa | caggcgcggc | gaacaaatgg | ggcgtctgta | gtccggaggc | 60  |
| cttcttagtt | taggggctct | ggcccargtc | gacctgtgtt | tttttttcca | atagcggatt | 120 |
| arcccaacag | agaacctttc | acggccctgc | tagagagagt | ttaacaatca | aaatagaaaa | 180 |
| cagaaacaaa | attcatcaga | gtgagagttc | atcttcttct | ccaagctgat | ttctgcttgt | 240 |
| tagctactca | cgtcaacaga | aaatctcgcg | ttcagctcct | ctccagtcct | tccgcctccc | 300 |
| gcttacttct | ctgactctgt | cctctttcgt | ttctttcttg | tcggcgacgg | ctggcggtg  | 360 |
| gggtgctgcg | ccgctctcac | cttcaccgcc | gacgagcatt | cacaagtagt | ggtctcttac | 420 |
| wggtggcggc | gtagaggtga | cgaaaaagcc | ttgacaatga | gcagcatagg | cacaggttat | 480 |
| gatctgtctg | tcaccacctt | ctctcccgat | ggccgcgtct | tccaggtcga | gtatgccacg | 540 |
| aargctgtcg | acaacagcgg | gac        |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Val Thr Thr Phe Ser  
1 5 10 15  
Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Thr Xaa Ala Val Asp  
20 25 30  
Asn Ser Gly

35

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..567
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| agggcaaaaag aggaaatttc tttgggctgg gtctaataaa ccctaattggg ctgcgggcctc | 60  |
| gtagataaac cagcactact catccgtcgc cccacggaag ttctcggcggc gcsgcgtgct   | 120 |
| cgtgatctca accaaggcgt gtctccgctc cggtcacccg tcaactccacg caaacatgtc   | 180 |
| gaggaggaag accaggggagc ccaaggagga gaacgtcacc cttggaccca ctgtccgtga   | 240 |
| aggagagtat gtctttrgtg tcgctcacat ctttgcaccc ttcaatgaca ccttcattca    | 300 |
| tatcactgat ttgtctggga gggaaactct ggttcggatc accggtggca tgaagggtgaa   | 360 |
| ggctgaccgt gacgagtcgt caccttacgc tgctatgctt gctgctcaag acgtcgcaca    | 420 |
| gcgctgcaag gagcttggca ttactgcact gcacattaag cttcgtgcca ccggaggcaa    | 480 |
| caagaccaag acccccggac ctggtgcccc gtctgccctc agggcgcttg ctcgttcttg    | 540 |
| gatgaaaatc ggacgcattg aggcgt                                         |     |

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Cys Gly Leu Val Asp Lys Pro Ala Leu Leu Ile Arg Arg Pro |  |
| 1 5 10 15                                                       |  |
| Thr Glu Val Ser Ala Ala Xaa Arg Ala Arg Asp Leu Asn Gln Gly Val |  |
| 20 25 30                                                        |  |
| Ser Pro Leu Arg Ser Pro Val Thr Pro Arg Lys His Val Glu Glu Glu |  |
| 35 40 45                                                        |  |
| Asp Gln Gly Ala Gln Gly Gly Glu Arg His Pro Trp Thr His Cys Pro |  |
| 50 55 60                                                        |  |

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu |  |
| 1 5 10 15                                                       |  |
| Gly Pro Thr Val Arg Glu Gly Glu Tyr Val Phe Xaa Val Ala His Ile |  |
| 20 25 30                                                        |  |

Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly  
35 40 45  
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp  
50 55 60  
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val  
65 70 75 80  
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu  
85 90 95  
Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr Pro Gly Pro Gly Ala Gln  
100 105 110  
Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly Met Lys Ile Gly Arg Ile  
115 120 125  
Glu Asp  
130

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

Met Lys Val Lys Ala Asp Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met  
1 5 10 15  
Leu Ala Ala Gln Asp Val Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr  
20 25 30  
Ala Leu His Ile Lys Leu Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr  
35 40 45  
Pro Gly Pro Gly Ala Gln Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly  
50 55 60  
Met Lys Ile Gly Arg Ile Glu Asp  
65 70

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

gtcatcaatc aaatactcag acaaccatgg ggcaccagca ggcgcasacg gcaaggacga 60  
caccgaggag ctgcttcgag cccaccggca gctgtrgtgc catgccctgg gctacgtcaa 120  
gtccatggcg ctcaagtgcg ccctggacct gcgcaccccc gacaccatcg accgctgcgg 180  
cgggagcgcc accctgggcg agctgctcgc cgccagcgag atcccggcgt ccaaccacga 240  
ctacctccgg cgggtcatgc gcacgctgac agccatgcgc atcttcgcgg ccagccacga 300  
ccccgccaaag gccgacgacg cggccgccat ctccctaccag ctgacccccg cgtccccggct 360  
gctcgtcagc agcagcagca gcgtcgacga cgccgcgggg cctcgaagga gaacactact 420  
accccgagca tcctcccaa catcgccac ctggtccgcc ccaacacat ctccctgctg 480  
ttcagcatgg gcgag

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..165
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501572
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

Val Ile Asn Gln Ile Leu Arg Gln Pro Trp Gly Thr Ser Arg Arg Xaa  
1 5 10 15  
Arg Gln Gly Arg His Arg Gly Ala Ala Cys Ser Pro Pro Ala Ala Xaa  
20 25 30  
Val Pro Cys Pro Gly Leu Arg Gln Val His Gly Ala Gln Val Arg Pro  
35 40 45  
Gly Pro Ala His Pro Arg His His Arg Pro Leu Arg Arg Glu Arg His  
50 55 60  
Pro Gly Arg Ala Ala Arg Arg Gln Arg Asp Pro Gly Val Gln Pro Arg  
65 70 75 80  
Leu Pro Pro Ala Gly His Ala His Ala Asp Ser His Ala His Leu Arg  
85 90 95  
Gly Gln Pro Arg Pro Arg Gln Gly Arg Arg Gly Arg His Leu Leu  
100 105 110  
Pro Ala Asp Pro Gly Val Pro Ala Ala Arg Gln Gln Gln Gln Gln Arg  
115 120 125  
Arg Arg Arg Arg Arg Ala Ser Lys Glu Asn Thr Thr Thr Pro Ser Ile  
130 135 140  
Leu Pro Asn Ile Ala His Leu Val Arg Pro Asn Thr Ile Ser Leu Leu  
145 150 155 160  
Phe Ser Met Gly Glu  
165

(2) INFORMATION FOR SEQ ID NO:1880:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..164
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501573
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:

Ser Ser Ile Lys Tyr Ser Asp Asn His Gly Ala Pro Ala Gly Ala Xaa  
1 5 10 15  
Gly Lys Asp Asp Thr Glu Glu Leu Leu Ala Ala His Arg Gln Leu Xaa  
20 25 30  
Cys His Ala Leu Gly Tyr Val Lys Ser Met Ala Leu Lys Cys Ala Leu  
35 40 45  
Asp Leu Arg Ile Pro Asp Thr Ile Asp Arg Cys Gly Gly Ser Ala Thr  
50 55 60  
Leu Gly Glu Leu Leu Ala Ala Ser Glu Ile Pro Ala Ser Asn His Asp  
65 70 75 80  
Tyr Leu Arg Arg Val Met Arg Thr Leu Thr Ala Met Arg Ile Phe Ala  
85 90 95  
Ala Ser His Asp Pro Ala Lys Ala Asp Asp Ala Ala Ala Ile Ser Tyr  
100 105 110  
Gln Leu Thr Pro Ala Ser Arg Leu Leu Val Ser Ser Ser Ser Ser Val  
115 120 125  
Asp Asp Ala Ala Gly Pro Arg Arg Arg Thr Leu Leu Pro Arg Ala Ser  
130 135 140  
Ser Pro Thr Ser Pro Thr Trp Ser Ala Pro Thr Pro Ser Pro Cys Cys

145  
Ser Ala Trp Ala

150

155

160

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

```
Met Ala Leu Lys Cys Ala Leu Asp Leu Arg Ile Pro Asp Thr Ile Asp
1 5 10 15
Arg Cys Gly Gly Ser Ala Thr Leu Gly Glu Leu Leu Ala Ala Ser Glu
20 25 30
Ile Pro Ala Ser Asn His Asp Tyr Leu Arg Arg Val Met Arg Thr Leu
35 40 45
Thr Ala Met Arg Ile Phe Ala Ala Ser His Asp Pro Ala Lys Ala Asp
50 55 60
Asp Ala Ala Ala Ile Ser Tyr Gln Leu Thr Pro Ala Ser Arg Leu Leu
65 70 75 80
Val Ser Ser Ser Ser Ser Val Asp Asp Ala Ala Gly Pro Arg Arg Arg
85 90 95
Thr Leu Leu Pro Arg Ala Ser Ser Pro Thr Ser Pro Thr Trp Ser Ala
100 105 110
Pro Thr Pro Ser Pro Cys Cys Ser Ala Trp Ala
115 120
```

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

```
atcttaacag ccaggaagct ggcgtcttgc ttgtccttgc tcttttccca cccggctacc 60
cccgtcgtcg ccgccgcttt ccccggtggt tcagagctcg agtcggctag ctaggccgcc 120
tggtaatct ccctgccttc tataagtaca ggttcattgt gtgctgtgct ccagctcca 180
tcactgacac aagagagcac gctactactc atcactcgcc aacgtgcaga gatcagggag 240
gcggcacact ccattccactg accgctcatg gcgaaggctc acctctacgt cgccgcggcc 300
tgccgcgtcg tctcgcgcgt cgccgccccg gccctcgccg ggcaccccgga catgctgcag 360
gacgtctgcc cggtgacta cgcctccccg gtgaagctga acgggttcgc gtgcaaggcg 420
aacttttcgg cggacgactt cttcttcgac gggctgagga acccgggcaa caccaacaac 480
ccggcgggct ccgtggtgac
```

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide



(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1501583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

```
Met Ala Lys Val His Leu Tyr Val Ala Ala Ala Cys Ala Val Val Leu
1 5 10 15
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp
20 25 30
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala
35 40 45
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg
50 55 60
Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val Val
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1501584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

```
Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu
1 5 10 15
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe
20 25 30
Asp Gly Leu Arg Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val
35 40 45
Val
```

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

```
agtggacagg tggcatcttc tgcgctcgca acacctcggc gcccaaacgt aaccgtccca 60
acaaactcct ctccctcccc ttcccagcag aagtaccagc gccggccatg gacatgcagt 120
tcttccccga caggcgcact tgcgcctgcg gascgctggc acggcatgta ccttcacgcc 180
gaggaagacg ggggtgaggat caccctgcgc cggcgccgtg ggacgctgaa cgaggcgtgg 240
gtrgtgcacc acctcgagcg caacggcgctc aactacgtcc tcctccacag cgccgcctac 300
ggcgttacc tcgccatcgt aagcatggaa gcgactccgg cgccgtcttc gggccaaggt 360
caaggcgccc gccgcacctg cctcgccgtc cagcgccttt acgacgcccc agggcagaac 420
gacgtcctgt ggcagttccg cttcgcgacg acgggtccga cgatgtcgtc atgcgcaatc 480
gcgtgtacgg cacctggcac aactacggcg acgag
```

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1501590

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Thr | Gly | Gly | Ile | Phe | Cys | Ala | Arg | Asn | Thr | Ser | Ala | Pro | Lys | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Arg | Pro | Asn | Lys | Leu | Leu | Ser | Leu | Pro | Phe | Pro | Ala | Glu | Val | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Pro | Ala | Met | Asp | Met | Gln | Phe | Pro | Asp | Arg | Arg | Thr | Cys | Ala |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Gly | Xaa | Leu | Ala | Arg | His | Val | Pro | Ser | Arg | Arg | Gly | Arg | Arg | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Asp | His | Pro | Ala | Pro | Ala | Pro | Trp | Asp | Ala | Glu | Arg | Gly | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Ala | Pro | Pro | Arg | Ala | Gln | Arg | Arg | Gln | Leu | Arg | Pro | Pro | Pro | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Arg | Leu | Arg | Pro | Leu | Pro | Arg | His | Arg | Lys | His | Gly | Ser | Asp | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ala | Val | Phe | Gly | Pro | Arg | Ser | Arg | Arg | Pro | Pro | His | Leu | Pro | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Ala | Pro | Leu | Arg | Arg | Pro | Arg | Ala | Glu | Arg | Arg | Pro | Val | Ala |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Pro | Leu | Arg | Asp | Asp | Gly | Ser | Asp | Asp | Val | Val | Met | Arg | Asn | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | Tyr | Gly | Thr | Trp | His | Asn | Tyr | Gly | Asp | Glu |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

```
Met Asp Met Gln Phe Pro Asp Arg Thr Cys Ala Cys Gly Xaa
1 5 10 15
Leu Ala Arg His Val Pro Ser Arg Arg Gly Arg Arg Gly Glu Asp His
20 25 30
Pro Ala Pro Ala Pro Trp Asp Ala Glu Arg Gly Val Gly Xaa Ala Pro
35 40 45
Pro Arg Ala Gln Arg Arg Gln Leu Arg Pro Pro Pro Gln Arg Arg Leu
50 55 60
Arg Pro Leu Pro Arg His Arg Lys His Gly Ser Asp Ser Gly Ala Val
65 70 75 80
Phe Gly Pro Arg Ser Arg Arg Pro Pro His Leu Pro Arg Arg Pro Ala
85 90 95
Pro Leu Arg Arg Pro Arg Ala Glu Arg Arg Pro Val Ala Val Pro Leu
100 105 110
Arg Asp Asp Gly Ser Asp Asp Val Val Met Arg Asn Arg Val Tyr Gly
115 120 125
Thr Trp His Asn Tyr Gly Asp Glu
130 135
```

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

```
atcacaagca atcgatcaag ctagcatggc ggtgaagggtg tgggtgttcg ccgtggcact 60
gatgatgtgc gctggtgtag ggcttggagc tgacgacgac ggcggcagsc cttattagcc 120
gctgtcgtct garctcgccc aactaccgcg ggcgcctggc aaaggccatc ctcttcttcg 180
argggcagcg gtcggggcg gctgccggcaa accagagagt caggtggcgc ggggactcgg 240
cgctcaccga cggccaaccc gaaaacgtga acttgacggg tggctactac gacgccggag 300
acaacgtcaa gttcgggttc ccgatggcgt tcagcgtcac cctcctgarc tggagcrccg 360
tcgagtaccg cbacgaggtg gcggcgggcg gtcagctccg cmacctccg tccgccatcc 420
agtkggggcg cgacttcctt ctccgtdecc ac
```

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:  
Ser Gln Ala Ile Asp Gln Ala Ser Met Ala Val Lys Val Trp Val Phe  
1                   5                   10                   15  
Ala Val Ala Leu Met Met Cys Ala Gly Val Gly Leu Gly Ala Asp Asp  
                  20                   25                   30  
Asp Gly Gly Xaa Pro Tyr  
                  35

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

Met Ala Val Lys Val Trp Val Phe Ala Val Ala Leu Met Met Cys Ala  
1                   5                   10                   15  
Gly Val Gly Leu Gly Ala Asp Asp Asp Gly Gly Xaa Pro Tyr  
                  20                   25                   30

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

Met Ala Phe Ser Val Thr Leu Leu Xaa Trp Ser Xaa Val Glu Tyr Arg  
1                   5                   10                   15  
Xaa Glu Val Ala Ala Gly Gln Leu Arg Xaa Leu Arg Ser Ala Ile  
                  20                   25                   30  
Gln Xaa Gly Ala Asp Phe Leu Leu Arg Xaa His  
                  35                   40

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaactgctgg aatatactta caccgggaag aaggcgaagg ccgtcgcgct ctccggcrgcg | 60  |
| gcggcgggcg cggcagcggc gatgcttgcg ttcgagcagc aggtgttggc ggatctggtg  | 120 |
| gaagatccga acggaggtct ggtggtgctc tcctcgggtc tcctctcgcg ttccctagcc  | 180 |
| gctaccctcc tcctccatct ccaccagacc cccggcaacg cggctggagg aggatgtctc  | 240 |
| ctcgtcctct ccgccaccga taccctcaag gcccggatcc ggcgccgcct ccaagacaag  | 300 |
| ctgcaggttc acgacgtgcc ccctgacctc gccgcgcasa gcgcgenmam cctttacgcc  | 360 |
| tctgggctgc tctcttcctc tctccccgcg cmctcgcmgc cgacctctc amctcccgcg   | 420 |
| tcctccctcc ccgcgtccaa gccctactcc tcctctccgc cccacmgctc camcgatacc  | 480 |

tcctccgatg ccttcacgtg c

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1501625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Leu | Leu | Glu | Tyr | Thr | Tyr | Thr | Gly | Lys | Lys | Ala | Lys | Ala | Val | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Ser | Xaa | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Met | Leu | Ala | Phe | Glu |     |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Val | Leu | Ala | Asp | Leu | Val | Glu | Asp | Pro | Asn | Gly | Gly | Leu | Val |     |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Ser | Ser | Gly | Leu | Pro | Leu | Ala | Ser | Leu | Ala | Ala | Thr | Leu | Leu |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | His | Leu | His | Gln | Thr | Pro | Gly | Asn | Ala | Ala | Gly | Gly | Gly | Cys | Leu |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Val | Leu | Ser | Ala | Thr | Asp | Thr | Leu | Lys | Ala | Arg | Ile | Arg | Arg | Arg |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Gln | Asp | Lys | Leu | Gln | Val | His | Asp | Val | Pro | Pro | Asp | Leu | Ala | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Xaa | Ser | Ala | Xaa | Xaa | Leu | Tyr | Ala | Ser | Gly | Leu | Leu | Ser | Ser | Ser | Leu |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Ala | Xaa | Ser | Xaa | Pro | Thr | Ser | Ser | Xaa | Pro | Xaa | Ser | Ser | Pro | Pro |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Ala | Ser | Lys | Pro | Tyr | Ser | Ser | Ser | Pro | Pro | His | Xaa | Ser | Xaa | Asp | Thr |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Ser | Asp | Ala | Phe | Ile | Cys |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 165 |

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1501626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Ala | Gly | Ile | Tyr | Leu | His | Arg | Glu | Glu | Gly | Glu | Gly | Arg | Arg | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Leu | Gly | Xaa | Gly | Gly | Gly | Gly | Gly | Ser | Gly | Asp | Ala | Cys | Val | Arg | Ala |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Ala | Gly | Val | Gly | Gly | Ser | Gly | Gly | Arg | Ser | Glu | Arg | Arg | Ser | Gly | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Ala | Leu | Leu | Gly | Ser | Pro | Ser | Arg | Phe | Pro | Ser | Arg | Tyr | Pro | Pro | Pro |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Pro | Ser | Pro | Pro | Asp | Pro | Arg | Gln | Arg | Gly | Trp | Arg | Arg | Met | Ser | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | Pro | Leu | Arg | His | Arg | Tyr | Pro | Gln | Gly | Pro | Asp | Pro | Ala | Pro | Pro |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Pro | Arg | Gln | Ala | Ala | Gly | Ser | Arg | Arg | Ala | Pro |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

```
Met Leu Ala Phe Glu Gln Gln Val Leu Ala Asp Leu Val Glu Asp Pro
1 5 10 15
Asn Gly Gly Leu Val Val Leu Ser Ser Gly Leu Pro Leu Ala Ser Leu
20 25 30
Ala Ala Thr Leu Leu Leu His Leu His Gln Thr Pro Gly Asn Ala Ala
35 40 45
Gly Gly Gly Cys Leu Leu Val Leu Ser Ala Thr Asp Thr Leu Lys Ala
50 55 60
Arg Ile Arg Arg Arg Leu Gln Asp Lys Leu Gln Val His Asp Val Pro
65 70 75 80
Pro Asp Leu Ala Ala Xaa Ser Ala Xaa Xaa Leu Tyr Ala Ser Gly Leu
85 90 95
Leu Ser Ser Ser Leu Pro Ala Xaa Ser Xaa Pro Thr Ser Ser Xaa Pro
100 105 110
Xaa Ser Ser Pro Pro Ala Ser Lys Pro Tyr Ser Ser Ser Pro Pro His
115 120 125
Xaa Ser Xaa Asp Thr Ser Ser Asp Ala Phe Ile Cys
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

```
aaactctgct gcatcttctt ccactctoca gtctccacta gcatcagtcg ccgctgccta 60
tcctcgagca ccatttccat caacagcatc cgctctggc aagctagcga casaactcat 120
ggcactccgc ggcgtcgaca acacgatgcc cgcmgccgtc gaggagcggc ccaagaaggt 180
ggctaagggtg ggcgtccccg cmgcmgccgc caaggccgcm gcctcccccg ggagtggcgg 240
caagaagaag aaggggaacg acgagaactc ggcgccaagg gccacggccg cggcgggcga 300
gcaggcmgtg gagtacatct cgtcggagga gctggaggcg gcggccaacc ctaaggccaa 360
ggccgcgggg ctggtcgcgg gccttgactc caaggactgg gtcaggacct gcraggcgct 420
caacgac
```

(2) INFORMATION FOR SEQ ID NO:1898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Ala | Ala | Ser | Ser | Ser | Thr | Leu | Gln | Ser | Pro | Leu | Ala | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ala | Ala | Tyr | Pro | Arg | Ala | Pro | Phe | Pro | Ser | Thr | Ala | Ser | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Lys | Leu | Ala | Thr | Xaa | Leu | Met | Ala | Leu | Arg | Ala | Leu | Asp | Asn | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Met | Pro | Xaa | Ala | Val | Glu | Glu | Arg | Pro | Lys | Lys | Val | Ala | Lys | Val | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Pro | Xaa | Xaa | Ala | Ala | Lys | Ala | Xaa | Ala | Ser | Pro | Gly | Ser | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Lys | Lys | Lys | Gly | Asn | Asp | Glu | Asn | Ser | Ala | Pro | Arg | Ala | Thr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Ala | Glu | Gln | Xaa | Val | Glu | Tyr | Ile | Ser | Ser | Glu | Glu | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ala | Ala | Asn | Pro | Lys | Ala | Lys | Ala | Ala | Gly | Leu | Val | Ala | Gly | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ser | Lys | Asp | Trp | Val | Arg | Thr | Cys | Xaa | Ala | Leu | Asn | Asp |     |     |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Arg | Ala | Leu | Asp | Asn | Thr | Met | Pro | Xaa | Ala | Val | Glu | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Pro | Lys | Lys | Val | Ala | Lys | Val | Gly | Val | Pro | Xaa | Xaa | Ala | Ala | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Xaa | Ala | Ser | Pro | Gly | Ser | Gly | Gly | Lys | Lys | Lys | Lys | Gly | Asn | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Ser | Ala | Pro | Arg | Ala | Thr | Ala | Ala | Ala | Ala | Glu | Gln | Xaa | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Tyr | Ile | Ser | Ser | Glu | Glu | Leu | Glu | Ala | Ala | Ala | Asn | Pro | Lys | Ala |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ala | Ala | Gly | Leu | Val | Ala | Gly | Leu | Asp | Ser | Lys | Asp | Trp | Val | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Cys | Xaa | Ala | Leu | Asn | Asp |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Xaa | Ala | Val | Glu | Glu | Arg | Pro | Lys | Lys | Val | Ala | Lys | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Xaa | Xaa | Ala | Ala | Lys | Ala | Xaa | Ala | Ser | Pro | Gly | Ser | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala  
35 40 45  
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu  
50 55 60  
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu  
65 70 75 80  
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp  
85 90

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..541
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

|            |             |              |            |             |            |     |
|------------|-------------|--------------|------------|-------------|------------|-----|
| ccggaacgcc | cgtcccggtcc | gtcctctctccc | catccacatc | catcccggtgt | gctcctactg | 60  |
| ctcctcgatt | tgatcaccga  | ttaggggagg   | cggtttacca | gtgagcacgc  | gcgagarata | 120 |
| ggataggagg | aaaggggaagc | tagcggsttc   | gctctcgcg  | ggagatggcg  | cargcggtkg | 180 |
| aggagtggta | ccggcagatg  | cccacatcatc  | cgcgctccta | cctcamcgcc  | gctgtcgta  | 240 |
| ccaccgtcgg | ctgcamcctc  | gaaatcattt   | cgcggtatca | cctgtacott  | aaccggaagc | 300 |
| tcgtggtgca | gcactacgag  | atttrgcgcc   | tcgtcaccaa | sttsctctan  | yttccgcaaa | 360 |
| gatggatttg | gatcttctat  | tccacatgtw   | ctttcttgca | cgatactgca  | agcttctgga | 420 |
| ggaaaactca | tttagaggaa  | gaactgctga   | ctttttttac | atgcwcttgt  | ttggtgctac | 480 |
| tgtcctaact | ggcattggtt  | ctgatcggag   | ggatgatacc | ttacatttct  | gagacatttg | 540 |

c

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Xaa | Ala | Xaa | Glu | Glu | Trp | Tyr | Arg | Gln | Met | Pro | Ile | Ile | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Ser | Tyr | Leu | Xaa | Ala | Ala | Val | Val | Thr | Thr | Val | Gly | Cys | Xaa | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ile | Ile | Ser | Pro | Tyr | His | Leu | Tyr | Leu | Asn | Pro | Lys | Leu | Val | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | His | Tyr | Glu | Ile | Xaa | Arg | Leu | Val | Thr | Xaa | Xaa | Leu | Xaa | Xaa | Pro |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Gln | Arg | Trp | Ile | Trp | Ile | Phe | Tyr | Ser | Thr | Cys | Xaa | Phe | Leu | His | Asp |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |     |
| Thr | Ala | Ser | Phe | Trp | Arg | Lys | Thr | His | Leu | Glu | Glu | Glu | Leu | Leu | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Phe | Thr | Cys | Xaa | Cys | Leu | Val | Leu | Leu | Ser |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..96  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501641  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:  
Met Pro Ile Ile Thr Arg Ser Tyr Leu Xaa Ala Ala Val Val Thr Thr  
1                    5                    10                    15  
Val Gly Cys Xaa Leu Glu Ile Ile Ser Pro Tyr His Leu Tyr Leu Asn  
                    20                    25                    30  
Pro Lys Leu Val Val Gln His Tyr Glu Ile Xaa Arg Leu Val Thr Xaa  
                    35                    40                    45  
Xaa Leu Xaa Xaa Pro Gln Arg Trp Ile Trp Ile Phe Tyr Ser Thr Cys  
50                    55                    60  
Xaa Phe Leu His Asp Thr Ala Ser Phe Trp Arg Lys Thr His Leu Glu  
65                    70                    75                    80  
Glu Glu Leu Leu Thr Phe Phe Thr Cys Xaa Cys Leu Val Leu Leu Ser  
                    85                    90                    95

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 56 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..56  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501642  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:  
Met Asp Leu Asp Phe Leu Phe His Met Xaa Phe Leu Ala Arg Tyr Cys  
1                    5                    10                    15  
Lys Leu Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe  
                    20                    25                    30  
Tyr Met Xaa Leu Phe Gly Ala Thr Val Leu Thr Gly Ile Gly Ser Asp  
35                    40                    45  
Arg Arg Asp Asp Thr Leu His Phe  
50                    55

(2) INFORMATION FOR SEQ ID NO:1905:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1144 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1144  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501643  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:  
tttacaggca cagctaaagc aagagtcact gctaaggcaa caggagcaac aacaattagc 60  
tgaacaatcc cagctgaggc aacaagagca agaaaaacta gccaaagagc aaaccctgat 120  
tgctttctctg gaggtgaaa agcaacagtt ggaagaccaa attactatgt tgacaaagaa 180  
agctacagag gacgcttctg agtttgctgc acgcaaggca ttttcaatgc aagataggga 240  
aaaacttgaa cagcagttgc atgacatggc tttgatgatt gagaggctag aggggagtcg 300  
tcaaaaactg ctaatggaga ttgattctca atcgtcagaa atagagaaac tgtttgagga 360  
gaactcagcc ttatctgctt cttatcaaga agccattgat gttactgtac aatgggaaaa 420  
ccagaaaatt tcagggttaga gactgtctga agcaaaatga agagctccgt tctcacttgg 480

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| agaaaactaag | acttgaacaa  | gtagcctgt  | tgaagtaag  | caatatcgct  | acccaatcag  | 540  |
| atggggcaaac | tgaaaacagt  | atctcaaacc | caccacaaat | ggatcatcgag | aatatattctc | 600  |
| taaarggwtc  | agcttataaa  | agwacagwgc | agatctgagg | gggtgtcggc  | agagataatg  | 660  |
| aaactttcag  | ctgagccttag | gaaagcagtc | catgcacaga | ataaccttgc  | acgcttatac  | 720  |
| agacctgtat  | taagagacat  | tgagagcaat | ctgatgaaaa | tgaacaaga   | aacttatgcg  | 780  |
| acgatccagt  | gatacatgtt  | gacatgtttg | gaaactcagt | cctctggcat  | ggccgcatgg  | 840  |
| gctccacgtt  | actgattttc  | gtcgtggatg | tatttatctc | atgccatctt  | caagatgctg  | 900  |
| gtgcaaagca  | gttcttttcg  | tggccaccat | ttataagtag | agttcagtcg  | agatcgttgt  | 960  |
| acttgatca   | tactcatgta  | taccggattc | ccagactggg | tcatctcgta  | aattggaagc  | 1020 |
| gatgtttgga  | tgcctatgta  | tcaagtggat | cataaacatc | caaacaacgc  | cttaaaaatag | 1080 |
| atcgtttcga  | cattattatt  | ttcctgcttg | caatccaggc | tctaacaact  | tctcggtctt  | 1140 |
| gttt        |             |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Ala | Gln | Leu | Lys | Gln | Glu | Ser | Leu | Leu | Arg | Gln | Gln | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Gln | Leu | Ala | Glu | Gln | Ser | Gln | Leu | Arg | Gln | Gln | Glu | Gln | Glu | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Ala | Lys | Glu | Gln | Thr | Arg | Ile | Ala | Ser | Leu | Glu | Ala | Glu | Lys | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gln | Leu | Glu | Asp | Gln | Ile | Thr | Met | Leu | Thr | Lys | Lys | Ala | Thr | Glu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Ser | Glu | Phe | Ala | Ala | Arg | Lys | Ala | Phe | Ser | Met | Gln | Asp | Arg | Glu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Lys | Leu | Glu | Gln | Gln | Leu | His | Asp | Met | Ala | Leu | Met | Ile | Glu | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |
| Glu | Gly | Ser | Arg | Gln | Lys | Leu | Leu | Met | Glu | Ile | Asp | Ser | Gln | Ser | Ser |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Glu | Ile | Glu | Lys | Leu | Phe | Glu | Glu | Asn | Ser | Ala | Leu | Ser | Ala | Ser | Tyr |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Gln | Glu | Ala | Ile | Asp | Val | Thr | Val | Gln | Trp | Glu | Asn | Gln | Lys | Ile | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Thr | Lys | Lys | Ala | Thr | Glu | Asp | Ala | Ser | Glu | Phe | Ala | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ala | Phe | Ser | Met | Gln | Asp | Arg | Glu | Lys | Leu | Glu | Gln | Gln | Leu | His |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Met | Ala | Leu | Met | Ile | Glu | Arg | Leu | Glu | Gly | Ser | Arg | Gln | Lys | Leu |

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| 35                                                              | 40 | 45 |
| Leu Met Glu Ile Asp Ser Gln Ser Ser Glu Ile Glu Lys Leu Phe Glu |    |    |
| 50                                                              | 55 | 60 |
| Glu Asn Ser Ala Leu Ser Ala Ser Tyr Gln Glu Ala Ile Asp Val Thr |    |    |
| 65                                                              | 70 | 75 |
| Val Gln Trp Glu Asn Gln Lys Ile Ser Gly                         |    | 80 |
|                                                                 | 85 | 90 |

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1501646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

|                                                                 |    |
|-----------------------------------------------------------------|----|
| Met Leu Leu Tyr Asn Gly Lys Thr Arg Lys Phe Gln Val Arg Asp Cys |    |
| 1                                                               | 15 |
| Leu Lys Gln Asn Glu Glu Leu Arg Ser His Leu Glu Lys Leu Arg Leu |    |
| 20                                                              | 30 |
| Glu Gln Val Ser Leu Leu Lys Val Ser Asn Ile Ala Thr Gln Ser Asp |    |
| 35                                                              | 45 |
| Gly Gln Thr Glu Asn Ser Ile Ser Asn Pro Pro Gln Met Val Ile Glu |    |
| 50                                                              | 60 |
| Asn Ile Ser Leu Xaa Xaa Ser Ala Tyr Lys Xaa Thr Xaa Gln Ile     |    |
| 65                                                              | 75 |

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 597 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..597

(D) OTHER INFORMATION: / Ceres Seq. ID 1501689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ttttttcgcc tataattact cttccccgtg cgccctcgcg aggtcgaacc cccaaggcga | 60  |
| ggcgacgaaa ccctcgccag tccccaactc gaacctcagt caggcggcgt gagggaggga | 120 |
| gagttcgagg accgaggcgg cgtcgggcga gatgaagctt aacgtcaaga ccctcaaggg | 180 |
| caccaacttc gagatcgagg cgagccccga tgcgtcggtt gctgacgtga agaggatcat | 240 |
| tgagaccact cagggtcaga gtacctaccg ggcggaccag caaatgctta tataccaagg | 300 |
| gaaaattctc aaggatgaga ccactttgga aagcaacgga gttctganga acagcttcct | 360 |
| tgttataatg ttgtccaagg ctaaggcatc gtcgagtgga gttctacca ctactgctgc  | 420 |
| aaaagctcct gcaactctgg cccaacctgc tgcccctgtg cccctgctg catcagttgc  | 480 |
| aagaacacca acacaggctc ctgttgccac agctgaaacg gcacctcaa gtgccaacc   | 540 |
| tcaggctgct cagctgctac ggttgctgct actgatgatg ctgatgtgta cagtcag    |     |

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu  
1 5 10 15  
Ala Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr  
20 25 30  
Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr  
35 40 45  
Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val  
50 55 60  
Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser  
65 70 75 80  
Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala Pro Ala Thr Leu  
85 90 95  
Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser Val Ala Arg Thr  
100 105 110  
Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Ala  
115 120 125  
Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu Met Met Leu  
130 135 140  
Met Cys Thr Val  
145

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1501691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:

Met Leu Ile Tyr Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu  
1 5 10 15  
Ser Asn Gly Val Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys  
20 25 30  
Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala  
35 40 45  
Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser  
50 55 60  
Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala  
65 70 75 80  
Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu  
85 90 95  
Leu Met Met Leu Met Cys Thr Val  
100

(2) INFORMATION FOR SEQ ID NO:1912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1501692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

Met Leu Ser Lys Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr

(2) INFORMATION FOR SEQ ID NO:1913:

(A) LENGTH: 272 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1501701

| (X1) SEQUENCE DESCRIPTION: SEQ ID: 1 |            |            |            |            |            |     |
|--------------------------------------|------------|------------|------------|------------|------------|-----|
| ccgctcgatc                           | gcgcccccac | caatcaatca | atcaattctc | gacctacta  | ctcgatctct | 60  |
| cgtctcatca                           | gtgtgactgt | gtgagtgtcc | gagcacggt  | gcaacgcgaa | tggacgctct | 120 |
| gctcgtgact                           | accttctcgc | tccccctgg  | ggcgctcctc | ctcggttccg | ggtccgggtc | 180 |
| cgcggcaccg                           | ctgcmgcgcg | ccttcttcgt | gttcggtgac | tccctcgtgg | acaacggcaa | 240 |
| caacaactac                           | ctgatgacga | cgcgcgcgcg | cg         |            |            |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1501702

Ala Arg Ser Arg Pro His Gln Ser Ile Asn Gln Phe Ser Thr Ser Leu  
1 5 10 15  
Leu Asp Leu Ser Ser His Gln Cys Asp Cys Val Ser Val Arg Ala Arg  
20 25 30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1501703

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ala | Leu | Leu | Val | Thr | Thr | Phe | Leu | Val | Pro | Val | Val | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Leu | Gly | Ser | Gly | Ser | Gly | Ser | 25  | Ala | Pro | Leu | Xaa | Arg | Ala | Phe |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     | 30  |     |     |
| Phe | Val | Phe | Gly | Asp | Ser | Leu | Val | Asp | Asn | Gly | Asn | Asn | Asn | Tyr | Leu |

35  
Met Thr Thr Ala Arg Ala  
50

40

45

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..562
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gacgaccgca ttctctttcc tctctctcgc agtctcgcct cgcccaaccc agtccctcgc  | 60  |
| gcgcgctctc tctcctgcaa ggaccgccag ggaaggacct gctgtttcaa agtattgtgc  | 120 |
| gagacaccta cacgctgagc ttgcgcgaca tgaaagtttt cgggataatc tccagactgc  | 180 |
| aattgagaga acgttcttaa ggatggatga gatgatgaga gacaggaggg cagggagggg  | 240 |
| attatctggg tacgggtgtaa tgacaattgg aaagcatata gaaaggctat caacatgagt | 300 |
| ctatttctac ccttctgtca gaagccagct tatcaggggc cagtaatgga tggatgtacc  | 360 |
| gcgtgtgtgg ttctcattag agacaaccga atcattgtgg gaaatgctgg tgattctcgt  | 420 |
| tgtgtactct caaggaataa tcaggcgatt gatctatcca ccgattttta accaaacctt  | 480 |
| ccagacgaaa gacaaagaat agaagctgca rgacatgtgg taacttttag cgagagagga  | 540 |
| aatgtgcatc gtattgatga tg                                           |     |

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr Thr Ala Phe Ser Phe Leu Ser Leu Ala Val Ser Pro Arg Pro Thr |  |
| 1 5 10 15                                                       |  |
| Gln Ser Leu Ala Arg Ala Leu Ser Pro Ala Arg Thr Ala Arg Glu Gly |  |
| 20 25 30                                                        |  |
| Pro Ala Val Ser Lys Tyr Cys Ala Arg His Leu His Ala Glu Leu Arg |  |
| 35 40 45                                                        |  |
| Arg His Glu Ser Phe Arg Asp Asn Leu Gln Thr Ala Ile Glu Arg Thr |  |
| 50 55 60                                                        |  |
| Phe Leu Arg Met Asp Glu Met Met Arg Asp Arg Arg Ala Gly Arg Glu |  |
| 65 70 75 80                                                     |  |
| Leu Ser Gly Tyr Gly Val Met Thr Ile Gly Lys His Ile Glu Arg Leu |  |
| 85 90 95                                                        |  |
| Ser Thr                                                         |  |

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:

```
Met Ser Leu Phe Pro Phe Cys Gln Lys Pro Ala Tyr Gln Gly Pro
1 5 10 15
Val Met Asp Gly Cys Thr Ala Cys Val Val Leu Ile Arg Asp Asn Arg
20 25 30
Ile Ile Val Gly Asn Ala Gly Asp Ser Arg Cys Val Leu Ser Arg Asn
35 40 45
Asn Gln Ala Ile Asp Leu Ser Thr Asp Phe Lys Pro Asn Leu Pro Asp
50 55 60
Glu Arg Gln Arg Ile Glu Ala Ala Xaa His Val Val Thr Phe Ser Glu
65 70 75 80
Arg Gly Asn Val His Arg Ile Asp Asp
85
```

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

```
Met Asp Gly Cys Thr Ala Cys Val Val Leu Ile Arg Asp Asn Arg Ile
1 5 10 15
Ile Val Gly Asn Ala Gly Asp Ser Arg Cys Val Leu Ser Arg Asn Asn
20 25 30
Gln Ala Ile Asp Leu Ser Thr Asp Phe Lys Pro Asn Leu Pro Asp Glu
35 40 45
Arg Gln Arg Ile Glu Ala Ala Xaa His Val Val Thr Phe Ser Glu Arg
50 55 60
Gly Asn Val His Arg Ile Asp Asp
65 70
```

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1501718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

```
aaggcagcaa ggccactaac actagttatc acatccacca taacgaccat ggctaccacc 60
tcagctttgc tagctcttgt cttgttagcc agcctccttg caggcacggt gttcagtgat 120
gatatcgtac ccatccatat acccttggtg gatcggttcc aagcctggca ggccgaatac 180
aaccgcacat atgcgacccc agaggaattc cagcaacgct tcatgggtcta tagcgagaat 240
gtcaagttca tcgagaccat gaaccagcct gggagctcat atgagctcgg tgagaaccga 300
ttcgctgacc tcaccgagga ggagttcaag gacacgtatc ttatgaagct tgacaacgtg 360
gcctcgtccc ctgaggccat ggcactgacc gtcgatacca tgaatagagc aggcacatct 420
ggcggcagca acaccaacga ggctcccaat agtgtggact ggaggaccaa gggagcagtg 480
acgccggtca agagccagca acattgtg
```

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..169  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501719  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Ala | Arg | Pro | Leu | Thr | Leu | Val | Ile | Thr | Ser | Thr | Ile | Thr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Ala | Thr | Thr | Ser | Ala | Leu | Leu | Ala | Leu | Val | Leu | Leu | Ala | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Gly | Thr | Val | Phe | Ser | Asp | Asp | Ile | Val | Pro | Ile | His | Ile | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Leu | Asp | Arg | Phe | Gln | Ala | Trp | Gln | Ala | Glu | Tyr | Asn | Arg | Thr | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Pro | Glu | Glu | Phe | Gln | Gln | Arg | Phe | Met | Val | Tyr | Ser | Glu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Lys | Phe | Ile | Glu | Thr | Met | Asn | Gln | Pro | Gly | Ser | Ser | Tyr | Glu | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Glu | Asn | Arg | Phe | Ala | Asp | Leu | Thr | Glu | Glu | Glu | Phe | Lys | Asp | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Leu | Met | Lys | Leu | Asp | Asn | Val | Ala | Ser | Ser | Pro | Glu | Ala | Met | Ala |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Thr | Val | Asp | Thr | Met | Asn | Arg | Ala | Gly | Thr | Ser | Gly | Gly | Ser | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asn | Glu | Ala | Pro | Asn | Ser | Val | Asp | Trp | Arg | Thr | Lys | Gly | Ala | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Pro | Val | Lys | Ser | Gln | Gln | His | Cys |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1922:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 153 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..153  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Thr | Ser | Ala | Leu | Leu | Ala | Leu | Val | Leu | Leu | Ala | Ser | Leu |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Gly | Thr | Val | Phe | Ser | Asp | Asp | Ile | Val | Pro | Ile | His | Ile | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Asp | Arg | Phe | Gln | Ala | Trp | Gln | Ala | Glu | Tyr | Asn | Arg | Thr | Tyr |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Thr | Pro | Glu | Glu | Phe | Gln | Gln | Arg | Phe | Met | Val | Tyr | Ser | Glu | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Phe | Ile | Glu | Thr | Met | Asn | Gln | Pro | Gly | Ser | Ser | Tyr | Glu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Glu | Asn | Arg | Phe | Ala | Asp | Leu | Thr | Glu | Glu | Glu | Phe | Lys | Asp | Thr |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Tyr | Leu | Met | Lys | Leu | Asp | Asn | Val | Ala | Ser | Ser | Pro | Glu | Ala | Met | Ala |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Thr | Val | Asp | Thr | Met | Asn | Arg | Ala | Gly | Thr | Ser | Gly | Gly | Ser | Asn |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Glu | Ala | Pro | Asn | Ser | Val | Asp | Trp | Arg | Thr | Lys | Gly | Ala | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Pro | Val | Lys | Ser | Gln | Gln | His | Cys |     |     |     |     |     |     |     |



145

150

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Tyr | Ser | Glu | Asn | Val | Lys | Phe | Ile | Glu | Thr | Met | Asn | Gln | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Ser | Ser | Tyr | Glu | Leu | Gly | Glu | Asn | Arg | Phe | Ala | Asp | Leu | Thr | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Glu | Phe | Lys | Asp | Thr | Tyr | Leu | Met | Lys | Leu | Asp | Asn | Val | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Pro | Glu | Ala | Met | Ala | Leu | Thr | Val | Asp | Thr | Met | Asn | Arg | Ala | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ser | Gly | Gly | Ser | Asn | Thr | Asn | Glu | Ala | Pro | Asn | Ser | Val | Asp | Trp |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Arg | Thr | Lys | Gly | Ala | Val | Thr | Pro | Val | Lys | Ser | Gln | Gln | His | Cys |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..911
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| gacgccgaca  | tatggggccc | gcttgagaag | taagggccac  | atgtcggtgg | gaactctccc | 60  |
| ggagtcggca  | actaatcgac | cccgtgcgcc | ggctccaccc  | gaagcgcaag | aggaagaggt | 120 |
| ggccatacgc  | aacaagcaaa | gcatancccc | aaatccccaa  | tccccaatcc | ccaatcccca | 180 |
| aaccctaggt  | tatctcggcg | cggcagcgan | tggcggcggc  | gggcctgagg | aaggggaatg | 240 |
| cgcgcctccc  | gccggaggtg | aaccgggtgc | tctacgtgcg  | gaacctgccg | ttcaacatct | 300 |
| cgagcggagga | gatgtacgac | atcttcggca | agtacggcgc  | gatccggcag | atccgtcttg | 360 |
| gcaacgccaa  | ggacacgcgc | gggaccgctt | acgttgctta  | csaggacatc | tacgacgcca | 420 |
| agaacgccgt  | cgaccacctc | tmcggtttca | acgtcgccaa  | ccgctacett | atcgtgctct | 480 |
| actaccagcc  | cgccaagats | tccaagaagy | cggatatcam  | gaagaaggag | gacgagatcc | 540 |
| accaggetcc  | aggagaagta | cggaatcggg | tccaagacgc  | ccggcccggg | ctccagcgac | 600 |
| tgagcggcca  | gggtattgcc | tctgcagcct | cttgatgat   | gaagagcaat | caaaaggaac | 660 |
| aaattgggtg  | cgctgtgctg | tgttacatcc | agcgtcgcta  | attactctgt | tgttattcag | 720 |
| gctccataac  | aattgaatag | atatgtgctt | gtctaatacgc | cagcgataat | gtttagtttc | 780 |
| tacaaaaaac  | aagaggaatg | agtagtgtac | acctcacacc  | tgtggctatg | cttgaattgt | 840 |
| tgatctatat  | tctgttgtga | gactgagagt | agcatggtta  | ggctgttaaa | tttgtgcttc | 900 |
| tattattggt  | t          |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1501723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Thr | Tyr | Gly | Pro | Arg | Leu | Arg | Ser | Lys | Gly | His | Met | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Thr | Leu | Pro | Glu | Ser | Ala | Thr | Asn | Arg | Pro | Arg | Ala | Pro | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Glu | Ala | Gln | Glu | Glu | Glu | Val | Ala | Ile | Arg | Asn | Lys | Gln | Ser | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Pro | Asn | Pro | Gln | Ser | Pro | Ile | Pro | Asn | Pro | Gln | Thr | Leu | Gly | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Gly | Ala | Ala | Ala | Xaa | Gly | Gly | Gly | Gly | Pro | Glu | Glu | Gly | Glu | Cys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ala | Pro | Pro | Ala | Gly | Gly | Glu | Pro | Gly | Ala | Leu | Arg | Ala | Glu | Pro | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Gln | His | Leu | Glu | Arg | Gly | Asp | Val | Arg | His | Leu | Arg | Gln | Val | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Asp | Pro | Ala | Asp | Pro | Ser | Gly | Gln | Arg | Gln | Gly | His | Ala | Arg | Asp |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Leu | Arg | Cys | Leu | Xaa | Gly | His | Leu | Arg | Arg | Gln | Glu | Arg | Arg | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Pro | Xaa | Arg | Leu | Gln | Arg | Arg | Gln | Pro | Leu | Pro | Tyr | Arg | Ala | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Pro | Ala | Arg | Gln | Asp | Xaa | Gln | Glu | Xaa | Gly | Tyr | Xaa | Glu | Glu | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Arg | Asp | Pro | Pro | Gly | Ser | Arg | Arg | Ser | Thr | Glu | Ser | Gly | Pro | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Pro | Ala | Arg | Ala | Pro | Ala | Thr | Glu | Arg | Pro | Gly | Tyr | Cys | Leu | Cys |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Leu | Tyr | Asp | Glu | Glu | Gln | Ser | Lys | Gly | Thr | Asn | Trp | Leu | Arg |     |
|     | 210 |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Cys | Ala | Val | Leu | His | Pro | Ala | Ser | Leu | Ile | Thr | Leu | Leu | Leu | Phe | Arg |
| 225 |     |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |
| Leu | His | Asn | Asn |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1501724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Val | Gly | Thr | Leu | Pro | Glu | Ser | Ala | Thr | Asn | Arg | Pro | Arg | Ala |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Pro | Ala | Pro | Pro | Glu | Ala | Gln | Glu | Glu | Glu | Val | Ala | Ile | Arg | Asn | Lys |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Gln | Ser | Ile | Xaa | Pro | Asn | Pro | Gln | Ser | Pro | Ile | Pro | Asn | Pro | Gln | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Tyr | Leu | Gly | Ala | Ala | Xaa | Gly | Gly | Gly | Gly | Pro | Glu | Glu |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Glu | Cys | Ala | Pro | Pro | Ala | Gly | Gly | Glu | Pro | Gly | Ala | Leu | Arg | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Pro | Ala | Val | Gln | His | Leu | Glu | Arg | Gly | Asp | Val | Arg | His | Leu | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Val | Arg | Arg | Asp | Pro | Ala | Asp | Pro | Ser | Gly | Gln | Arg | Gln | Gly | His |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 100                                                             | 105 | 110 |
| Ala Arg Asp Arg Leu Arg Cys Leu Xaa Gly His Leu Arg Arg Gln Glu |     |     |
| 115                                                             | 120 | 125 |
| Arg Arg Arg Pro Pro Xaa Arg Leu Gln Arg Arg Gln Pro Leu Pro Tyr |     |     |
| 130                                                             | 135 | 140 |
| Arg Ala Leu Leu Pro Ala Arg Gln Asp Xaa Gln Glu Xaa Gly Tyr Xaa |     |     |
| 145                                                             | 150 | 155 |
| Glu Glu Gly Gly Arg Asp Pro Pro Gly Ser Arg Arg Ser Thr Glu Ser |     |     |
| 165                                                             | 170 | 175 |
| Gly Pro Arg Arg Pro Ala Arg Ala Pro Ala Thr Glu Arg Pro Gly Tyr |     |     |
| 180                                                             | 185 | 190 |
| Cys Leu Cys Ser Leu Leu Tyr Asp Glu Glu Gln Ser Lys Gly Thr Asn |     |     |
| 195                                                             | 200 | 205 |
| Trp Leu Arg Cys Ala Val Leu His Pro Ala Ser Leu Ile Thr Leu Leu |     |     |
| 210                                                             | 215 | 220 |
| Leu Phe Arg Leu His Asn Asn                                     |     |     |
| 225                                                             | 230 |     |

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501725

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Tyr Asp Ile Phe Gly Lys Tyr Gly Ala Ile Arg Gln Ile Arg Leu |     |     |
| 1                                                               | 5   | 10  |
| Gly Asn Ala Lys Asp Thr Arg Gly Thr Ala Tyr Val Val Tyr Xaa Asp |     |     |
| 20                                                              | 25  | 30  |
| Ile Tyr Asp Ala Lys Asn Ala Val Asp His Leu Xaa Gly Phe Asn Val |     |     |
| 35                                                              | 40  | 45  |
| Ala Asn Arg Tyr Leu Ile Val Leu Tyr Tyr Gln Pro Ala Lys Xaa Ser |     |     |
| 50                                                              | 55  | 60  |
| Lys Lys Xaa Asp Ile Xaa Lys Lys Glu Asp Glu Ile His Gln Ala Pro |     |     |
| 65                                                              | 70  | 75  |
| Gly Glu Val Arg Asn Arg Val Gln Asp Ala Arg Pro Gly Leu Gln Arg |     |     |
| 85                                                              | 90  | 95  |
| Leu Ser Gly Gln Gly Ile Ala Ser Ala Ala Ser Cys Met Met Lys Ser |     |     |
| 100                                                             | 105 | 110 |
| Asn Gln Lys Glu Gln Ile Gly Cys Ala Val Leu Cys Tyr Ile Gln Arg |     |     |
| 115                                                             | 120 | 125 |

Arg

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..916
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atccatgtca tgacgatact gcaggctcca attgtcagct gaactgtggt tgcattctgt | 60  |
| ccagctatag ctcatittgt tctacttgtc gacatagact caagcttgct tattagtacg | 120 |

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| tccaagaacg | acgtacatgg | cttcagctgc  | tgcggctagc | gctgttaagg | aggccttgg  | 180 |
| cgtcgtcgcc | gtgtgcatcg | tgtgtgtgct  | ccactcttcg | gcgggacatc | agccgccc   | 240 |
| gtcgccgcct | ccaccgcatt | gccattacac  | ggggcagcag | ccaccgccct | cgccggtgcc | 300 |
| agcgtcggtt | tactcgccgc | cgccaccacc  | accagtacca | gcgcccattg | cgtcgccgtc | 360 |
| gccgcccgcc | ccgccagtag | aagcgcccat  | gccgcccgcg | ccgccggcac | caacgccgac | 420 |
| acctgcgcc  | acgcccammg | egtcgcccgc  | gccggmaccc | gtcaataact | gcagctacat | 480 |
| gtactgcgcc | atgcaatgta | gcccgggtct  | ccaagccaaa | ccamgacgcc | ggcatcgcca | 540 |
| agtgcgaaag | cgacctcgcc | accaaactac  | aacgggtgct | acgacagctg | caccagccat | 600 |
| gtctgccccg | gcgactcctg | cgccggcgagt | ggctgcgggt | tgggccactg | cccctgcgac | 660 |
| aacgccaacg | cgaccagctg | ctgccaatcc  | tgcggcaacg | ttctgtaccg | cgaggagcag | 720 |
| cgctgccgga | attactacga | cagggtgtg   | gagtactgca | tgatcgactg | ccaggacacc | 780 |
| tgctacaaga | actgcactca | gggcgcgtag  | agagctcttg | attggtcttg | tcacttcagt | 840 |
| tagtctgaat | gtttctgtat | gttcatgacg  | tttctaogat | tgatcaaata | aaacaaggtg | 900 |
| atgagcattg | agctcc     |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1501731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ala | Ala | Ala | Ala | Ser | Ala | Val | Lys | Glu | Ala | Leu | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ala | Val | Cys | Ile | Val | Leu | Leu | Leu | His | Ser | Ser | Ala | Gly | His | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Lys | Ser | Pro | Pro | Pro | Pro | His | Cys | His | Tyr | Thr | Gly | Gln | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Pro | Pro | Ser | Pro | Val | Pro | Ala | Ser | Leu | Tyr | Ser | Pro | Pro | Pro | Pro |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Pro | Val | Pro | Ala | Pro | Met | Pro | Ser | Pro | Ser | Pro | Pro | Pro | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Gln | Ala | Pro | Met | Pro | Pro | Pro | Pro | Pro | Ala | Pro | Thr | Pro | Thr | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Pro | Thr | Pro | Xaa | Pro | Ser | Pro | Ser | Pro | Xaa | Pro | Val | Asn | Asn | Cys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ser | Tyr | Met | Tyr | Cys | Ala | Met | Gln | Cys | Ser | Pro | Val | Cys | Gln | Ala | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Xaa | Arg | Arg | His | Arg | Gln | Val | Arg | Lys | Arg | Pro | Arg | His | Gln | Thr |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Thr | Gly | Ala | Thr | Thr | Ala | Ala | Pro | Ala | Met | Ser | Ala | Pro | Ala | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Ala | Pro | Ala | Val | Ala | Ala | Ala | Ser | Ala | Thr | Ala | Pro | Ala | Thr | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Pro | Thr | Arg | Pro | Ala | Ala | Ala | Asn | Pro | Ala | Ala | Thr | Phe | Cys | Thr | Ala |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Arg | Ser | Ser | Ala | Ala | Gly | Ile | Thr | Thr | Thr | Gly | Leu | Trp | Ser | Thr | Ala |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1501732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met Pro Ser Pro Ser Pro Pro Pro Pro Pro Val Gln Ala Pro Met Pro  
1 5 10 15  
Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro Ala Pro Thr Pro Xaa Pro  
20 25 30  
Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys Ser Tyr Met Tyr Cys Ala  
35 40 45  
Met Gln Cys Ser Pro Val Cys Gln Ala Lys Pro Xaa Arg Arg His Arg  
50 55 60  
Gln Val Arg Lys Arg Pro Arg His Gln Thr Thr Thr Gly Ala Thr Thr  
65 70 75 80  
Ala Ala Pro Ala Met Ser Ala Pro Ala Thr Pro Ala Pro Ala Val Ala  
85 90 95  
Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr Pro Thr Arg Pro Ala Ala  
100 105 110  
Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala Arg Ser Ser Ala Ala Gly  
115 120 125  
Ile Thr Thr Thr Gly Leu Trp Ser Thr Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

Met Pro Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro Ala Pro Thr Pro  
1 5 10 15  
Xaa Pro Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys Ser Tyr Met Tyr  
20 25 30  
Cys Ala Met Gln Cys Ser Pro Val Cys Gln Ala Lys Pro Xaa Arg Arg  
35 40 45  
His Arg Gln Val Arg Lys Arg Pro Arg His Gln Thr Thr Thr Gly Ala  
50 55 60  
Thr Thr Ala Ala Pro Ala Met Ser Ala Pro Ala Thr Pro Ala Pro Ala  
65 70 75 80  
Val Ala Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr Pro Thr Arg Pro  
85 90 95  
Ala Ala Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala Arg Ser Ser Ala  
100 105 110  
Ala Gly Ile Thr Thr Thr Gly Leu Trp Ser Thr Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1501737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| attctgttcg gttccttccg aaaacacaaac aggaaaacac acgcacaaaa ctgccgtttc | 60  |
| cgaatggcca cggccgtgct ccgccgcca ttccctgcgcg cgctcctccc cgccgccgga  | 120 |
| ggggcggtccg ggacctcctc ttggttccgt ccccgagac gtaggtcctc tccttccgtg  | 180 |
| cgcgcggtgt cttccgactc ccccaagccc gtcgcctcca cctcctcccc caccggcggt  | 240 |
| gacagccccg acgaggaacc accggtccta ccgctcctcc aggagcttgc ggattgcttg  | 300 |
| attcttccac ccaagctcct cgctcagctc ccgagcgacc ttctgtctga cctcaatgac  | 360 |
| gctgcgtttg atctctccaa cgggccaagt ctcgacgagt gtggccaaga agtgggtgat  | 420 |
| ctgctcctga acctggcaaa agcatgggag ttagctgata cgtcaacatc aaatagcatt  | 480 |
| gccaaagcagc tgc                                                    |     |

(2) INFORMATION FOR SEQ ID NO:1933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1501738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Leu | Phe | Gly | Ser | Phe | Arg | Lys | His | Asn | Arg | Lys | Thr | His | Ala | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Cys | Arg | Phe | Arg | Met | Ala | Thr | Ala | Val | Leu | Arg | Arg | Pro | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Leu | Leu | Pro | Ala | Ala | Gly | Gly | Ala | Ser | Gly | Thr | Ser | Ser | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Arg | Pro | Arg | Arg | Arg | Arg | Ser | Ser | Pro | Ser | Val | Arg | Ala | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asp | Ser | Pro | Lys | Pro | Val | Ala | Ser | Thr | Ser | Ser | Pro | Thr | Gly | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ser | Pro | Asp | Glu | Glu | Pro | Pro | Val | Leu | Pro | Leu | Leu | Gln | Glu | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Asp | Cys | Leu | Ile | Leu | Pro | Pro | Lys | Leu | Leu | Ala | Gln | Leu | Pro | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Arg | Leu | Asp | Leu | Asn | Asp | Ala | Ala | Phe | Asp | Leu | Ser | Asn | Gly |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Pro | Val | Leu | Asp | Glu | Cys | Gly | Gln | Glu | Val | Gly | Asp | Leu | Leu | Leu | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Leu | Ala | Lys | Ala | Trp | Glu | Leu | Ala | Asp | Thr | Ser | Thr | Ser | Asn | Ser | Ile |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |
| Ala | Lys | Gln | Leu |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1501739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Cys | Ser | Val | Pro | Ser | Glu | Asn | Thr | Thr | Gly | Lys | His | Thr | His | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ala | Val | Ser | Glu | Trp | Pro | Arg | Pro | Cys | Ser | Ala | Ala | His | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Pro Arg Ser Ser Pro Pro Pro Glu Gly Arg Pro Gly Pro Pro Leu Gly  
35 40 45  
Ser Val Pro Gly Asp Val Gly Pro Leu Leu Pro Cys Ala Arg Cys Leu  
50 55 60  
Pro Thr Pro Pro Ser Pro Ser Pro Pro Pro Pro Pro Pro Pro Ala Val  
65 70 75 80  
Thr Ala Pro Thr Arg Asn His Arg Ser Tyr Arg Ser Ser Arg Ser Leu  
85 90 95  
Arg Ile Ala

(2) INFORMATION FOR SEQ ID NO:1935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

Met Ala Thr Ala Val Leu Arg Arg Pro Phe Leu Ala Ala Leu Leu Pro  
1 5 10 15  
Ala Ala Gly Gly Ala Ser Gly Thr Ser Ser Trp Phe Arg Pro Arg Arg  
20 25 30  
Arg Arg Ser Ser Pro Ser Val Arg Ala Val Ser Ser Asp Ser Pro Lys  
35 40 45  
Pro Val Ala Ser Thr Ser Ser Pro Thr Gly Gly Asp Ser Pro Asp Glu  
50 55 60  
Glu Pro Pro Val Leu Pro Leu Leu Gln Glu Leu Ala Asp Cys Leu Ile  
65 70 75 80  
Leu Pro Pro Lys Leu Leu Ala Gln Leu Pro Ser Asp Leu Arg Leu Asp  
85 90 95  
Leu Asn Asp Ala Ala Phe Asp Leu Ser Asn Gly Pro Val Leu Asp Glu  
100 105 110  
Cys Gly Gln Glu Val Gly Asp Leu Leu Asn Leu Ala Lys Ala Trp  
115 120 125  
Glu Leu Ala Asp Thr Ser Thr Ser Asn Ser Ile Ala Lys Gln Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1501741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

acaaacttcc cctgtcacga gagtacgaga ccacgccttc cgtgggatca atcggttagg 60  
gtttcggaga tggtcggccg cgcgccgaag aagagcgaca acacccggta ctacgagatc 120  
ctgggggttt ccaaggacgc gtcacaggat gacctcaaga aggcctaccg caaggccgcc 180  
atcaagaacc accccgacaa gggcggcgac cccgagaagt tcaaggagct atgtatgctg 240  
tatgcatgtg gtgaagcaag tgctcgtcgg tgtgtagtgt tcgctctttt gatccattgt 300  
ctgtgctctg tactgtagtg atcagcgtca aaataaagaa atgcctgtcc ttgtttagaa 360  
ttg

(2) INFORMATION FOR SEQ ID NO:1937:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..105  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501742  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:  
Thr Asn Phe Pro Cys His Glu Ser Thr Arg Pro Arg Leu Pro Trp Asp  
1                  5                  10                  15  
Gln Ser Ala Arg Val Ser Glu Met Phe Gly Arg Ala Pro Lys Lys Ser  
                  20                  25                  30  
Asp Asn Thr Arg Tyr Tyr Glu Ile Leu Gly Val Ser Lys Asp Ala Ser  
                  35                  40                  45  
Gln Asp Asp Leu Lys Lys Ala Tyr Arg Lys Ala Ala Ile Lys Asn His  
                  50                  55                  60  
Pro Asp Lys Gly Gly Asp Pro Glu Lys Phe Lys Glu Leu Cys Met Leu  
65                  70                  75                  80  
Tyr Ala Cys Gly Glu Ala Ser Ala Arg Arg Cys Val Val Phe Ala Leu  
                  85                  90                  95  
Leu Ile His Cys Leu Cys Ser Val Leu  
                  100                  105  
(2) INFORMATION FOR SEQ ID NO:1938:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 91 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..91  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1501743  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:  
Gln Thr Ser Pro Val Thr Arg Val Arg Asp His Ala Phe Arg Gly Ile  
1                  5                  10                  15  
Asn Arg Leu Gly Phe Arg Arg Cys Ser Ala Ala Arg Arg Arg Ala  
                  20                  25                  30  
Thr Thr Pro Gly Thr Thr Arg Ser Trp Gly Phe Pro Arg Thr Arg His  
                  35                  40                  45  
Arg Met Thr Ser Arg Arg Pro Thr Ala Arg Pro Pro Ser Arg Thr Thr  
                  50                  55                  60  
Pro Thr Arg Ala Ala Thr Pro Arg Ser Ser Arg Ser Tyr Val Cys Cys  
65                  70                  75                  80  
Met His Val Val Lys Gln Val Leu Val Gly Val  
                  85                  90  
(2) INFORMATION FOR SEQ ID NO:1939:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 82 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..82  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1501744  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:  
Met Phe Gly Arg Ala Pro Lys Lys Ser Asp Asn Thr Arg Tyr Tyr Glu



|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| 1                                                               | 5  | 10 | 15 |
| Ile Leu Gly Val Ser Lys Asp Ala Ser Gln Asp Asp Leu Lys Lys Ala |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Tyr Arg Lys Ala Ala Ile Lys Asn His Pro Asp Lys Gly Gly Asp Pro |    |    |    |
|                                                                 | 35 | 40 | 45 |
| Glu Lys Phe Lys Glu Leu Cys Met Leu Tyr Ala Cys Gly Glu Ala Ser |    |    |    |
|                                                                 | 50 | 55 | 60 |
| Ala Arg Arg Cys Val Val Phe Ala Leu Leu Ile His Cys Leu Cys Ser |    |    |    |
| 65                                                              | 70 | 75 | 80 |
| Val Leu                                                         |    |    |    |

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| ctcgttttac cgcacccgc cgcagccgc aacgccgaga agacgcgaga kgaagggagg    | 60  |
| aggtgagcca ccgaagcgga gacgtgagta gtcgaccaac cccgtcggtc cggcgactcc  | 120 |
| ggctgcggcg cggcgtgcta gatcgctacc gaccatggtg gtggaggaga tcgccgaggg  | 180 |
| ggtgaaaaac ctcaccgtta ccggagatgc ggcggcttca ggcggagagg ggcagaggag  | 240 |
| ggcgggcggc ggcacagcaa ccgcatccag gtgtccaaca ccaagaagcc cctcttcttc  | 300 |
| tacgtcaacc tcgccaagag tatatgcaac agcacgacga tgtagagcta tccgctcttg  | 360 |
| ggatggccat agcaacagtt gtgaccgtgg cagaaattct gaagaacaat ggatttgccg  | 420 |
| ttgaaaagaa aattaggacc tctactgttg aaataaacga cgaatcaaga gggcgctccat | 480 |
| tcc                                                                |     |

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| Arg Phe Thr Arg Thr Arg Arg Ser Pro Gln Arg Arg Glu Asp Ala Arg |    |    |    |
| 1                                                               | 5  | 10 | 15 |
| Xaa Arg Glu Glu Val Ser His Arg Ser Gly Asp Val Ser Ser Arg Pro |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Thr Pro Ser Val Arg Arg Leu Arg Leu Arg Arg Gly Val Leu Asp Arg |    |    |    |
|                                                                 | 35 | 40 | 45 |
| Tyr Arg Pro Trp Trp Trp Arg Arg Ser Pro Arg Gly                 |    |    |    |
| 50                                                              | 55 | 60 |    |

(2) INFORMATION FOR SEQ ID NO:1942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

Met Val Val Glu Glu Ile Ala Glu Gly Val Lys Asn Leu Thr Val Thr  
1 5 10 15  
Gly Asp Ala Ala Ala Ser Gly Gly Glu Gly Gln Arg Arg Gly Gly Gly  
20 25 30  
Gly Thr Ala Thr Ala Ser Arg Cys Pro Thr Pro Arg Ser Pro Ser Ser  
35 40 45  
Ser Thr Ser Thr Ser Pro Arg Val Tyr Ala Thr Ala Arg Arg Cys Arg  
50 55 60  
Ala Ile Arg Ser Trp Asp Gly His Ser Asn Ser Cys Asp Arg Gly Arg  
65 70 75 80  
Asn Ser Glu Glu Gln Trp Ile Cys Arg  
85

(2) INFORMATION FOR SEQ ID NO:1943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1501758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

Met Arg Arg Leu Gln Ala Glu Arg Gly Arg Gly Ala Ala Ala Ala  
1 5 10 15  
Gln Gln Pro His Pro Gly Val Gln His Gln Glu Ala Pro Leu Leu Leu  
20 25 30  
Arg Gln Pro Arg Gln Glu Tyr Met Gln Gln His Asp Asp Val Glu Leu  
35 40 45  
Ser Ala Leu Gly Met Ala Ile Ala Thr Val Val Thr Val Ala Glu Ile  
50 55 60  
Leu Lys Asn Asn Gly Phe Ala Val Glu Lys Lys Ile Arg Thr Ser Thr  
65 70 75 80  
Val Glu Ile Asn Asp Glu Ser Arg Gly Arg Pro Phe  
85 90

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1501763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

|             |            |             |            |            |             |     |
|-------------|------------|-------------|------------|------------|-------------|-----|
| aagattgggt  | ccaacaccag | ccgcccgcct  | gtcgaagcga | ggcargggag | gttcggcggg  | 60  |
| gaacaagtgc  | cgcattgtgc | tgggtctgcc  | agtggccgcg | acggtgaact | gcgcggacaa  | 120 |
| caccggcgcc  | aagaacctct | acatcatctc  | cgtaaggggc | atcaaggggc | gcctcaatcg  | 180 |
| cctcccgtcc  | gcctgcgttg | gcgacatggt  | catggccacc | gtcaagaagg | ggaagcccga  | 240 |
| cctcaggaag  | aaggtgatgc | ccgcccgtcat | cgtccgccag | cgcaagccgt | ggcggcgcaa  | 300 |
| ggacgggggtc | tacatgtact | tcgaagataa  | tgctggagtg | attgtgaatc | ccaaggggtga | 360 |
| gatgaaaggt  | tccgctatca | ctggacctat  | cggcaaggag | tgtgctgata | tttggcctag  | 420 |
| gattgctagc  | gcagcaaacg | ccattgtttg  | agagcttggt | ggaatatggt | cagacttcta  | 480 |
| tatgatcatc  | ttattatcag | ttgctagact  | gcaattgggc | ttatgtttgt | tcactcaatt  | 540 |
| ttgtagtaaa  | cagaatttgg | tataccaagg  | ggatct     |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1501764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

```
Arg Leu Gly Pro Thr Pro Ala Ala Ala Met Ser Lys Arg Gly Xaa Gly
1 5 10 15
Gly Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala
20 25 30
Ala Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile
35 40 45
Ile Ser Val Lys Gly Ile Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala
50 55 60
Cys Val Gly Asp Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp
65 70 75 80
Leu Arg Lys Lys Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Pro
85 90 95
Trp Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly
100 105 110
Val Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly
115 120 125
Pro Ile Gly Lys Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala
130 135 140
Ala Asn Ala Ile Val
145
```

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1501765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

```
Met Ser Lys Arg Gly Xaa Gly Gly Ser Ala Gly Asn Lys Phe Arg Met
1 5 10 15
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr
20 25 30
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg
35 40 45
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr
50 55 60
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val
65 70 75 80
Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr Met
85 90 95
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met
100 105 110
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu
115 120 125
Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val
```

130 135 140  
(2) INFORMATION FOR SEQ ID NO:1947:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501766  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:  
Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn  
1 5 10 15  
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly  
20 25 30  
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala  
35 40 45  
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala  
50 55 60  
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr  
65 70 75 80  
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu  
85 90 95  
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp  
100 105 110  
Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1948:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 554 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..554  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501771  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:  
attattctat caagtgtgtg tgcttttatt ttatgtgctg gagctgcact agtgctttat 60  
ttcaagcttc gaaaccacat ccatttaact gaagcgtcac ttgtgccaac aaaacctaca 120  
ggctctgttt ctgcaatggt tgggaacagg ctagaaagca gacctatttc ggcatcacca 180  
tccttcagct caagtttggt ggcatataaa ggatctgcc aacatttta cctggttgag 240  
atggagagag ctacactagg atttgatgag tccagaatta ttggtgaggg tggttttggg 300  
cgtgtctatg aaggtattct tgaggatgga gaacgggttg ctatcaaggt tttaaagcgg 360  
gacgatcaac aaggtacccg ggagtttttg gctgargtcg agatgcttag ccgattgcat 420  
cataggaact tggttaagct gataggtata tgcacagagg ggcatagccg atgtttgggt 480  
tatgagcttg ttccgaatgg cagtgtggga atctcacttg catggatcag ataaaggag 540  
ctgctcagtt tgat

(2) INFORMATION FOR SEQ ID NO:1949:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1501772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

Ile Ile Leu Ser Ser Val Cys Ala Phe Ile Leu Cys Ala Gly Ala Ala  
1 5 10 15  
Leu Val Leu Tyr Phe Lys Leu Arg Asn His Ile His Leu Thr Glu Ala  
20 25 30  
Ser Leu Val Pro Thr Lys Pro Thr Gly Pro Val Ser Ala Met Val Gly  
35 40 45  
Asn Arg Leu Glu Ser Arg Pro Ile Ser Ala Ser Pro Ser Phe Ser Ser  
50 55 60  
Ser Leu Val Ala Tyr Lys Gly Ser Ala Lys Thr Phe Asn Leu Val Glu  
65 70 75 80  
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu  
85 90 95  
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg  
100 105 110  
Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly Thr Arg Glu  
115 120 125  
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu  
130 135 140  
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val  
145 150 155 160  
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile  
165 170 175  
Arg

(2) INFORMATION FOR SEQ ID NO:1950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1501773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

Met Val Gly Asn Arg Leu Glu Ser Arg Pro Ile Ser Ala Ser Pro Ser  
1 5 10 15  
Phe Ser Ser Ser Leu Val Ala Tyr Lys Gly Ser Ala Lys Thr Phe Asn  
20 25 30  
Leu Val Glu Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile  
35 40 45  
Ile Gly Glu Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp  
50 55 60  
Gly Glu Arg Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly  
65 70 75 80  
Thr Arg Glu Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His  
85 90 95  
Arg Asn Leu Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg  
100 105 110  
Cys Leu Val Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu  
115 120 125  
Ala Trp Ile Arg  
130

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..97  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501774  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:  
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu  
1                  5                  10                  15  
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg  
                  20                  25                  30  
Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly Thr Arg Glu  
                  35                  40                  45  
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu  
                  50                  55                  60  
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val  
65                  70                  75                  80  
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile  
                  85                  90                  95  
Arg

(2) INFORMATION FOR SEQ ID NO:1952:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 420 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..420  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:  
aaaaacctcg caagcgaccc cagtaatggc gaccaaggcg ctatccgtct cctcgctcac 60  
ctccacggcc ttgacctct ttcccttgcc gcgccccgc aggccttcac cttcgcttcc 120  
cctcctccgc cttctcgccc ctccgccccg cgctccact ctctccgccg ccgctcccg 180  
cgacgaggac ggcgtcgaca ccgtggagca gctcctccac ccamgcccgc ctgagacctc 240  
agccccgcc ggatccccgc gccggatcga mcgctcatg aagctccagc gcmgcccga 300  
cgggamgccg tgcccggggg ccggaggagg tggttccctt acctggacgc gttccggccc 360  
cgggccgngn ggcgcggaat gtccagcggg gaggtcatag aggtgctgga gccgcacatc 420

(2) INFORMATION FOR SEQ ID NO:1953:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 77 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..77  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:  
Lys Asn Leu Ala Ser Asp Pro Ser Asn Gly Asp Gln Gly Ala Ile Arg  
1                  5                  10                  15  
Leu Leu Ala His Leu His Gly Leu Cys Leu Leu Phe Leu Ala Ala Ala  
                  20                  25                  30  
Pro Gln Ala Phe Thr Phe Ala Ser Pro Pro Pro Pro Ser Arg Pro Ser  
                  35                  40                  45  
Pro Pro Arg Leu His Ser Leu Arg Arg Arg Ser Arg Arg Arg Gly Arg  
50                  55                  60

Arg Arg His Arg Gly Ala Ala Pro Pro Pro Xaa Pro Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

Lys Thr Ser Gln Ala Thr Pro Val Met Ala Thr Lys Ala Leu Ser Val  
1 5 10 15  
Ser Ser Leu Thr Ser Thr Ala Phe Ala Ser Phe Ser Leu Pro Arg Pro  
20 25 30  
Arg Arg Pro Ser Pro Ser Pro Leu Leu Arg Leu Leu Gly Pro Arg  
35 40 45  
Pro Arg Ala Ser Thr Leu Ser Ala Ala Pro Gly Asp Glu Asp Gly  
50 55 60  
Val Asp Thr Val Glu Gln Leu Leu His Pro Xaa Pro Pro Glu Thr Ser  
65 70 75 80  
Ala Pro Ala Gly Ser Arg Gly Arg Ile Xaa Arg Leu Met Lys Leu Gln  
85 90 95  
Arg Xaa Ala Asp Gly Xaa Pro Cys Pro Gly Ala Gly Gly Gly Ser  
100 105 110  
Leu Thr Trp Thr Arg Ser Gly Pro Arg Pro Xaa Gly Ala Xaa Cys Pro  
115 120 125  
Ala Gly Arg Ser  
130

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Met Ala Thr Lys Ala Leu Ser Val Ser Ser Leu Thr Ser Thr Ala Phe  
1 5 10 15  
Ala Ser Phe Ser Leu Pro Arg Pro Arg Arg Pro Ser Pro Ser Pro Pro  
20 25 30  
Leu Leu Arg Leu Leu Gly Pro Arg Pro Arg Ala Ser Thr Leu Ser Ala  
35 40 45  
Ala Ala Pro Gly Asp Glu Asp Gly Val Asp Thr Val Glu Gln Leu Leu  
50 55 60  
His Pro Xaa Pro Pro Glu Thr Ser Ala Pro Ala Gly Ser Arg Gly Arg  
65 70 75 80  
Ile Xaa Arg Leu Met Lys Leu Gln Arg Xaa Ala Asp Gly Xaa Pro Cys  
85 90 95  
Pro Gly Ala Gly Gly Gly Gly Ser Leu Thr Trp Thr Arg Ser Gly Pro  
100 105 110  
Arg Pro Xaa Gly Ala Xaa Cys Pro Ala Gly Arg Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:1956:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 493 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..493  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501794  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

```
aacctaacc tcgtctcgcc tcgcctccgc cagtcagccc cctcaacccc ggcggccaaa 60
agtcgacgca ccgaagcggc ggccatggcg gactaaagcg gctgtcagag agccgggacc 120
tgacgcggat cgagccatcg gcgcgcactc ccacatccgg gggctagggc tggactcctc 180
catggaggcg cgcgacgcct cggaggggcat ggtcggggcag ctgcccgcgc gccgsscgcg 240
gngctcata ctccagctca tccgccaggg caagatcgcc ggccgcgccg ttctcctcgc 300
gggccagccc ggtaccggca agaccgcgct cgccatggcg atcgccaagt cgctcggcgc 360
ggagacgccc ttgcctccg tcgcagcctc ggagctcttc tcgctcgamc tctccaagam 420
ggaggcgctc acgcaggcct tccgccgcgc catcgggtgc gcatcaagga ggagacggaa 480
atcatcgagg gcg
```

(2) INFORMATION FOR SEQ ID NO:1957:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 54 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..54  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501795  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

```
Pro Lys Pro Arg Leu Ala Ser Pro Pro Pro Val Ser Pro Leu Asn Pro
1 5 10 15
Gly Gly Gln Lys Ser Thr His Arg Ser Gly Gly His Gly Gly Leu Lys
 20 25 30
Arg Leu Ser Glu Ser Arg Asp Leu Thr Arg Ile Glu Pro Ser Ala Arg
 35 40 45
Thr Pro Thr Ser Gly Gly
50
```

(2) INFORMATION FOR SEQ ID NO:1958:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 104 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..104  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501796  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

```
Met Glu Ala Arg Asp Ala Ser Glu Gly Met Val Gly Gln Leu Pro Ala
1 5 10 15
Arg Xaa Xaa Arg Xaa Leu Ile Leu Gln Leu Ile Arg Gln Gly Lys Ile
 20 25 30
Ala Gly Arg Ala Val Leu Leu Ala Gly Gln Pro Gly Thr Gly Lys Thr
 35 40 45
Ala Leu Ala Met Gly Ile Ala Lys Ser Leu Gly Ala Glu Thr Pro Phe
 50 55 60
Ala Ser Val Ala Ala Ser Glu Leu Phe Ser Leu Xaa Leu Ser Lys Xaa
```



(2) INFORMATION FOR SEQ ID NO:1959:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1501797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

(2) INFORMATION FOR SEQ ID NO:1960:

(A) LENGTH: 461 base pairs

(B) TYPE: nucleic acid

```
{C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1501804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

(2) INFORMATION FOR SEQ ID NO:1961:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

Ile Pro Lys Ser Thr Gln Arg Xaa Leu Lys His His Phe Leu His Ser  
1 5 10 15  
Leu Leu Ala Ala His Thr Val Leu Val Thr Val His His Gln Ser Pro  
20 25 30  
Pro Met Ala Pro Lys Val Ala Leu Phe Leu Ala Leu Gly Leu Leu Phe  
35 40 45  
Ala Ala Ala Ala Asn Gly Cys Glu Pro Tyr Cys Pro Gly Pro Val Val  
50 55 60  
Pro Thr Pro Pro Val Val Pro Thr Pro Ser Ser His Ser His Gly Arg  
65 70 75 80  
Cys Pro Ile Asp Ala Leu Lys Ile Met Cys Ala Pro Thr Cys  
85 90

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

Pro Lys Glu His Ala Ala Xaa Thr Glu Ala Pro Leu Pro Ala Leu Thr  
1 5 10 15  
Ala Ser Cys Ser His Arg Ala Ser Asn Ser Pro Ser Pro Val Thr Thr  
20 25 30  
Asn Gly Ser Gln Gly Cys Ala Leu Pro Cys Pro Arg Pro Ser Leu Arg  
35 40 45  
Cys Arg Arg Glu Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro  
50 55 60  
Asn Ala Ala Ser Arg Ala Asp Ala Val Val Ala Gln Pro Arg Ala Leu  
65 70 75 80  
Pro Asp Arg Arg Ala Gln Asn His Val Cys Ala Asn Val Leu Gly Leu  
85 90 95  
Val Lys Val Gly Leu Pro Gln His Glu Gln Cys Cys Pro Leu Leu Glu  
100 105 110  
Gly Leu Val Asp Leu Asp Ala Ala Leu Cys Leu Cys Thr Xaa Ile Lys  
115 120 125  
Ala Asn Gly Val Asp Phe Tyr Ile Asn Gly His Asp His Cys Leu Glu  
130 135 140  
His Ile Ser Ser Arg Asp Ser Pro Ile  
145 150

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

Met Ala Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Gln  
1 5 10 15  
Ser Cys Arg Arg Arg Arg Arg Thr Ala Thr Gly Ala Ala Arg Ser Thr  
20 25 30  
Arg Ser Lys Ser Cys Val Arg Gln Arg Ala Arg Pro Arg Gln Gly Arg

```

 35 40 45
Pro Ala Pro Ala Arg Ala Met Leu Pro Thr Ser Gly Gly Ala Gly Gly
 50 55 60
Pro Arg Arg Arg Thr Val Pro Leu His Xaa His Gln Gly Gln Arg Arg
 65 70 75 80
Arg Phe Leu His Gln Arg Ala
 85
```

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

```

agacaacat agaccgacga ggtgtgaact gtaatttcag atttcagagc gcgcaagaac 60
cctcttgacc accgcccgcg ccgcccgcgaa scaagccaaa ctgagtaagc agctatggag 120
ggatccgcgc ccgctccgct ccgcacgcgc atctgcatca tcgggagcgc tcccgcctgcg 180
cacacggcag ccatctacgc ggcccgcgcg gagctcaagc ctgtdctctt cgagggctgg 240
atggccaacg acatcgccgc gggcgggcag ctcaccacca ccaccgacgt cgagaacttc 300
ccgggcttcc ccaacggcat catgggcgcc gacctcatgg acaactgccg cgcgcagtcc 360
ctgcgctttg gcaccaacat cctctccgag accgtcaccg ccgtcgactt ttcggcctgc 420
ccattccgag ttagtgcaga ctccac
```

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

```

Met Glu Gly Ser Ala Ala Pro Leu Arg Thr Arg Ile Cys Ile Ile
 1 5 10 15
Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala
 20 25 30
Glu Leu Lys Pro Xaa Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala
 35 40 45
Ala Gly Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly
 50 55 60
Phe Pro Asn Gly Ile Met Gly Ala Asp Leu Met Asp Asn Cys Arg Ala
 65 70 75 80
Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu Ser Glu Thr Val Thr Ala
 85 90 95
Val Asp Phe Ser Ala Cys Pro Phe Arg Val Ser Ala Asp Ser
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO:1966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1501812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

```
Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr Thr Asp
 1 5 10 15
Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala Asp Leu
 20 25 30
Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu
 35 40 45
Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe Arg Val
 50 55 60
Ser Ala Asp Ser
65
```

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..758

(D) OTHER INFORMATION: / Ceres Seq. ID 1501813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

```
aaattcccaa ccgccgcacg gcaacaccag cggtcggatc gggggagaaa cggaagggca 60
acagcagagc gcgaattcca ccgacaaatc caagatttcg agcacagaca caggcgaaac 120
tcgatggcgg aggggtccaa gccggacgtg ccgctgttcc agctcctcag cgatcttctc 180
cagcaggtgg agtcaatgag caatcaggaa gaagtagagc tgccgcgctaa gattgaagca 240
ttaggattag aagtcactaa ggtaccagag cagcccgcga atmatctcag cgagctagaa 300
matagctgca gagttggaca aagctgtcat cgcggcttga ataatgtcg acaaagatga 360
tatcatctgc catggcctca gatccagagg tgaagtctct tctgagcagc acatctgata 420
tctggatgcc ggtcataaca gcgtctgcca atgagaggcg ggggtttgtt gggacgagca 480
gcgaaggcag ccagaaagag caggagaatt ccaagaaata gctggtatat gggctgttaa 540
tagtttcgtt ttgtgggtct gtaccgacct tatctatgtt cattcaaact agtgtttcca 600
tgccaaaaag tttgtggcgt aataaacaat aaaaacccat gtccttcatt cggattagta 660
atgagtgatg atagatctaa attactatct tggtcgcccg ttagttcatt tttgaactaa 720
aacgcgaata atagaaaaga acggagggag tatgattt
```

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1501814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

```
Lys Phe Pro Thr Ala Ala Arg Gln His Gln Arg Ser Asp Arg Gly Arg
 1 5 10 15
Asn Gly Arg Ala Thr Ala Glu Arg Glu Phe His Arg Gln Ile Gln Asp
 20 25 30
Phe Glu His Arg His Arg Arg Asn Ser Met Ala Glu Gly Ser Lys Pro
 35 40 45
Asp Val Pro Leu Phe Gln Leu Leu Ser Asp Leu Leu Gln Gln Val Glu
 50 55 60
Ser Met Ser Asn Gln Glu Glu Val Glu Leu Arg Ala Lys Ile Glu Ala
 65 70 75 80
```

Leu Gly Leu Glu Val Thr Lys Val Pro Glu Gln Pro Ala Asn Xaa Leu  
85 90 95  
Ser Glu Leu Glu Xaa Ser Cys Arg Val Gly Gln Ser Cys His Arg Gly  
100 105 110  
Leu Asn Lys Cys Arg Gln Arg  
115

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1501815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

Ile Pro Asn Arg Arg Thr Ala Thr Pro Ala Val Gly Ser Gly Glu Lys  
1 5 10 15  
Arg Lys Gly Asn Ser Arg Ala Arg Ile Pro Pro Thr Asn Pro Arg Phe  
20 25 30  
Arg Ala Gln Thr Gln Ala Lys Leu Asp Gly Gly Gly Val Gln Ala Gly  
35 40 45  
Arg Ala Ala Val Pro Ala Pro Gln Arg Ser Ser Pro Ala Gly Gly Val  
50 55 60  
Asn Glu Gln Ser Gly Arg Ser Arg Ala Ala Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1501816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

Met Ala Glu Gly Ser Lys Pro Asp Val Pro Leu Phe Gln Leu Leu Ser  
1 5 10 15  
Asp Leu Leu Gln Gln Val Glu Ser Met Ser Asn Gln Glu Glu Val Glu  
20 25 30  
Leu Arg Ala Lys Ile Glu Ala Leu Gly Leu Glu Val Thr Lys Val Pro  
35 40 45  
Glu Gln Pro Ala Asn Xaa Leu Ser Glu Leu Glu Xaa Ser Cys Arg Val  
50 55 60  
Gly Gln Ser Cys His Arg Gly Leu Asn Lys Cys Arg Gln Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1501824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

|            |             |            |            |             |            |     |
|------------|-------------|------------|------------|-------------|------------|-----|
| aaaacgcaca | ggagataact  | agcgagcgag | agcgtngaga | tcgaggagaa  | gaaggcaagc | 60  |
| aggcagagaa | agagagagag  | agatggatga | ggagtacgac | gtgatcgtgt  | tggggacggg | 120 |
| gctcaaggag | tgcatacatca | gcggcctcct | ctccgtcgat | ggcctcaagg  | tccttcacat | 180 |
| ggacaggaat | gactactacg  | gaggagaatc | ttcgtccctg | aatctaacca  | agctctggaa | 240 |
| taggttcaag | ggcaacgaca  | gccctcccg  | gcacctgggc | gtcaciaaaga | gtacaacgtc | 300 |
| gacatggtgc | ccaagttcat  | gatggcaaac | ggcgcgctgg | tccgcgtcct  | gatccgcacc | 360 |
| agcgtgacca | agtatctcaa  | cttcaaggct | gttgacggga | gctttgtgta  | caacaatggc | 420 |
| aagatccaca | aagtcgccgg  | aaccgacgtg | gaggccctca | agtcgaacct  | gatgggcctg | 480 |
| ttcgagaagc | ggcgcgcccc  | gaagttcttc | atatacgtdc | aggactacga  | ggaggacgac | 540 |
| cccaagtccc | acgagggcct  | ggacctcaac | aaggtcacca | ccaggggaagt | catctccaaa | 600 |
| tacggat    |             |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1501825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Pro | Lys | Phe | Met | Met | Ala | Asn | Gly | Ala | Leu | Val | Arg | Val | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Arg | Thr | Ser | Val | Thr | Lys | Tyr | Leu | Asn | Phe | Lys | Ala | Val | Asp | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Phe | Val | Tyr | Asn | Asn | Gly | Lys | Ile | His | Lys | Val | Pro | Ala | Thr | Asp |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Val | Glu | Ala | Leu | Lys | Ser | Asn | Leu | Met | Gly | Leu | Phe | Glu | Lys | Arg | Arg |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Arg | Lys | Phe | Phe | Ile | Tyr | Xaa | Gln | Asp | Tyr | Glu | Glu | Asp | Asp | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Ser | His | Glu | Gly | Leu | Asp | Leu | Asn | Lys | Val | Thr | Thr | Arg | Glu | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Ile | Ser | Lys | Tyr | Gly |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1501826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Met | Ala | Asn | Gly | Ala | Leu | Val | Arg | Val | Leu | Ile | Arg | Thr | Ser | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Lys | Tyr | Leu | Asn | Phe | Lys | Ala | Val | Asp | Gly | Ser | Phe | Val | Tyr | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Gly | Lys | Ile | His | Lys | Val | Pro | Ala | Thr | Asp | Val | Glu | Ala | Leu | Lys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ser | Asn | Leu | Met | Gly | Leu | Phe | Glu | Lys | Arg | Arg | Ala | Arg | Lys | Phe | Phe |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Tyr | Xaa | Gln | Asp | Tyr | Glu | Glu | Asp | Asp | Pro | Lys | Ser | His | Glu | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Leu | Asp | Leu | Asn | Lys | Val | Thr | Thr | Arg | Glu | Val | Ile | Ser | Lys | Tyr | Gly |  |

85

90

95

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asn | Gly | Ala | Leu | Val | Arg | Val | Leu | Ile | Arg | Thr | Ser | Val | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Tyr | Leu | Asn | Phe | Lys | Ala | Val | Asp | Gly | Ser | Phe | Val | Tyr | Asn | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Lys | Ile | His | Lys | Val | Pro | Ala | Thr | Asp | Val | Glu | Ala | Leu | Lys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Leu | Met | Gly | Leu | Phe | Glu | Lys | Arg | Arg | Ala | Arg | Lys | Phe | Phe | Ile |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Tyr | Xaa | Gln | Asp | Tyr | Glu | Glu | Asp | Asp | Pro | Lys | Ser | His | Glu | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Asp | Leu | Asn | Lys | Val | Thr | Thr | Arg | Glu | Val | Ile | Ser | Lys | Tyr | Gly |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| tctgttcccc | tttccctcct | gcgacccccg | tcttctcctc | cccgcgtcaa  | accccagcac | 60  |
| aaaaagcaac | cgccccgcgc | ctcctcgctc | ctctcccgaa | tcagccgtcg  | cggtgcctaa | 120 |
| tccggccgac | ccccctccg  | atccgcgggt | gcccgccgca | gaggcgcgcc  | tccgggcctc | 180 |
| ccccgatgta | tagcaacttc | aaggagcagg | cgatcgagta | cgtaagcag   | gcagtcagg  | 240 |
| aggacaatgc | cggsaactac | gtcaaggcgt | tccctctcta | catgaacgcg  | ctcgagtact | 300 |
| tcaaaaccca | cctcaagtac | gagaagaacc | ccaagatcaa | ggaggccatc  | accgccaagt | 360 |
| tcaccgagta | cctccgcmgc | gccgaggaga | tccgggcggt | cctcgatgag  | ggcggcgcar | 420 |
| ggcctggggc | caacggtggc | gacgcagctg | tmgccacgcg | ccccaaagacc | caagggcaag | 480 |
| gatkgggacg | gargcaacgg | argggatgac | tccgagcagt | ccaagc      |            |     |

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Cys Ser Pro Phe Pro Pro Ala His Pro Val Phe Ser Ser Pro Arg Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   |     | 5   |     | 10  |     | 15  |     |     |     |     |     |     |     |     |     |
| Thr | Pro | Ala | Gln | Lys | Ala | Thr | Ala | Arg | Leu | Leu | Ala | Pro | Leu | Pro |     |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asn | Gln | Pro | Ser | Arg | Cys | Leu | Ile | Arg | Pro | Thr | Pro | Pro | Pro | Ile | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Cys | Pro | Pro | Gln | Arg | Arg | Ala | Ser | Gly | Pro | Pro | Pro | Met | Tyr | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Phe | Lys | Glu | Gln | Ala | Ile | Glu | Tyr | Val | Lys | Gln | Ala | Val | Gln | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Asn | Ala | Xaa | Asn | Tyr | Val | Lys | Ala | Phe | Pro | Leu | Tyr | Met | Asn | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Tyr | Phe | Lys | Thr | His | Leu | Lys | Tyr | Glu | Lys | Asn | Pro | Lys | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Glu | Ala | Ile | Thr | Ala | Lys | Phe | Thr | Glu | Tyr | Leu | Arg | Xaa | Ala | Glu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Glu | Ile | Arg | Ala | Val | Leu | Asp | Glu | Gly | Gly | Ala | Xaa | Pro | Gly | Ala | Asn |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Gly | Asp | Ala | Ala | Xaa | Ala | Thr | Arg | Pro | Lys | Thr | Gln | Gly | Gln | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Xaa | Gly | Arg | Xaa | Gln | Arg | Xaa | Gly |     |     |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Ser | Asn | Phe | Lys | Glu | Gln | Ala | Ile | Glu | Tyr | Val | Lys | Gln | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Gln | Glu | Asp | Asn | Ala | Xaa | Asn | Tyr | Val | Lys | Ala | Phe | Pro | Leu | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Met | Asn | Ala | Leu | Glu | Tyr | Phe | Lys | Thr | His | Leu | Lys | Tyr | Glu | Lys | Asn |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Lys | Ile | Lys | Glu | Ala | Ile | Thr | Ala | Lys | Phe | Thr | Glu | Tyr | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Xaa | Ala | Glu | Glu | Ile | Arg | Ala | Val | Leu | Asp | Glu | Gly | Gly | Ala | Xaa | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ala | Asn | Gly | Gly | Asp | Ala | Ala | Xaa | Ala | Thr | Arg | Pro | Lys | Thr | Gln |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Gln | Gly | Xaa | Gly | Arg | Xaa | Gln | Arg | Xaa | Gly |     |     |     |     |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| atttttttta | tatggagatt | atttctggwt | tatataaaaag | gacacaagtg | gggacgaata | 60  |
| gcagaagact | tcccttcgtc | tgcttcccag | agacccagcc  | atggcgatct | cccagatctc | 120 |



```
acgcatattc ctggccatcc ttctcctggm cgccgccttc gccgccgcc cagctgcgct 180
tgccggacggc gacgacgtgg tggcccttac cgaatccacg ttcgagaagg aggtcggaaa 240
ggaccgcggc gccctcgtcg agttctacgc cccctggtgt ggtcactgca agaagcttgc 300
tcctgagtat gaaagacttg gtgcaagttt taagaaagct aaatctgtct tgattgcyaa 360
ggttgattgt ratgagcaca agartttgtg cagcaagtat ggagtttccg ggtatccaac 420
aatccaatgg ttcccgaaag gatccttgga gcccaaaaag tatgaaggac aacgcactgc 480
agaagccctt gctgaatttc tcaatactga aggaggcaca aatgtaaagc tggc
```

(2) INFORMATION FOR SEQ ID NO:1979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

```
Phe Phe Tyr Met Glu Ile Ile Ser Xaa Leu Tyr Lys Arg Thr Gln Val
1 5 10 15
Gly Thr Asn Ser Arg Arg Leu Pro Phe Val Cys Phe Pro Glu Thr Gln
 20 25 30
Pro Trp Arg Ser Pro Arg Ser His Ala Tyr Ser Trp Pro Ser Phe Ser
 35 40 45
Trp Xaa Pro Pro Ser Pro Pro Pro Gln Leu Arg Leu Arg Thr Ala Thr
 50 55 60
Thr Trp Trp Pro Leu Pro Asn Pro Arg Ser Arg Arg Ser Glu Arg
65 70 75 80
Thr Ala Ala Pro Ser Ser Ser Thr Pro Pro Gly Val Val Thr Ala
 85 90 95
Arg Ser Leu Leu Leu Ser Met Lys Asp Leu Val Gln Val Leu Arg Lys
 100 105 110
Leu Asn Leu Ser
 115
```

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1501852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

```
Met Glu Ile Ile Ser Xaa Leu Tyr Lys Arg Thr Gln Val Gly Thr Asn
1 5 10 15
Ser Arg Arg Leu Pro Phe Val Cys Phe Pro Glu Thr Gln Pro Trp Arg
 20 25 30
Ser Pro Arg Ser His Ala Tyr Ser Trp Pro Ser Phe Ser Trp Xaa Pro
 35 40 45
Pro Ser Pro Pro Pro Gln Leu Arg Leu Arg Thr Ala Thr Thr Trp Trp
 50 55 60
Pro Leu Pro Asn Pro Arg Ser Arg Arg Arg Ser Glu Arg Thr Ala Ala
65 70 75 80
Pro Ser Ser Ser Ser Thr Pro Pro Gly Val Val Thr Ala Arg Ser Leu
 85 90 95
Leu Leu Ser Met Lys Asp Leu Val Gln Val Leu Arg Lys Leu Asn Leu
 100 105 110
```

Ser

(2) INFORMATION FOR SEQ ID NO:1981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Ser | Gln | Ile | Ser | Arg | Ile | Phe | Leu | Ala | Ile | Leu | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Xaa | Ala | Ala | Phe | Ala | Ala | Ala | Pro | Ala | Ala | Leu | Ala | Asp | Gly | Asp | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Val | Val | Ala | Leu | Thr | Glu | Ser | Thr | Phe | Glu | Lys | Glu | Val | Gly | Lys | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Gly | Ala | Leu | Val | Glu | Phe | Tyr | Ala | Pro | Trp | Cys | Gly | His | Cys | Lys |
|     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |
| Lys | Leu | Ala | Pro | Glu | Tyr | Glu | Arg | Leu | Gly | Ala | Ser | Phe | Lys | Lys | Ala |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Lys | Ser | Val | Leu | Ile | Xaa | Lys | Val | Asp | Cys | Xaa | Glu | His | Lys | Xaa | Leu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Cys | Ser | Lys | Tyr | Gly | Val | Ser | Gly | Tyr | Pro | Thr | Ile | Gln | Trp | Phe | Pro |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Lys | Gly | Ser | Leu | Glu | Pro | Lys | Lys | Tyr | Glu | Gly | Gln | Arg | Thr | Ala | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Leu | Ala | Glu | Phe | Leu | Asn | Thr | Glu | Gly | Gly | Thr | Asn | Val | Lys | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..569
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acagcctctc | cgctccgct  | cctcgcgccg | cgcgcgctc  | tcctcctgta | caggtaagga | 60  |
| gaggaagagg | gcgaaatggt | gaagcacaac | aacgtcatcc | ccaacgggca | cttcaagaag | 120 |
| cactggcaga | actatgtcaa | gacatggttc | aaccagcccc | cccgaagca  | gaggcgccgc | 180 |
| atcgctcgtc | aaaagaaggc | tgtgaagata | ttccccgcc  | cgactgctgg | tcctctacgc | 240 |
| cccattgttc | aatgccagac | tttaaagtac | aacatgaagt | caagggctgg | gagaggcttt | 300 |
| acccttgagg | agctgaaggc | tgggctcacc | ggcgagygga | ggcgcgcgcg | ggactacctg | 360 |
| tgcgcgctgc | cgcacaagat | aaagaggatg | gaagagaagg | cccacgatag | arcggtcaaa | 420 |
| gcacaaaaga | aaccacacac | catccccatc | aactggatct | tcgataggac | cattcctgtc | 480 |
| attctacctt | agtgtttatc | tttttcgatc | tttgtttg   | tatctatgct | gttattgtaa | 540 |
| gctaattcca | tgaccttga  | tagcgtcgt  |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..101
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Leu | Ser | Ala | Ser | Ala | Pro | Arg | Ala | Ala | Ala | Ala | Ser | Pro | Pro | Val |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gln | Val | Arg | Arg | Gly | Arg | Gly | Arg | Asn | Gly | Glu | Ala | Gln | Gln | Arg | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Gln | Arg | Ala | Leu | Gln | Glu | Ala | Leu | Ala | Glu | Leu | Cys | Gln | Asp | Met |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Gln | Pro | Ala | Arg | Pro | Gln | Ala | Glu | Ala | Pro | His | Arg | Ser | Ser | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu | Gly | Cys | Glu | Asp | Ile | Pro | Pro | Pro | Asp | Cys | Trp | Ser | Ser | Thr | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| His | Cys | Ser | Met | Pro | Asp | Phe | Lys | Val | Gln | His | Glu | Val | Lys | Gly | Trp |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Arg | Leu | Tyr | Pro |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1984:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 138 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..138
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Lys | His | Asn | Asn | Val | Ile | Pro | Asn | Gly | His | Phe | Lys | Lys | His |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Trp | Gln | Asn | Tyr | Val | Lys | Thr | Trp | Phe | Asn | Gln | Pro | Ala | Arg | Lys | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Arg | Arg | Ile | Ala | Arg | Gln | Lys | Lys | Ala | Val | Lys | Ile | Phe | Pro | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Thr | Ala | Gly | Pro | Leu | Arg | Pro | Ile | Val | Gln | Cys | Gln | Thr | Leu | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Tyr | Asn | Met | Lys | Ser | Arg | Ala | Gly | Arg | Gly | Phe | Thr | Leu | Glu | Glu | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Lys | Ala | Gly | Leu | Thr | Gly | Glu | Gly | Arg | Arg | Ala | Arg | Asp | Tyr | Leu | Cys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ala | Leu | Pro | His | Lys | Ile | Lys | Arg | Met | Glu | Glu | Lys | Ala | His | Asp | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Xaa | Val | Lys | Ala | Gln | Lys | Lys | Pro | Thr | Pro | Ile | Pro | Ile | Asn | Trp | Ile |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Phe | Asp | Arg | Thr | Ile | Pro | Val | Ile | Leu | Pro |     |     |     |     |     |     |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1985:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

```
Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu Lys Ala
1 5 10 15
Gly Leu Thr Gly Glu Gly Arg Arg Ala Arg Asp Tyr Leu Cys Ala Leu
20 25 30
Pro His Lys Ile Lys Arg Met Glu Glu Lys Ala His Asp Arg Xaa Val
35 40 45
Lys Ala Gln Lys Lys Pro Thr Pro Ile Pro Ile Asn Trp Ile Phe Asp
50 55 60
Arg Thr Ile Pro Val Ile Leu Pro
65 70
```

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1501872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

```
atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag ctctgggcag cgtgcgcacg 60
trgggtacct agctcgtctt gctagcctac catggctgat caccaccggg gcgcgacggg 120
argtgscggg ggctacggcg acctccagcg cgggggcggc atgcacggcg aggcgcagca 180
gcagcagaag cagggcgcca tgatgacggc gctcaaggcc gcgacggccg cgacctcctt 240
gaaccactgc cggcgcgggcg gcatatggcc cttaaaggcg gtggctgctg ctacgtacgc 300
tgccgtagag tctcggctgc cgcgatatgt ctagctagtc gtttatgtgt tgtgctttgt 360
gtgtgcatgc ttgtgtctgg gggcatgcag tgcagtgcag tactatatgc tgtatgcgtc 420
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggatgtcatg 480
tttatgatga ggaataaaat gcagtgttca ggtg
```

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1501873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

```
Arg Thr Arg Ser Arg Ser Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln
1 5 10 15
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu
20 25 30
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser
35 40 45
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Ser Arg Ser Arg
50 55 60
Ala Pro
65
```

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..78  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501874  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:  
Met Ala Asp His His Arg Gly Ala Thr Gly Xaa Xaa Gly Gly Tyr Gly  
1                    5                    10                    15  
Asp Leu Gln Arg Gly Gly Gly Met His Gly Glu Ala Gln Gln Gln Gln  
                    20                    25                    30  
Lys Gln Gly Ala Met Met Thr Ala Leu Lys Ala Ala Thr Ala Ala Thr  
                    35                    40                    45  
Ser Leu Asn His Cys Arg Arg Gly Gly Ile Trp Pro Leu Lys Ala Val  
50                    55                    60  
Ala Ala Ala Thr Tyr Ala Ala Val Glu Ser Arg Ser Pro Arg  
65                    70                    75

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 55 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..55

    (D) OTHER INFORMATION: / Ceres Seq. ID 1501875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

Met His Gly Glu Ala Gln Gln Gln Gln Gln Gly Ala Met Met Thr  
1                    5                    10                    15  
Ala Leu Lys Ala Ala Thr Ala Ala Thr Ser Leu Asn His Cys Arg Arg  
                    20                    25                    30  
Gly Gly Ile Trp Pro Leu Lys Ala Val Ala Ala Ala Thr Tyr Ala Ala  
                    35                    40                    45  
Val Glu Ser Arg Ser Pro Arg  
50                    55

(2) INFORMATION FOR SEQ ID NO:1990:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 556 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

    (A) NAME/KEY: -

    (B) LOCATION: 1..556

    (D) OTHER INFORMATION: / Ceres Seq. ID 1501884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aagggtgcgc | cctgcgccgc | accaaacgta | ggagacccat | tcacccatct | cctctctttt  | 60  |
| ctttccaaga | aaagtcttct | cttctctgtc | tcagcgccga | cgcttcccaa | ttccttccaa  | 120 |
| tcgattcttc | gtctcgctct | cgtgtaatcc | ccagcttgcc | ctcctcgctc | ttccctccca  | 180 |
| aaaccctacg | cctccctgac | caagctccgc | ggacgaatgg | acggaggagc | cggttccct   | 240 |
| ggcacgcmgg | tcgcgcgtc  | gccggaggac | gttttcggg  | actaccgcgc | gcgccaggcc  | 300 |
| ggcctaata  | gggcgctcac | caccgatgtt | gagaagtct  | acgtgatgtg | cgacccagag  | 360 |
| aaggataatt | tatgtttata | tggaattccc | aatgagacat | gggaagtaaa | cttgccctgct | 420 |
| gaggagggtc | ctcctgaact | cccagagcca | gctctcgaa  | ttaatattgc | tcgtgatggg  | 480 |
| atgaatgaaa | aagattggct | atcacttggt | gcagtgcata | gtgattcttg | gctaattgtct | 540 |
| gttgcatatt | attttg     |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1991:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 109 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..109  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501885  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:  
Gly Leu Arg Leu Arg Pro Thr Lys Arg Arg Arg Pro Ile His Pro Ser  
1                   5                   10                   15  
Pro Leu Phe Ser Phe Gln Glu Lys Ser Ser Leu Leu Cys Leu Ser Ala  
                  20                   25                   30  
Asp Ala Ser Gln Phe Leu Pro Ile Asp Ser Ser Ser Arg Pro Arg Val  
                  35                   40                   45  
Ile Pro Ser Leu Pro Ser Ser Leu Phe Pro Pro Lys Thr Leu Arg Leu  
                  50                   55                   60  
Pro Asp Gln Ala Pro Gly Thr Asn Gly Arg Arg Ser Arg Leu Pro Trp  
65                   70                   75                   80  
His Xaa Gly Pro Ala Leu Ala Gly Gly Arg Phe Pro Gly Leu Pro Arg  
                  85                   90                   95  
Ala Pro Gly Arg Pro Asn Gln Gly Ala His His Arg Cys  
                  100                   105  
(2) INFORMATION FOR SEQ ID NO:1992:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 113 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..113  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1501886  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:  
Met Asp Gly Gly Ala Gly Phe Pro Gly Thr Xaa Val Pro Arg Ser Pro  
1                   5                   10                   15  
Glu Asp Val Phe Arg Asp Tyr Arg Ala Arg Gln Ala Gly Leu Ile Arg  
                  20                   25                   30  
Ala Leu Thr Thr Asp Val Glu Lys Phe Tyr Val Met Cys Asp Pro Glu  
                  35                   40                   45  
Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn Glu Thr Trp Glu Val  
                  50                   55                   60  
Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu Pro Ala Leu  
65                   70                   75                   80  
Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp Trp Leu Ser  
                  85                   90                   95  
Leu Val Ala Val His Ser Asp Ser Trp Leu Met Ser Val Ala Phe Tyr  
                  100                   105                   110  
Phe

(2) INFORMATION FOR SEQ ID NO:1993:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 70 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1501887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:

```
Met Cys Asp Pro Glu Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn
1 5 10 15
Glu Thr Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu
20 25 30
Pro Glu Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu
35 40 45
Lys Asp Trp Leu Ser Leu Val Ala Val His Ser Asp Ser Trp Leu Met
50 55 60
Ser Val Ala Phe Tyr Phe
65 70
```

(2) INFORMATION FOR SEQ ID NO:1994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1501888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

```
gagccttttcg gtttttctct gtcttcatgt gtgtttgtta tagagaccct gccttgctcg 60
ggcagcacac ttgggacgcg aggaggagga gttggtgagc gaactcggga tcagtgggtg 120
accgcagagt tcttgcttct tcctcttgga ggargagggc tgcagcctgc agggggccgga 180
gagagcagga ggaggcggag acatgggtag cttcgctaag ctggcgagga gggcggtgga 240
gacggacgct ccggtcatgg tgaagataca agaactgctc cgargggcca aggatgtrat 300
gtcgcttgcg cagggagttg tttactggca acctcccag tcagctatgg ataagatcga 360
aaagatcatc agggaaaccaa tagtcagtaa atatggttct ratgatgggc ttcttgagct 420
tcgagaagca cttctcgaaa agctaagcag agagaacaag cttaccaaat catctgtcat 480
ggtcactgct ggtgcaaatac aggccttttgk gaacttggtc ctcactcttt gt
```

(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1501889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

```
Met Gly Ser Phe Ala Lys Leu Ala Arg Arg Ala Val Glu Thr Asp Ala
1 5 10 15
Pro Val Met Val Lys Ile Gln Glu Leu Arg Xaa Ala Lys Asp Xaa
20 25 30
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala
35 40 45
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr
50 55 60
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys
65 70 75 80
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala
85 90 95
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
100 105 110
```

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501890  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:  
Met Val Lys Ile Gln Glu Leu Leu Arg Xaa Ala Lys Asp Xaa Met Ser  
1 5 10 15  
Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala Met Asp  
20 25 30  
Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr Gly Ser  
35 40 45  
Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys Leu Ser  
50 55 60  
Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala Gly Ala  
65 70 75 80  
Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys  
85 90

(2) INFORMATION FOR SEQ ID NO:1997:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1501891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:

Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala  
1 5 10 15  
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr  
20 25 30  
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys  
35 40 45  
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala  
50 55 60  
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..569

(D) OTHER INFORMATION: / Ceres Seq. ID 1501895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aggatcgag aacatccgcc ggcactccat gctccaggag atcaagtctg cctaccagat  | 60  |
| tcttgcccac aagtaccatc ctgatatgaa taagagtccc gaagcagaag aaaagttcaa | 120 |
| ggagatcagt gctgcatatg agccaagctt ggatctgacc gctgtacttt gtgtcgccgc | 180 |
| ttgaatctac ggttctcttc ttccttggtc atcccgtgga tctgtcccgt ggtggtccaa | 240 |
| gcattcgatt tctgctatta taacatccaa cgttggcggt gaagagcaag gggacagata | 300 |



```
agcccaaagg cagcaagggg aacgtcgaca aggaccccaa caagcctgac tcccaacatt 360
ttttgtccgc cgggtgctgta gcggaagccc aaaggcagca aggggaacgt cgacaaggac 420
cccaacaagg ctgactccca acatttttttg tccgccggtg ctgtarcggc ggcgctggtg 480
arctcccca tgctgggctc tgggatgctc ccaggcgccg gggttcggcg agacggggac 540
tgawctggtg ctgggctctg ggatgctcc
```

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

```
Gly Ser Glu Asn Ile Arg Arg Asp Ser Met Leu Gln Glu Ile Lys Ser
1 5 10 15
Ala Tyr Gln Ile Leu Ala His Lys Tyr His Pro Asp Met Asn Lys Ser
20 25 30
Pro Glu Ala Glu Glu Lys Phe Lys Glu Ile Ser Ala Ala Tyr Glu Pro
35 40 45
Ser Leu Asp Leu Thr Ala Val Leu Cys Val Ala Ala
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

```
Met Leu Gln Glu Ile Lys Ser Ala Tyr Gln Ile Leu Ala His Lys Tyr
1 5 10 15
His Pro Asp Met Asn Lys Ser Pro Glu Ala Glu Glu Lys Phe Lys Glu
20 25 30
Ile Ser Ala Ala Tyr Glu Pro Ser Leu Asp Leu Thr Ala Val Leu Cys
35 40 45
Val Ala Ala
50
```

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

```
Met Asn Lys Ser Pro Glu Ala Glu Glu Lys Phe Lys Glu Ile Ser Ala
1 5 10 15
Ala Tyr Glu Pro Ser Leu Asp Leu Thr Ala Val Leu Cys Val Ala Ala
20 25 30
```

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ccatccagtc | ctggagcctg  | cgcggctgcs | cttgcacgc  | atctccgtcg | tcgtcctcgc | 60  |
| ccacggaatc | cgtccaattc  | cccacgccgc | ccgtcgtcct | tttctataaa | attcactccg | 120 |
| ccaccaaadc | tcgaatcccc  | atcgcgctgc | ttttccaccg | accccgacgc | cgacgccgac | 180 |
| gccaccgccg | ctccctcccc  | agtcccact  | ccccttcccg | ggccgcggac | agagatccgg | 240 |
| ggcgccgcgc | gatggcgaaac | atcgacatgg | cgaagatcct | ggcggacctg | gaccgcggcg | 300 |
| ccagcgccgg | ncgacgcgcg  | ggtgcccaag | accaagctcg | tatgcacgct | cggcccggcc | 360 |
| tcccgaccgc | tgcccatgct  | cgagaagctg | ctccgcgcmg | gcacgaacgt | cgcgcgcttc | 420 |
| aacttctccc | ac          |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Ser | Pro | Gly | Ala | Cys | Ala | Ala | Xaa | Leu | Ala | Ser | His | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Pro | Arg | Pro | Arg | Asn | Pro | Ser | Asn | Ser | Pro | Arg | Arg | Pro | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Ser | Ile | Lys | Phe | Thr | Pro | Pro | Pro | Asn | Leu | Glu | Ser | Pro | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Cys | Phe | Ser | Thr | Asp | Pro | Asp | Ala | Asp | Ala | Asp | Ala | Thr | Ala | Ala |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Pro | Ser | Pro | Val | Pro | Thr | Pro | Leu | Pro | Gly | Pro | Arg | Thr | Glu | Ile | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ala | Ala | Arg | Trp | Arg | Thr | Ser | Thr | Trp | Arg | Arg | Ser | Trp | Arg | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Trp | Thr | Ala | Ala | Pro | Ala | Ala | Xaa | Asp | Ala | Arg | Val | Pro | Lys | Thr | Lys |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Val | Cys | Thr | Leu | Gly | Pro | Ala | Ser | Arg | Thr | Val | Pro | Met | Leu | Glu |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Lys | Leu | Leu | Arg | Xaa | Gly | Met | Asn | Val | Ala | Arg | Phe | Asn | Phe | Ser | His |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

```
Ile Gln Ser Trp Ser Leu Arg Gly Cys Xaa Cys Ile Ala Ser Pro Ser
1 5 10 15
Ser Ser Ser Pro Thr Glu Ser Val Gln Phe Pro Thr Pro Pro Val Val
20 25 30
Leu Phe Tyr Lys Ile His Ser Ala Thr Lys Ser Arg Ile Pro Ile Ala
35 40 45
Leu Leu Phe His Arg Pro Arg Arg Arg Arg Arg His Arg Arg Ser
50 55 60
Leu Pro Ser Pro His Ser Pro Ser Arg Ala Ala Asp Arg Asp Pro Gly
65 70 75 80
Arg Arg Ala Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala Asp Leu
85 90 95
Asp Arg Gly Ala Ser Gly Xaa Arg Arg Ala Gly Ala Gln Asp Gln Ala
100 105 110
Arg Met His Ala Arg Pro Gly Leu Pro His Arg Ala His Ala Arg Glu
115 120 125
Ala Ala Pro Arg Xaa His Glu Arg Arg Ala Leu Gln Leu Leu Pro
130 135 140
```

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1501902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

```
aagctcctgc ttttccactg ctctgcgtct gcgctctgcgt ctgcgtctgc actgcttcgc 60
gtctccctcc ccccgccctcc gccccgggaa aaaaaaaagc aaaacacggc catggaaggc 120
tacgaccgcg agttctacca gttcagcgac cagctgcgcc tgcagacggc cgccttctcg 180
ggcctctccc tcggcgactc catctggtcc cccgcgggcc ggcgcaacaa cagcaacgac 240
gtcctcttcg ccgctcggc gtcgcccggc gacgcggccg ccaagaccaa cgccgtcgtc 300
ggcctcaagc tcaacgacgg agggcccggc ctcctcggtt ccgggaagct ggccttcggc 360
ggcggcgcca ccaaggccga ccgctacaac aacaacaacc tctccaacac cgacaacaag 420
accgtgtac
```

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

```
Lys Leu Leu Leu Phe His Cys Ser Ala Ser Ala Ser Ala Ser
1 5 10 15
Ala Leu Leu Arg Val Ser Leu Pro Pro Pro Pro Pro Arg Glu Lys Lys
20 25 30
Lys Gln Asn Thr Ala Met Glu Gly Tyr Asp Arg Glu Phe Tyr Gln Phe
35 40 45
```

Ser Asp Gln Leu Arg Leu Gln Thr Ala Ala Phe Ser Gly Leu Ser Leu  
50 55 60  
Gly Asp Ser Ile Trp Ser Pro Ala Gly Arg Arg Asn Asn Ser Asn Asp  
65 70 75 80  
Val Leu Phe Ala Ala Ser Ala Ser Pro Ala Asp Ala Ala Lys Thr  
85 90 95  
Asn Ala Val Val Gly Leu Lys Leu Asn Asp Gly Gly Pro Gly Leu Ile  
100 105 110  
Gly Ser Gly Lys Leu Ala Phe Gly Gly Gly Gly Thr Lys Ala Asp Arg  
115 120 125  
Tyr Asn Asn Asn Asn Leu Ser Asn Thr Asp Asn Lys Thr Val Tyr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Ser Ser Cys Phe Ser Thr Ala Leu Arg Leu Arg Leu Arg Leu Arg Leu  
1 5 10 15  
His Cys Phe Ala Ser Pro Ser Pro Arg Leu Arg Pro Gly Lys Lys Lys  
20 25 30  
Ser Lys Thr Arg Pro Trp Lys Ala Thr Thr Ala Ser Ser Thr Ser Ser  
35 40 45  
Ala Thr Ser Cys Ala Cys Arg Arg Pro Pro Ser Arg Ala Ser Pro Ser  
50 55 60  
Ala Thr Pro Ser Gly Pro Pro Pro Ala Gly Ala Thr Thr Ala Thr Thr  
65 70 75 80  
Ser Ser Ser Pro Pro Arg Arg Arg Pro Pro Thr Pro Pro Pro Arg Pro  
85 90 95  
Thr Pro Ser Ser Ala Ser Ser Ser Thr Thr Glu Gly Pro Ala Ser Ser  
100 105 110  
Ala Pro Gly Ser Trp Pro Ser Ala Ala Ala Pro Arg Pro Thr Ala  
115 120 125  
Thr Thr Thr Thr Thr Ser Pro Thr Pro Thr Thr Arg Pro Cys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Ala Pro Ala Phe Pro Leu Leu Cys Val Cys Val Cys Val Cys Val Cys  
1 5 10 15  
Thr Ala Ser Arg Leu Pro Pro Pro Ala Ser Ala Pro Gly Lys Lys Lys  
20 25 30  
Ala Lys His Gly His Gly Arg Leu Arg Pro Arg Val Leu Pro Val Gln  
35 40 45  
Arg Pro Ala Ala Pro Ala Asp Gly Arg Leu Leu Gly Pro Leu Pro Arg

50 55 60  
Arg Leu His Leu Val Pro Arg Arg Pro Ala Gln Gln Gln Arg Arg  
65 70 75 80  
Pro Leu Arg Arg Leu Gly Val Ala Arg Arg Arg Arg Gln Asp Gln  
85 90 95  
Arg Arg Arg Arg Pro Gln Ala Gln Arg Arg Arg Ala Arg Pro His Arg  
100 105 110  
Leu Arg Glu Ala Gly Leu Arg Arg Arg Arg His Gln Gly Arg Pro Leu  
115 120 125  
Gln Gln Gln Gln Pro Leu Gln His Arg Gln Gln Asp Arg Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaatatctct | gcacactatg | acctgagtaa | tgatttcttt | gctctttttc | tggatccgac | 60  |
| gatgacttac | tottgtggta | ttttcaakgm | rraagatgag | agtttagaag | cagcgcasta | 120 |
| cgtaaacttg | acaatcta   | taataaggct | aaggtggatc | cggggcatca | tgctcctgac | 180 |
| attggctgtg | gttggggctc | attggcaata | cgtttggtga | agagaactgg | ctgcaagtgc | 240 |
| acaggaatta | cattatcgga | ggagcaactg | aaatatggaa | agagaaaggt | gaaagaattt | 300 |
| ggattagagg | accgcataac | tctcctgctt | tgtgattacc | gtcaaatacc | gaacggccag | 360 |
| aagtttgata | ggattathag | ttgtgggatg | cttgaacacg | ttggccatga | gttctacgaa | 420 |
| gatttctttg | cctcctgcga | gtatcatttg | gccgaacacg | gcctacttgt | cctccagtcc | 480 |
| atcgcggtcc | cagaggaact | gtacgacaaa | atgag      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asn Ile Ser Ala His Tyr Asp Leu Ser Asn Asp Phe Phe Ala Leu Phe |  |
| 1 5 10 15                                                       |  |
| Leu Asp Pro Thr Met Thr Tyr Ser Cys Gly Ile Phe Xaa Xaa Xaa Asp |  |
| 20 25 30                                                        |  |
| Glu Ser Leu Glu Ala Ala Xaa Tyr Val Asn Leu Thr Ile             |  |
| 35 40 45                                                        |  |

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:  
Met Leu Glu His Val Gly His Glu Phe Tyr Glu Asp Phe Phe Ala Ser  
1 5 10 15  
Cys Glu Tyr His Leu Ala Glu His Gly Leu Leu Val Leu Gln Ser Ile  
20 25 30  
Ala Val Pro Glu Glu Leu Tyr Asp Lys Met  
35 40

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

Met Ser Ser Thr Lys Ile Ser Leu Pro Pro Ala Ser Ile Ile Trp Pro  
1 5 10 15  
Asn Thr Ala Tyr Leu Ser Ser Ser Pro Ser Arg Ser Gln Arg Asn Cys  
20 25 30  
Thr Thr Lys  
35

(2) INFORMATION FOR SEQ ID NO:2013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..549
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acaacaagca gaagcagaag cagaagctag cagctagtag acgagcgacg agtagctagc  | 60  |
| tagctagcta tctagagagc tcatcatatc gctgctcgct ctcattccacc attatagaga | 120 |
| agagcagatc gagctgcagc tggcagaggc cgagttgttg ctagctagct cctgcttgct  | 180 |
| aaatttgcat cgtatccgat ccattccatg aagaagtcgt cgatgatggc gcccatgacg  | 240 |
| atcatggcga gagggtgccg tgtgctcgtc ctctcgtcgg ctgccatggc ttccgccgca  | 300 |
| ggagcagctg ggctggacat gaatttctac ggcagcacgt gccgcgcgt ggaggccatc   | 360 |
| gtcaaggagg agatggtggc gatcctcaag gcggcgccga cgctggccgg cccgctgctc  | 420 |
| cgctccatt tccacgactg cttcgtcagg ggctgcgacg cctccgtgct cctggactcg   | 480 |
| actcccacca gcacggcgga gaaggacgcc accccgaacc tcaccctccg gggcttcggc  | 540 |
| tccgtgcag                                                          |     |

(2) INFORMATION FOR SEQ ID NO:2014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014:

Met Lys Lys Ser Ser Met Met Ala Pro Met Thr Ile Met Ala Arg Val  
1 5 10 15

Ala Ala Val Leu Val Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly  
20 25 30  
Ala Ala Gly Leu Asp Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val  
35 40 45  
Glu Ala Ile Val Lys Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro  
50 55 60  
Thr Leu Ala Gly Pro Leu Leu Arg Leu His Phe His Asp Cys Phe Val  
65 70 75 80  
Arg Gly Cys Asp Ala Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr  
85 90 95  
Ala Glu Lys Asp Ala Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser  
100 105 110  
Val Gln

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

Met Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val  
1 5 10 15  
Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp  
20 25 30  
Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys  
35 40 45  
Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro  
50 55 60  
Leu Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala  
65 70 75 80  
Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr Ala Glu Lys Asp Ala  
85 90 95  
Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser Val Gln  
100 105

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val Leu  
1 5 10 15  
Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp Met  
20 25 30  
Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys Glu  
35 40 45  
Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro Leu  
50 55 60  
Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala Ser

(2) INFORMATION FOR SEQ ID NO:2017:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..555

(D) OTHER INFORMATION: / Ceres Seq. ID 1501926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NUMBER |             |            |            |            |            |     |
|------------------------------------------|-------------|------------|------------|------------|------------|-----|
| ctggctgcgc                               | gtcattctct  | tcctcttccg | gtgctcgtgc | tgtgtctcgt | gctctccgcc | 60  |
| ctccccctcc                               | gccacctcgc  | gcggaacgga | accagggccg | ccgccgacct | agccaccgct | 120 |
| aggcgaccgc                               | gcggcatggt  | ggcgctttta | cactacctat | gctagtttgc | ctgatgctac | 180 |
| atttccacga                               | tggttaagct  | gactatgata | gcgcgtgtca | ctgatggcct | tccattgtcg | 240 |
| gagggattag                               | atgatatgct  | ggatctgaaa | gatgctgact | tctacaagca | gcaagcaaaa | 300 |
| ctgttggtca                               | agaacttgct  | cagagggcag | catgaggcgt | caaggatgtc | aattgagaca | 360 |
| ggaccatacc                               | ttttccacta  | catcatagaa | ggcctgtgtt | gctatttgac | tttgtgtgac | 420 |
| cgttcttatt                               | ccaagaaact  | tgcattccag | tatctcgaag | atctcaaaaa | tgaatttgag | 480 |
| aaagtcattg                               | gcagccaaaat | tgaaacagct | gcaaggccat | atgsatttat | taaatttgat | 540 |
| gcattcatac                               | agaag       |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1501927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

|     |      |                                   |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|------|-----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     | (X1) | SEQUENCE DESCRIPTION: See Table 1 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| Met | Val  | Lys                               | Leu | Thr | Met | Ile | Ala | Arg | Val | Thr | Asp | Gly | Leu | Pro | Leu |  |  |
| 1   |      |                                   |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Glu  | Gly                               | Leu | Asp | Asp | Ser | Arg | Asp | Leu | Lys | Asp | Ala | Asp | Phe | Tyr |  |  |
|     |      |                                   | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Lys | Gln  | Gln                               | Ala | Lys | Leu | Leu | Phe | Lys | Asn | Leu | Ser | Arg | Gly | Gln | His |  |  |
|     |      | 35                                |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Glu | Ala  | Ser                               | Arg | Met | Ser | Ile | Glu | Thr | Gly | Pro | Tyr | Leu | Phe | His | Tyr |  |  |
|     | 50   |                                   |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |  |
| Ile | Ile  | Glu                               | Gly | Arg | Val | Cys | Tyr | Leu | Thr | Leu | Cys | Asp | Arg | Ser | Tyr |  |  |
| 65  |      |                                   |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Pro | Lys  | Lys                               | Leu | Ala | Phe | Gln | Tyr | Leu | Glu | Asp | Leu | Lys | Asn | Glu | Phe |  |  |
|     |      |                                   | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Glu | Lys  | Val                               | Asn | Gly | Ser | Gln | Ile | Glu | Thr | Ala | Ala | Arg | Pro | Tyr | Xaa |  |  |
|     |      |                                   | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Phe | Ile  | Lys                               | Phe | Asp | Ala | Phe | Ile | Gln | Lys |     |     |     |     |     |     |  |  |
|     |      | 115                               |     |     |     |     | 120 |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1501928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

```
Met Ile Ala Arg Val Thr Asp Gly Leu Pro Leu Ser Glu Gly Leu Asp
1 5 10 15
Asp Ser Arg Asp Leu Lys Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys
20 25 30
Leu Leu Phe Lys Asn Leu Ser Arg Gly Gln His Glu Ala Ser Arg Met
35 40 45
Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly Arg
50 55 60
Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu Ala
65 70 75 80
Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn Gly
85 90 95
Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe Asp
100 105 110
Ala Phe Ile Gln Lys
115
```

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1501929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

```
Met Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly
1 5 10 15
Arg Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu
20 25 30
Ala Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn
35 40 45
Gly Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe
50 55 60
Asp Ala Phe Ile Gln Lys
65 70
```

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1501930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

```
aagtctcttt gtgtttttta taggcttgag agcttggaat agcggggggt ggaggaagcg 60
gaagaggagc ttcgttttgt gttctagagg ggagtcattg tccatggcgg caggcctctg 120
tccctccggg ggtctctcaa ggcgcttgaa gctgatatcc accatgccaa caccctggcg 180
catgctatac acagggcgta trggggtgcc tgcgcagatg naggctgtcc tacagctcca 240
tggtctcaat ctttctcaac cttatccaat ggatggactg cagctgctcc ctgtcataca 300
```

```
cgctccctag ctaccttggc ctgctcgagg ttctcgtcta caaggtttat gtcgatgaag 360
atgcctccat atccaccata gaaaggaggg cgagcctgaa ggaattctac actatcatat 420
accctttctt gcaacaactg gaggacaact tgatggacaa ggactgcaag gacaaagggt 480
ggtctgctgc tgc
```

(2) INFORMATION FOR SEQ ID NO:2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

```
Ser Leu Phe Val Phe Phe Ile Gly Leu Arg Ala Trp Asn Ser Gly Gly
1 5 10 15
Trp Arg Lys Arg Lys Arg Ser Phe Val Leu Cys Ser Arg Gly Glu Ser
20 25 30
Cys Ser Met Ala Ala Gly Leu Cys Pro Ser Gly Gly Leu Ser Arg Arg
35 40 45
Leu Lys Leu Ile Ser Thr Met Pro Thr Pro Trp Arg Met Leu Tyr Thr
50 55 60
Gly Arg Xaa Gly Val Pro Ala Gln Met Xaa Ala Val Leu Gln Leu His
65 70 75 80
Gly Ser Asn Leu Ser Gln Pro Tyr Pro Met Asp Gly Leu Gln Leu Leu
85 90 95
Pro Val Ile His Ala Pro
100
```

(2) INFORMATION FOR SEQ ID NO:2023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

```
Met Phe His Gly Gly Arg Pro Leu Ser Leu Arg Gly Ser Leu Lys Ala
1 5 10 15
Leu Glu Ala Asp Ile His His Ala Asn Thr Leu Ala His Ala Ile His
20 25 30
Arg Ala Tyr Xaa Gly Ala Cys Ala Asp Xaa Gly Cys Pro Thr Ala Pro
35 40 45
Trp Leu Gln Ser Phe Ser Thr Leu Ser Asn Gly Trp Thr Ala Ala Ala
50 55 60
Pro Cys His Thr Arg Ser Leu Ala Thr Leu Ala Cys Ser Arg Phe Ser
65 70 75 80
Ser Thr Arg Phe Met Ser Met Lys Met Pro Pro Tyr Pro Pro
85 90
```

(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1501933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

```
Met Ala Pro Ile Phe Leu Asn Leu Ile Gln Trp Met Asp Cys Ser Cys
1 5 10 15
Ser Leu Ser Tyr Thr Leu Pro Ser Tyr Leu Gly Leu Leu Glu Val Leu
20 25 30
Val Tyr Lys Val Tyr Val Asp Glu Asp Ala Ser Ile Ser Thr Ile Glu
35 40 45
Arg Arg Ala Ser Leu Lys Glu Phe Tyr Thr Ile Ile Tyr Pro Phe Leu
50 55 60
Gln Gln Leu Glu Asp Asn Leu Met Asp Lys Asp Cys Lys Asp Lys Gly
65 70 75 80
Trp Ser Ala Ala
```

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..586

(D) OTHER INFORMATION: / Ceres Seq. ID 1501949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

```
ccgccgtcaa acgtcatccg aatccgcgcc gcgaccagcg aagaaggtag gaagcatccg 60
gaacggagac gcgcctcctg cctcgctttc ctcccatggc gccgccctc gccgccgtct 120
catcgtcgtc gccctattc tctccttcat cgtcccgccc catccgccgc tgccacgcac 180
ctcctccttc tatctccttc cagacgcggg gacgctcgcc cacggcggcg gcggcagctg 240
agtccctctgt cagtacgctt ctcgagggtgc gcggactcac cgcattccgtg aaggagactg 300
ggcagcagat cctcgccggc gtcgacctca ccatccgcca gggcgagatt catgcgatta 360
tgggaaaaaa cggctccggc aagagcaccc tcacgaaagt tctcgtaggc catcctcatt 420
atgaggtaac tgggtggtacc attctcttca agggtgagga cctggttgac atggagccag 480
aggacagatc tctagcaggc cttttcatga gtttccaagc acctattgag attccctgga 540
gtcagcaatt ttgattttct gctcatggct gtgaatgctc gcagag
```

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1501950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

```
Pro Pro Ser Asn Val Ile Arg Ile Arg Ala Ala Thr Ser Glu Glu Gly
1 5 10 15
Arg Lys His Pro Glu Arg Arg Arg Ala Ser Cys Leu Ala Phe Leu Pro
20 25 30
Trp Arg Arg Pro Ser Pro Pro Ser His Arg Arg Arg Pro Tyr Ser Leu
35 40 45
Leu His Arg Pro Ala Pro Ser Ala Ala Ala Thr His Leu Leu Leu Leu
50 55 60
Ser Pro Ser Arg Arg Gly Asp Ala Arg Pro Arg Arg Arg Arg Gln Leu
65 70 75 80
```

Ser Pro Leu Ser Val Arg Phe Ser Arg Cys Ala Asp Ser Pro His Pro  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Arg Arg Gln Thr Ser Ser Glu Ser Ala Pro Arg Pro Ala Lys Lys Val  
1 5 10 15  
Gly Ser Ile Arg Asn Gly Asp Ala Pro Pro Ala Ser Leu Ser Ser His  
20 25 30  
Gly Ala Ala Pro Arg Arg Arg Leu Ile Val Val Ala Pro Ile Leu Ser  
35 40 45  
Phe Ile Val Pro Pro His Pro Pro Leu Pro Arg Thr Ser Ser Phe Tyr  
50 55 60  
Leu Leu Pro Asp Ala Gly Thr Leu Ala His Gly Gly Gly Gly Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

Met Ala Pro Pro Leu Ala Ala Val Ser Ser Ser Ser Pro Leu Phe Ser  
1 5 10 15  
Pro Ser Ser Ser Arg Pro Ile Arg Arg Cys His Ala Pro Pro Pro Ser  
20 25 30  
Ile Ser Phe Gln Thr Arg Gly Arg Ser Pro Thr Ala Ala Ala Ala  
35 40 45  
Glu Ser Ser Val Ser Thr Leu Leu Glu Val Arg Gly Leu Thr Ala Ser  
50 55 60  
Val Lys Glu Thr Gly Gln Gln Ile Leu Ala Gly Val Asp Leu Thr Ile  
65 70 75 80  
Arg Glu Gly Glu Ile His Ala Ile Met Gly Lys Asn Gly Ser Gly Lys  
85 90 95  
Ser Thr Leu Thr Lys Val Leu Val Gly His Pro His Tyr Glu Val Thr  
100 105 110  
Gly Gly Thr Ile Leu Phe Lys Gly Glu Asp Leu Val Asp Met Glu Pro  
115 120 125  
Glu Asp Arg Ser Leu Ala Gly Leu Phe Met Ser Phe Gln Ala Pro Ile  
130 135 140  
Glu Ile Pro Trp Ser Gln Gln Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..657  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501976  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:  
agtgccggca cgcgcgctgt tgcagaagtt gcctcttttt tacgtcttgt ttctcctcca 60  
ccccggcgac gccaatggag aagggcagtg gaggcagcaa tcctccgccg ccaccgctcc 120  
acatggagga cttccaactg gaggggaaga agcccgtcaa gaaccctttt gtgcccacg 180  
gcgcactggg tactgctgga gttctgactg ctggtctgat cagtttccga tatgggaact 240  
ctcagctggg tcagaaactg atgagggcac gtgtagttgc tcaaggcgct acagtcgctc 300  
tgatgattgg cagtgcctac tactatggcg atcaaatcaa gctgttcaag aaagggtcga 360  
gcccatgata ttcccatgaa tattgctgtt tttggtgat ggaggaatgc cttgtatacg 420  
cataaatttc acctggactc tgctgcccct ttttaacatc attttggcct gacacgtggg 480  
agctaacaag aaatcgctgt tgggtccgatc ggcaggattg aaaataaata attttgtttg 540  
ttgatttttg tcaggatttg ttgggttgat taattaggct atatgcatca attgttatat 600  
ctttgtacaa acacgcgttc tgttgtctgc aatcagcggc tgaagtgacc attttgc  
(2) INFORMATION FOR SEQ ID NO:2030:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501977  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:  
Val Pro Ala Pro Pro Leu Leu Gln Lys Leu Pro Leu Phe Tyr Val Leu  
1 5 10 15  
Phe Leu Leu His Pro Gly Asp Ala Asn Gly Glu Gly Gln Trp Arg Gln  
20 25 30  
Gln Ser Ser Ala Ala Thr Ala Pro His Gly Gly Leu Pro Thr Gly Gly  
35 40 45  
Glu Glu Ala Arg Gln Glu Pro Leu Cys Ala His Arg Arg Thr Gly Tyr  
50 55 60  
Cys Trp Ser Ser Asp Cys Trp Ser Asp Gln Phe Pro Ile Trp Glu Leu  
65 70 75 80  
Ser Ala Gly Ser Glu Thr Asp Glu Gly Thr Cys Ser Cys Ser Arg Arg  
85 90 95  
Tyr Ser Arg Ser Asp Asp Trp Gln Cys Leu Leu Leu Trp Arg Ser Asn  
100 105 110  
Gln Ala Val Gln Glu Arg Val Glu Pro Met Ile Phe Pro  
115 120 125  
(2) INFORMATION FOR SEQ ID NO:2031:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..121  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501978  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:  
Cys Arg His Arg Arg Cys Cys Arg Ser Cys Leu Phe Phe Thr Ser Cys

1 5 10 15  
Phe Ser Ser Thr Pro Ala Thr Arg Met Glu Lys Gly Ser Gly Gly Ser  
20 25 30  
Asn Pro Pro Pro Pro Leu His Met Glu Asp Phe Gln Leu Glu Gly  
35 40 45  
Lys Lys Pro Val Lys Asn Pro Phe Val Pro Ile Gly Ala Leu Val Thr  
50 55 60  
Ala Gly Val Leu Thr Ala Gly Leu Ile Ser Phe Arg Tyr Gly Asn Ser  
65 70 75 80  
Gln Leu Gly Gln Lys Leu Met Arg Ala Arg Val Val Ala Gln Gly Ala  
85 90 95  
Thr Val Ala Leu Met Ile Gly Ser Ala Tyr Tyr Tyr Gly Asp Gln Ile  
100 105 110  
Lys Leu Phe Lys Lys Gly Ser Ser Pro  
115 120

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

Met Glu Lys Gly Ser Gly Gly Ser Asn Pro Pro Pro Pro Leu His  
1 5 10 15  
Met Glu Asp Phe Gln Leu Glu Gly Lys Lys Pro Val Lys Asn Pro Phe  
20 25 30  
Val Pro Ile Gly Ala Leu Val Thr Ala Gly Val Leu Thr Ala Gly Leu  
35 40 45  
Ile Ser Phe Arg Tyr Gly Asn Ser Gln Leu Gly Gln Lys Leu Met Arg  
50 55 60  
Ala Arg Val Val Ala Gln Gly Ala Thr Val Ala Leu Met Ile Gly Ser  
65 70 75 80  
Ala Tyr Tyr Tyr Gly Asp Gln Ile Lys Leu Phe Lys Lys Gly Ser Ser  
85 90 95  
Pro

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

atgcgcctcg cggccgcttc gacagtcctc cgcgttccat ttgcttcggc tcatctcaga 60  
tcaagctagc gcacctgaca cccaccacct ccctcccaga tccaccaccc cagccatggc 120  
caccgccttt gactccccga cctcctcccc cgccgcgcgc cccttcacg acgacccttt 180  
cctccatttc gacggctcgg cccccgcgcg cgccgacggc ttcccggcct ccccgacgc 240  
ctacgcgccc tcccccttcg gcatgcccc ctccaacggc gacctccacg acgacccttt 300  
cgccgcacct gctgactcca acggtgggccc catccttccg ccgcccaccg agatggggccg 360  
cgaggaggga ttctgtctcc gcgagtgggtg ccgacaaaat gctattcacc ttgaggaaaa 420  
agagaagaag gagaaggagc tgaggagcca aatcatcggt gatgctgaag agtttaag

(2) INFORMATION FOR SEQ ID NO:2034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:

```
Cys Ala Ser Arg Pro Leu Arg Gln Ser Leu Ala Phe His Leu Leu Arg
1 5 10 15
Leu Ile Ser Asp Gln Ala Ser Ala Pro Asp Thr His His Leu Pro Pro
20 25 30
Arg Ser Thr Thr Pro Ala Met Ala Thr Ala Phe Asp Ser Pro Thr Ser
35 40 45
Ser Pro Ala Ala Ala Pro Phe His Asp Asp Pro Phe Leu His Phe Asp
50 55 60
Gly Ser Ala Pro Ala Ala Asp Gly Phe Pro Ala Ser Pro Asp Ala
65 70 75 80
Tyr Ala Pro Ser Pro Phe Gly Met Pro His Ser Asn Gly Asp Leu His
85 90 95
Asp Asp Pro Phe Ala Ala Pro Ala Asp Ser Asn Gly Gly Pro Ile Leu
100 105 110
Pro Pro Pro Thr Glu Met Gly Arg Glu Glu Gly Phe Leu Leu Arg Glu
115 120 125
Trp Cys Arg Gln Asn Ala Ile His Leu Glu Glu Lys Glu Lys Lys Glu
130 135 140
Lys Glu Leu Arg Ser Gln Ile Ile Val Asp Ala Glu Glu Phe Lys
145 150 155
```

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1502005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

```
Ala Pro Arg Gly Arg Phe Asp Ser Pro Ser Arg Ser Ile Cys Phe Gly
1 5 10 15
Ser Ser Gln Ile Lys Leu Ala His Leu Thr Pro Thr Thr Ser Leu Pro
20 25 30
Asp Pro Pro Pro Gln Pro Trp Pro Pro Pro Leu Thr Pro Arg Pro Pro
35 40 45
Pro Pro Pro Pro Arg Pro Ser Thr Thr Thr Leu Ser Ser Ile Ser Thr
50 55 60
Ala Arg Pro Pro Pro Pro Thr Ala Ser Arg Pro Pro Arg Thr Pro
65 70 75 80
Thr Arg Pro Pro Pro Ser Ala Cys Pro Thr Pro Thr Ala Thr Ser Thr
85 90 95
Thr Thr Leu Ser Pro His Leu Leu Thr Pro Thr Val Gly Pro Ser Phe
100 105 110
Arg Arg Pro Pro Arg Trp Ala Ala Arg Arg Asp Ser Cys Ser Ala Ser
115 120 125
Gly Ala Asp Lys Met Leu Phe Thr Leu Arg Lys Lys Arg Arg Arg Arg
```

130 135 140  
Arg Ser  
145  
(2) INFORMATION FOR SEQ ID NO:2036:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 121 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..121  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502006  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:  
Met Ala Thr Ala Phe Asp Ser Pro Thr Ser Ser Pro Ala Ala Ala Pro  
1 5 10 15  
Phe His Asp Asp Pro Phe Leu His Phe Asp Gly Ser Ala Pro Ala Ala  
20 25 30  
Ala Asp Gly Phe Pro Ala Ser Pro Asp Ala Tyr Ala Pro Ser Pro Phe  
35 40 45  
Gly Met Pro His Ser Asn Gly Asp Leu His Asp Asp Pro Phe Ala Ala  
50 55 60  
Pro Ala Asp Ser Asn Gly Gly Pro Ile Leu Pro Pro Pro Thr Glu Met  
65 70 75 80  
Gly Arg Glu Glu Gly Phe Leu Leu Arg Glu Trp Cys Arg Gln Asn Ala  
85 90 95  
Ile His Leu Glu Glu Lys Glu Lys Lys Glu Lys Glu Leu Arg Ser Gln  
100 105 110  
Ile Ile Val Asp Ala Glu Glu Phe Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:2037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..713
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:

accaaaggta ccttgcaatc acaacgaaca gaagctctcg atctcaccga caccgaggaa 60  
gaagagatca atggcgtccg agcagggagt cgtgatcgcg tgccacagca aggctgagtt 120  
cgacgcccac atgaccaagg cccaggaagc cggcaagctg gtggtcatcg acttcactgc 180  
cgcttgagca gtactgcagg gacaccgtca tgaccatctg gcattaccac ggcgggtgcc 240  
aggtcggcgc cgtcgtggac gacgattacc ggggtgttcgg cgtgcagcga ctgatggtga 300  
tcgacagctc cacgttcaag tactcccccg gcaccaaccc gcaggccacc gtcatgatgc 360  
tcggaaggta tatgggtgtg aaaattcagg ccgagagatg gaggaaatga tcgagatttc 420  
aagtatcagc atgggtctagg gactaagcct ctactgtgtga taatgaacat caatcaacac 480  
atctgtaact gggtaactgc tctagcctct agagtagggt ttatttttct ctagatattt 540  
tttaatctcc tctagacata ctctagctt ccgcatgttg ttggttccat tccaccacac 600  
ccctagatgc attgttcagc atttcgcggg aataatgaga attatgctga aaaggcatga 660  
tcgctcctcc tgcctattct acagaaaatt aaataaagaa ccgccatttc atc

(2) INFORMATION FOR SEQ ID NO:2038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..61  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502012  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:  
Pro Lys Val Pro Cys Asn His Asn Glu Gln Lys Leu Ser Ile Ser Pro  
1                    5                    10                    15  
Thr Pro Arg Lys Lys Arg Ser Met Ala Ser Glu Gln Gly Val Val Ile  
                    20                    25                    30  
Ala Cys His Ser Lys Ala Glu Phe Asp Ala His Met Thr Lys Ala Gln  
                    35                    40                    45  
Glu Ala Gly Lys Leu Val Val Ile Asp Phe Thr Ala Ala  
50                    55                    60  
(2) INFORMATION FOR SEQ ID NO:2039:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 66 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..66  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502013  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:  
Met Thr Ile Trp His Tyr His Gly Gly Cys Gln Val Gly Ala Val Val  
1                    5                    10                    15  
Asp Asp Asp Tyr Arg Val Phe Gly Val Gln Arg Leu Met Val Ile Asp  
                    20                    25                    30  
Ser Ser Thr Phe Lys Tyr Ser Pro Gly Thr Asn Pro Gln Ala Thr Val  
                    35                    40                    45  
Met Met Leu Gly Arg Tyr Met Gly Val Lys Ile Gln Ala Glu Arg Trp  
50                    55                    60  
Arg Lys  
65  
(2) INFORMATION FOR SEQ ID NO:2040:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 46 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..46  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502014  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:  
Met Leu Leu Val Pro Phe His His Thr Pro Arg Cys Ile Val Gln His  
1                    5                    10                    15  
Phe Ala Gly Ile Met Arg Ile Met Leu Lys Arg His Asp Arg Ser Ser  
                    20                    25                    30  
Cys Leu Phe Tyr Arg Lys Leu Asn Lys Glu Pro Pro Phe His  
                    35                    40                    45  
(2) INFORMATION FOR SEQ ID NO:2041:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 567 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..567

(D) OTHER INFORMATION: / Ceres Seq. ID 1502015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| ctcgcaaacc | cacgtttcaa  | aaaaaagaga | ggaaagcaaa | gttccttctt | ccctcgaaaa | 60  |
| aaaaaatcag | tctcgccatg  | gagagcagcg | ttggcataga | gaaggccgca | gcggtggcgg | 120 |
| ttggtgcagg | tgtgggcggg  | ggaggtggag | ggtacggcts | cggcggggtg | gagacgccga | 180 |
| agcgcgagga | gtscgcgcatc | ccggcgacgc | tgccgtgccc | cgcggcgccg | aggaaggccg | 240 |
| tgccggactt | cgggaagcgg  | cgcagcccyg | cccaagaacg | gctacttcca | gccgcgggac | 300 |
| ctggaggcgc | tcttcgcgct  | cgcgcgcgcg | cgccaggcct | tctgcgcgtg | acttggcrcg | 360 |
| gacttgattt | tttggggagg  | gagttgtaga | tagcttgccg | gtctcgctct | gttgactctt | 420 |
| ttctagtggg | ggtgtttagt  | ggccscgggt | gtattagggg | ggcagtaggg | tggttttagg | 480 |
| gagtagtagg | taggtaggtg  | gtggactctt | aatcataag  | catactgttt | ggttaagctg | 540 |
| atgaaatcct | tatatatgtt  | tcttggc    |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1502016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Thr | His | Val | Ser | Lys | Lys | Arg | Glu | Ser | Lys | Val | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Glu | Lys | Lys | Asn | Gln | Ser | Arg | His | Gly | Glu | Gln | Arg | Trp |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  | His |
| Arg | Glu | Gly | Arg | Ser | Gly | Gly | Gly | Trp | Cys | Arg | Cys | Gly | Arg | Gly |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  | Arg |
| Trp | Arg | Val | Arg | Xaa | Arg | Arg | Val | Gly | Asp | Ala | Glu | Ala | Arg | Gly |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  | Xaa |
| Pro | His | Pro | Gly | Asp | Ala | Ala | Val | Pro | Arg | Gly | Ala | Glu | Glu | Gly |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 80  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |
| Ala | Gly | Leu | Arg | Glu | Ala | Ala | Gln | Pro | Xaa | Pro | Arg | Thr | Ala | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  | Ser |
| Ser | Arg | Arg | Thr | Trp | Arg | Arg | Ser | Ser | Arg | Ser | Arg | Arg | Ala | Ala |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 | Arg |
| Pro | Ser | Ala | Arg | Asp | Leu | Xaa | Arg | Thr |     |     |     |     |     |     |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Pro | Thr | Phe | Gln | Lys | Lys | Glu | Arg | Lys | Ala | Lys | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  | Leu |
| Pro | Ser | Lys | Lys | Lys | Ile | Ser | Leu | Ala | Met | Glu | Ser | Ser | Val | Gly |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  | Ile |
| Glu | Lys | Ala | Ala | Ala | Val | Ala | Val | Gly | Ala | Gly | Val | Gly | Gly | Gly |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Tyr | Gly | Xaa | Gly | Gly | Trp | Glu | Thr | Pro | Lys | Arg | Glu | Glu | Xaa |
| 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Pro | Ala | Thr | Leu | Pro | Cys | Pro | Ala | Ala | Pro | Arg | Lys | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Asp | Phe | Gly | Lys | Arg | Arg | Ser | Xaa | Ala | Gln | Glu | Arg | Leu | Leu | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Ala | Gly | Pro | Gly | Gly | Ala | Leu | Arg | Ala | Arg | Ala | Ala | Pro | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Arg | Val | Thr | Trp | Xaa | Gly | Leu | Asp | Phe | Leu | Gly | Arg | Glu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1502018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Ser | Val | Gly | Ile | Glu | Lys | Ala | Ala | Ala | Val | Ala | Val | Gly |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Ala | Gly | Val | Gly | Gly | Gly | Gly | Gly | Gly | Tyr | Gly | Xaa | Gly | Gly | Trp | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Pro | Lys | Arg | Glu | Glu | Xaa | Arg | Ile | Pro | Ala | Thr | Leu | Pro | Cys | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ala | Pro | Arg | Lys | Ala | Val | Pro | Asp | Phe | Gly | Lys | Arg | Arg | Ser | Xaa |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Gln | Glu | Arg | Leu | Leu | Pro | Ala | Ala | Gly | Pro | Gly | Gly | Ala | Leu | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Arg | Ala | Ala | Pro | Pro | Gly | Leu | Leu | Arg | Val | Thr | Trp | Xaa | Gly | Leu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Asp | Phe | Leu | Gly | Arg | Glu | Leu |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..542

(D) OTHER INFORMATION: / Ceres Seq. ID 1502023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggggtagcga | ttacaccttg | acacctaagg | ccagagattg | gagagagaaa | gaagcagctg | 60  |
| agtggagcaa | gaaagaagag | gtcatggcgg | tgtagtctat | cagctgagtg | ggaaagagtg | 120 |
| gagcaatggt | ggggggctgt | gccagcggcg | acggcgccgc | cgaagggacg | ctgcgcaggt | 180 |
| ggcggagggc | ggcggccaag | cggatcggcc | tctcatgcgc | ctccttcttc | tcctacgccg | 240 |
| cctctccctc | cccgcctcct | tccaagatca | tctcccactc | cgcactgaat | gcgcctgatg | 300 |
| gagagcagca | aaagatggag | gaaccaccca | gcaccagagt | ggctgacaag | aatctatgtg | 360 |
| caatatgttt | ggaactcctc | agcacgagca | tcagcagcga | tggtgacagt | ggtagggcgg | 420 |
| cagcaatcta | cacagcgcag | tgctcccact | cattccactt | yctatgcac  | gcctccaaca | 480 |
| tccggcatgg | caacgtcagc | tgccctatct | gccgtgcaca | atggtctgag | ctaccacgtg | 540 |
| ac         |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2046:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 139 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..139  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502024  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gly | Gly | Cys | Ala | Ser | Gly | Asp | Gly | Ala | Ala | Glu | Gly | Thr | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Arg | Trp | Arg | Arg | Ala | Ala | Ala | Lys | Arg | Ile | Gly | Leu | Ser | Cys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Phe | Ser | Tyr | Ala | Ala | Ser | Pro | Ser | Pro | Pro | Pro | Ser | Lys | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | His | Ser | Ala | Leu | Asn | Ala | Pro | Asp | Gly | Glu | Gln | Gln | Lys | Met |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Glu | Pro | Thr | Ser | Thr | Arg | Val | Ala | Asp | Lys | Asn | Leu | Cys | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Cys | Leu | Glu | Leu | Leu | Ser | Thr | Ser | Ile | Ser | Ser | Asp | Val | Asp | Ser | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Ala | Ala | Ala | Ile | Tyr | Thr | Ala | Gln | Cys | Ser | His | Ser | Phe | His | Xaa |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Cys | Ile | Ala | Ser | Asn | Ile | Arg | His | Gly | Asn | Val | Ser | Cys | Pro | Ile |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Cys | Arg | Ala | Gln | Trp | Ser | Glu | Leu | Pro | Arg | Asp |     |     |     |     |     |
| 130 |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2047:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 84 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..84  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502025  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Met | Glu | Ser | Ser | Lys | Arg | Trp | Arg | Asn | Pro | Pro | Ala | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Glu | Trp | Leu | Thr | Arg | Ile | Tyr | Val | Gln | Tyr | Val | Trp | Asn | Ser | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Ala | Ser | Ala | Ala | Met | Leu | Thr | Val | Val | Arg | Arg | Gln | Gln | Ser | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Arg | Ser | Ala | Pro | Thr | His | Ser | Thr | Xaa | Tyr | Ala | Ser | Pro | Pro | Thr |
| 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Gly | Met | Ala | Thr | Ser | Ala | Ala | Leu | Ser | Ala | Val | His | Asn | Gly | Leu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Tyr | His | Val |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2048:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 81 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..81
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Ser | Lys | Arg | Trp | Arg | Asn | Pro | Pro | Ala | Pro | Glu | Trp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Arg | Ile | Tyr | Val | Gln | Tyr | Val | Trp | Asn | Ser | Ser | Ala | Arg | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Met | Leu | Thr | Val | Val | Arg | Arg | Gln | Gln | Ser | Thr | Gln | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ala | Pro | Thr | His | Ser | Thr | Xaa | Tyr | Ala | Ser | Pro | Pro | Thr | Ser | Gly | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Thr | Ser | Ala | Ala | Leu | Ser | Ala | Val | His | Asn | Gly | Leu | Ser | Tyr | His |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| acagcacagc | agagaacgca  | ggcagaggca | ccataccagt | caaccaccac | cgcttcggtc  | 60  |
| tcctcccaca | ccgctcgccct | tcgcctcctt | ctgggtccca | tcttctatca | tccccgagct  | 120 |
| ccagttctcc | acacctcacg  | tctataaata | ataaataagg | cgcccgcggt | gccccatcaat | 180 |
| tcgtgtcacc | gcgtcccag   | agcgcaaata | attccgcgcg | acgcaaaaac | cctagcccag  | 240 |
| ccaccgatcc | ctctcatggc  | aaccaccacc | acccaggcga | gcctcctcct | ccagaagcag  | 300 |
| ctaagagatc | tcgcgaagca  | cccgggtgat | gggttctctg | ctgggctggt | cgacgacagc  | 360 |
| aatgtcttcg | agtggcaggt  | caccatcatc | ggaccgcctg | acactctata | tgatggaggt  | 420 |
| tacttcaatg | caataatgag  | cttcccacaa | aattacccaa | acagcccgcg | atcagtcaga  | 480 |
| tttacctctg | aaatgkggca  | tc         |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | His | Ser | Arg | Glu | Arg | Arg | Gln | Arg | His | His | Thr | Ser | Gln | Pro | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Leu | Arg | Ser | Pro | Pro | Thr | Pro | Leu | Ala | Phe | Ala | Ser | Phe | Trp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Ser | Ile | Ile | Pro | Glu | Leu | Gln | Phe | Ser | Thr | Pro | His | Val | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502029  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:  
Ser Thr Ala Glu Asn Ala Gly Arg Gly Thr Ile Pro Val Asn His His  
1 5 10 15  
Arg Phe Val Leu Leu Pro His Arg Ser Pro Ser Pro Pro Ser Gly Ser  
20 25 30  
His Leu Leu Ser Ser Pro Ser Ser Ser Ser Pro His Leu Thr Ser Ile  
35 40 45  
Asn Asn Lys  
50

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502030  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:  
Met Ala Thr Thr Thr Thr Gln Ala Ser Leu Leu Gln Lys Gln Leu  
1 5 10 15  
Arg Asp Leu Ala Lys His Pro Val Asp Gly Phe Ser Ala Gly Leu Val  
20 25 30  
Asp Asp Ser Asn Val Phe Glu Trp Gln Val Thr Ile Ile Gly Pro Pro  
35 40 45  
Asp Thr Leu Tyr Asp Gly Gly Tyr Phe Asn Ala Ile Met Ser Phe Pro  
50 55 60  
Gln Asn Tyr Pro Asn Ser Pro Pro Ser Val Arg Phe Thr Ser Glu Met  
65 70 75 80  
Xaa His

(2) INFORMATION FOR SEQ ID NO:2053:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 526 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..526  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502031  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:  
aattttctta tccccctca tctgctccac ctccgacctc gcgcgagacg agcaagccca 60  
agtatggccg gaggcagcag agccgccgtg gcgtccgggg tctcggcccg gccggccgcg 120  
ccgatgaggg cttctgcggg acgccgcgct cggctgtcgg tggcgcgggc cgcgatatcc 180  
ctcgagaagg gcgagaaggc gtacacggtg cagaagtccg aggagatcct caacgccgcc 240  
aaggagctga tgcctggagg tgtaactcgc ccagtcctgt ccttcaaadc tgttggtggg 300  
cagccagtag tgttcgactc tgtaaagggt tctcgtatgt gggatgttga tgggaatgag 360  
tacattgatt acgttggttc ctggggctcct gcaatcatcg gccatgcaga tgataagggt 420  
aatgtctgat tgattgaaac tctgaagaaa ggaactagct ttggtgctcc atgtttgctg 480  
gagaacgtat tggctgagat ggtcatctct gccgtgcaa gtatcgc

(2) INFORMATION FOR SEQ ID NO:2054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Phe | Leu | Ile | Pro | Pro | His | Leu | Leu | His | Leu | Arg | Pro | Arg | Ala | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Ala | Ser | Pro | Ser | Met | Ala | Gly | Ala | Ala | Ala | Ala | Ala | Val | Ala | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Val | Ser | Ala | Arg | Pro | Ala | Ala | Pro | Met | Arg | Ala | Ser | Ala | Gly | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Ala | Arg | Leu | Ser | Val | Val | Arg | Ala | Ala | Ile | Ser | Leu | Glu | Lys | Gly |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Glu | Lys | Ala | Tyr | Thr | Val | Gln | Lys | Ser | Glu | Glu | Ile | Phe | Asn | Ala | Ala |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | Glu | Leu | Met | Pro | Gly | Gly | Val | Asn | Ser | Pro | Val | Arg | Ala | Phe | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Val | Gly | Gly | Gln | Pro | Val | Val | Phe | Asp | Ser | Val | Lys | Gly | Ser | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Met | Trp | Asp | Val | Asp | Gly | Asn | Glu | Tyr | Ile | Asp | Tyr | Val | Gly | Ser | Trp |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Pro | Ala | Ile | Ile | Gly | His | Ala | Asp | Asp | Lys | Val | Asn | Ala | Ala | Leu |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Glu | Thr | Leu | Lys | Lys | Gly | Thr | Ser | Phe | Gly | Ala | Pro | Cys | Leu | Leu |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Glu | Asn | Val | Leu | Ala | Glu | Met | Val | Ile | Ser | Ala | Val | Pro | Ser | Ile |     |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |

(2) INFORMATION FOR SEQ ID NO:2055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Ala | Ala | Ala | Ala | Val | Ala | Ser | Gly | Val | Ser | Ala | Arg |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Ala | Ala | Pro | Met | Arg | Ala | Ser | Ala | Gly | Arg | Arg | Ala | Arg | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Val | Arg | Ala | Ala | Ile | Ser | Leu | Glu | Lys | Gly | Glu | Lys | Ala | Tyr | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gln | Lys | Ser | Glu | Glu | Ile | Phe | Asn | Ala | Ala | Lys | Glu | Leu | Met | Pro |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Gly | Val | Asn | Ser | Pro | Val | Arg | Ala | Phe | Lys | Ser | Val | Gly | Gly | Gln |
| 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Pro | Val | Val | Phe | Asp | Ser | Val | Lys | Gly | Ser | Arg | Met | Trp | Asp | Val | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Asn | Glu | Tyr | Ile | Asp | Tyr | Val | Gly | Ser | Trp | Gly | Pro | Ala | Ile | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Gly | His | Ala | Asp | Asp | Lys | Val | Asn | Ala | Ala | Leu | Ile | Glu | Thr | Leu | Lys |

115 120 125  
Lys Gly Thr Ser Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala  
130 135 140  
Glu Met Val Ile Ser Ala Val Pro Ser Ile  
145 150

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

Met Arg Ala Ser Ala Gly Arg Arg Ala Arg Leu Ser Val Val Arg Ala  
1 5 10 15  
Ala Ile Ser Leu Glu Lys Gly Glu Lys Ala Tyr Thr Val Gln Lys Ser  
20 25 30  
Glu Glu Ile Phe Asn Ala Ala Lys Glu Leu Met Pro Gly Gly Val Asn  
35 40 45  
Ser Pro Val Arg Ala Phe Lys Ser Val Gly Gly Gln Pro Val Val Phe  
50 55 60  
Asp Ser Val Lys Gly Ser Arg Met Trp Asp Val Asp Gly Asn Glu Tyr  
65 70 75 80  
Ile Asp Tyr Val Gly Ser Trp Gly Pro Ala Ile Ile Gly His Ala Asp  
85 90 95  
Asp Lys Val Asn Ala Ala Leu Ile Glu Thr Leu Lys Lys Gly Thr Ser  
100 105 110  
Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala Glu Met Val Ile  
115 120 125  
Ser Ala Val Pro Ser Ile  
130

(2) INFORMATION FOR SEQ ID NO:2057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

aaggcagggc actgcactgc acgcatgcac tgacctgacg acgcgcgccca cagtccactc 60  
cacactcagg catggcgatg ggcgccgctt ccattcctact gatgatgggtt tcgctggagg 120  
ccctgcttct cgcgcgccgc gccgccggcg ggaccatccg tctgcccagc gatgtcggag 180  
gcgttgctgc agacctgtc acggcgatgg cgagggcgag ggcaagggca aagcatcagc 240  
ttcgcgacga ggagaggccg tggggggaat gctgcgactt ggccgtatgc gtcaagacgt 300  
acccgctaac ttgctcgtgc ttgatcggg ttgagcgctg ctccgacgcc tgtaaggagt 360  
gcgtggaaac ggaggactcg cgccacgtct gcgtcgacag gtaccgtggc gaccccgggc 420  
ccaggtgccca cgacgaggac gggaggagcg gcggacccgc tgacgacgac gctg

(2) INFORMATION FOR SEQ ID NO:2058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1502036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

Met Ala Met Gly Ala Ala Ser Ile Leu Leu Met Met Val Ser Leu Glu  
1 5 10 15  
Ala Leu Leu Leu Ala Ala Ala Ala Gly Gly Thr Ile Arg Leu Pro  
20 25 30  
Ser Asp Val Gly Gly Val Ala Ala Asp Leu Val Thr Ala Met Ala Arg  
35 40 45  
Ala Arg Ala Arg Ala Lys His Gln Leu Arg Asp Glu Glu Arg Pro Trp  
50 55 60  
Gly Glu Cys Cys Asp Leu Ala Val Cys Val Lys Thr Tyr Pro Leu Thr  
65 70 75 80  
Cys Ser Cys Phe Asp Arg Val Glu Arg Cys Ser Asp Ala Cys Lys Glu  
85 90 95  
Cys Val Glu Thr Glu Asp Ser Arg His Val Cys Val Asp Arg Tyr Arg  
100 105 110  
Gly Asp Pro Gly Pro Arg Cys His Asp Glu Asp Gly Arg Ser Gly Gly  
115 120 125  
Pro Ala Asp Asp Asp Ala  
130

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1502037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

Met Gly Ala Ala Ser Ile Leu Leu Met Met Val Ser Leu Glu Ala Leu  
1 5 10 15  
Leu Leu Ala Ala Ala Ala Ala Gly Gly Thr Ile Arg Leu Pro Ser Asp  
20 25 30  
Val Gly Gly Val Ala Ala Asp Leu Val Thr Ala Met Ala Arg Ala Arg  
35 40 45  
Ala Arg Ala Lys His Gln Leu Arg Asp Glu Glu Arg Pro Trp Gly Glu  
50 55 60  
Cys Cys Asp Leu Ala Val Cys Val Lys Thr Tyr Pro Leu Thr Cys Ser  
65 70 75 80  
Cys Phe Asp Arg Val Glu Arg Cys Ser Asp Ala Cys Lys Glu Cys Val  
85 90 95  
Glu Thr Glu Asp Ser Arg His Val Cys Val Asp Arg Tyr Arg Gly Asp  
100 105 110  
Pro Gly Pro Arg Cys His Asp Glu Asp Gly Arg Ser Gly Gly Pro Ala  
115 120 125  
Asp Asp Asp Ala  
130

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1502038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

```
Met Met Val Ser Leu Glu Ala Leu Leu Leu Ala Ala Ala Ala Gly
1 5 10 15
Gly Thr Ile Arg Leu Pro Ser Asp Val Gly Gly Val Ala Ala Asp Leu
20 25 30
Val Thr Ala Met Ala Arg Ala Arg Ala Arg Ala Lys His Gln Leu Arg
35 40 45
Asp Glu Glu Arg Pro Trp Gly Glu Cys Cys Asp Leu Ala Val Cys Val
50 55 60
Lys Thr Tyr Pro Leu Thr Cys Ser Cys Phe Asp Arg Val Glu Arg Cys
65 70 75 80
Ser Asp Ala Cys Lys Glu Cys Val Glu Thr Glu Asp Ser Arg His Val
85 90 95
Cys Val Asp Arg Tyr Arg Gly Asp Pro Gly Pro Arg Cys His Asp Glu
100 105 110
Asp Gly Arg Ser Gly Gly Pro Ala Asp Asp Ala
115 120
```

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 895 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..895

(D) OTHER INFORMATION: / Ceres Seq. ID 1502048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

```
atcgaaaaaa aaaactcctc tcccagagtc ctctcctctc cgggggtattg aattcgaacc 60
aaaaaatcaa aacaactcag cgattcgatt cgcgggcgagt caagcgggat gccgccgcgc 120
acggctccgg cggcgacctc aaccccgccg cggaaggtgc ccctccggaa gctgctgcgt 180
gcggcgctcg tgcctgcggg ggtgcagttc ggctggggcg tgcagctgtc gttgctgacc 240
ccgtacgtgc aggagctggg catcccgcac gcccttgcca gtctcgtctg gctgtgcggg 300
ccgctgtccg gcctcctcgt ccagccccctc gtcgggccacc tctccgaccg catcggcccc 360
gccgcttcgc cgctcggggc ccgcaggccc ttcctcgccg ccggcgccgc gtgcatcgcc 420
gcagccgtgc tcaccgtcgg cttctccgct gacctcggcc gactcttcgg cgacgacgtc 480
accccgggct caacgcgcct cggcgccatc tgcgtctacc ttgtaggatt ctggctgctc 540
gacgtgggca acaacggcac gcagggggccc tgcagggcgt tctcgccga cctcacagag 600
aatgacccaa ggaggagagg cgggacacac cgataagtct gctcatttac cattacaggc 660
atcatcaagt ctggaaatc tttgtggggt ggagaagagc acgctgggag ctcttgaatg 720
ctgtgtgtc tttggtggtt tgccccgttg agctattttt tgccctgtct ccaaattctt 780
tggtgttcaa ttcaactcga atgtatgtac gcacgtatgc atgtatgtat ttgtatgtat 840
gtggatcatt ttagagagc ttaagcaatg aataaaagtt acaggagtta cgttc
```

(2) INFORMATION FOR SEQ ID NO:2062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1502049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Arg Lys Lys Lys Leu Leu Ser Pro Ser Pro Leu Leu Ser Gly Val Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Asn | Ser | Asn | Gln | Lys | Ile | Lys | Thr | Thr | Gln | Arg | Phe | Asp | Ser | Arg | Arg |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Val | Lys | Arg | Asp | Ala | Ala | Ala | His | Gly | Ser | Gly | Gly | Asp | Leu | Asn | Pro |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Ala | Ala | Glu | Gly | Ala | Pro | Pro | Glu | Ala | Ala | Ala | Cys | Gly | Val | Gly | Arg |  |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Leu | Arg | Gly | Ala | Val | Arg | Leu | Gly | Ala | Ala | Ala | Val | Val | Ala | Asp | Pro |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Val | Arg | Ala | Gly | Ala | Gly | His | Pro | Ala | Arg | Leu | Cys | Gln | Ser | Arg | Leu |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |  |
| Ala | Val | Arg | Ser | Ala | Val | Arg | Pro | Pro | Arg | Pro | Ala | Pro | Arg | Arg | Pro |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Pro | Leu | Arg | Pro | His | Arg | Pro | Arg | Arg | Phe | Ala | Ala | Arg | Ala | Pro | Gln |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |
| Ala | Leu | His | Arg | Arg | Arg | Arg | Arg | Val | His | Arg | Arg | Ser | Arg | Ala | His |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Arg | Arg | Leu | Leu | Arg |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Pro | Pro | Arg | Thr | Ala | Pro | Ala | Ala | Thr | Ser | Thr | Pro | Pro | Arg | Lys |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Val | Pro | Leu | Arg | Lys | Leu | Leu | Arg | Ala | Ala | Ser | Val | Ala | Cys | Gly | Val |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Gln | Phe | Gly | Trp | Ala | Leu | Gln | Leu | Ser | Leu | Leu | Thr | Pro | Tyr | Val | Gln |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Glu | Leu | Gly | Ile | Pro | His | Ala | Phe | Ala | Ser | Leu | Val | Trp | Leu | Cys | Gly |  |  |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Pro | Leu | Ser | Gly | Leu | Leu | Val | Gln | Pro | Leu | Val | Gly | His | Leu | Ser | Asp |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Arg | Ile | Gly | Pro | Ala | Ala | Ser | Pro | Leu | Gly | Arg | Arg | Arg | Pro | Phe | Ile |  |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |  |  |
| Ala | Ala | Gly | Ala | Ala | Cys | Ile | Ala | Ala | Val | Leu | Thr | Val | Gly | Phe |     |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Ser | Ala | Asp | Leu | Gly | Arg | Leu | Phe | Gly | Asp | Asp | Val | Thr | Pro | Gly | Ser |  |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |  |
| Thr | Arg | Leu | Gly | Ala | Ile | Cys | Val | Tyr | Leu | Val | Gly | Phe | Trp | Leu | Leu |  |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Asp | Val | Gly | Asn | Asn | Gly | Thr | Gln | Gly | Pro | Cys | Arg | Ala | Phe | Leu | Ala |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |  |
| Asp | Leu | Thr | Glu | Asn | Asp | Pro | Arg | Arg | Arg | Gly | Gly | Thr | His | Arg |     |  |  |
|     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..490

(D) OTHER INFORMATION: / Ceres Seq. ID 1502056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| atcttcgtct  | ctctccgact | ctccctcgcc | cgcgcacctt  | tccgcgccgc | ctccttcctt  | 60  |
| tcctcgcggtg | ctctggcgcg | cgcaaggatc | aaaaggcgcc  | ggccactaga | ggcgagttag  | 120 |
| tcgcatgtaa  | acgaccacca | gctgctgtga | tctcaaaagg  | gagcgagaga | caaaggagag  | 180 |
| gcgagcaggt  | cgtggcgcca | gcaatcggtg | cgaatccgcg  | cgggattctg | tcctctgcac  | 240 |
| cactgcttcc  | cgctttcctg | cccggcgcaa | gtggtataat  | tctccaacgc | ggttgactgt  | 300 |
| attgcctctc  | gctctcggtg | ggtgggggca | tggacgaggc  | agaggagatg | cagggtggaga | 360 |
| ggctgcacga  | ggaggccgat | gcggggggag | ccgacacgga  | caagctcagc | tacgagatat  | 420 |
| tctccatcct  | cgagagcaag | ttcctgttcg | gctataaccga | cccgcaccag | ctctggctgc  | 480 |
| ccaagccagc  |            |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1502057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Val | Ser | Leu | Arg | Leu | Ser | Leu | Ala | Arg | Ala | Pro | Phe | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Phe | Leu | Ser | Ser | Arg | Ala | Leu | Ala | Arg | Ala | Arg | Ile | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Pro | Leu | Glu | Ala | Ser | Glu | Ser | His | Val | Asn | Asp | His | Gln | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1502058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Glu | Ala | Glu | Glu | Met | Gln | Val | Glu | Arg | Leu | His | Glu | Glu | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ala | Gly | Gly | Ala | Asp | Thr | Asp | Lys | Leu | Ser | Tyr | Glu | Ile | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Leu | Glu | Ser | Lys | Phe | Leu | Phe | Gly | Tyr | Thr | Asp | Pro | His | Gln | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Leu | Pro | Lys | Pro |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..47  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

```
Met Gln Val Glu Arg Leu His Glu Glu Ala Asp Ala Gly Gly Ala Asp
1 5 10 15
Thr Asp Lys Leu Ser Tyr Glu Ile Phe Ser Ile Leu Glu Ser Lys Phe
 20 25 30
Leu Phe Gly Tyr Thr Asp Pro His Gln Leu Trp Leu Pro Lys Pro
 35 40 45
```

(2) INFORMATION FOR SEQ ID NO:2068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..566  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

```
aaaaatcaaa gtagcgctcgt gctgccccaa ctcggcaact ccccatcagc tcaccccgat 60
ctagggtttg ggcaccctcc gcttacgcgc ctccccacca agcaaagtgt agggcccgcg 120
gcatctccct tcgggcgtca tggcggctac agggcaggag ggggatgacg tcgaccacta 180
cgaggtactc tgcctcccgt cgggggagga aggcgcggcg ctgaccatcg agcatatcga 240
gaaggcctac cggacgcagt cgcggctgcg ccaccccgat aagcgccccg acgaccccaa 300
cgccaccgcc gacttcacgc tcctctcgag ttctacaaa ctctccgcg acgagtcctt 360
tcgccgccag ttcgacgcgc gcctccgcgg ccgccgcgag gccgcagccc gcgccgcgcg 420
cacgggcggt aagcgccgga agccgtctc cgacctcgag gagcgcgagc gcgccgycgy 480
cgngggccac cccgscgatc ccgaggagct cgccmagcgc gaggcccara gatggccscg 540
gacattgagc gcgagctcgc agcggt
```

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

```
Met Ala Ala Thr Gly Gln Glu Gly Asp Val Asp His Tyr Glu Val
1 5 10 15
Leu Cys Leu Pro Ser Gly Glu Glu Gly Ala Ala Leu Thr Ile Glu His
 20 25 30
Ile Glu Lys Ala Tyr Arg Thr Gln Ser Arg Leu Arg His Pro Asp Lys
 35 40 45
Arg Pro Asp Asp Pro Asn Ala Thr Ala Asp Phe Gln Leu Leu Ser Ser
 50 55 60
Ser Tyr Lys Leu Leu Arg Asp Glu Ser Leu Arg Arg Gln Phe Asp Ala
 65 70 75 80
Arg Leu Arg Gly Arg Arg Glu Ala Ala Ala Arg Ala Ala Ala Thr Gly
 85 90 95
Val Lys Arg Arg Lys Ala Val Ser Asp Leu Glu Glu Arg Glu Arg Ala
 100 105 110
Xaa Xaa Xaa Gly His Pro Xaa Asp Pro Glu Glu Leu Ala Xaa Arg Glu
 115 120 125
Ala Xaa Arg Trp Xaa Pro Thr Leu Ser Ala Ser Ser Gln Arg
```

130 135 140

(2) INFORMATION FOR SEQ ID NO:2070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1502074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aagaccacca | ctgcgccatt | ggccagctag | agccaaccag | aagagcttgc | agttactgag | 60  |
| agtgtttgag | agagagagga | tgatgggtgg | cagcggcagg | gctgctctgc | tgctggccct | 120 |
| ggtggccgtg | agcctggccg | tgagatcca  | ggccgacgcc | gggtacgggt | acaccccgac | 180 |
| gccgacgccg | gccaccccca | ccccgaagcc | ggagaagccc | cccaccaagg | ggcccaagcc | 240 |
| ggagaagccg | ccaaaggagc | acaagccgcc | caaggagcac | gggcccagc  | cggagaagcc | 300 |
| gccaagagag | cacaagccga | cgccgcccac | gtacaccccg | agccccaac  | ccacgcccgc | 360 |
| gacgtacact | cccaccccca | cgcccccaa  | gccgacgcca | cccacataca | ctcccgcgcc | 420 |
| tacgccccac | aaaccacctc | ccactcctcc | gacgtacacc | ccttc      |            |     |

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1502075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Pro | Pro | Leu | Arg | His | Trp | Pro | Ala | Arg | Ala | Asn | Gln | Lys | Ser | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Gln | Leu | Leu | Arg | Val | Phe | Glu | Arg | Glu | Arg | Met | Met | Gly | Gly | Ser | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Ala | Ala | Leu | Leu | Leu | Ala | Leu | Val | Ala | Val | Ser | Leu | Ala | Val | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Gln | Ala | Asp | Ala | Gly | Tyr | Gly | Tyr | Thr | Pro | Thr | Pro | Thr | Pro | Ala |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Pro | Thr | Pro | Lys | Pro | Glu | Lys | Pro | Pro | Thr | Lys | Gly | Pro | Lys | Pro |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Glu | Lys | Pro | Pro | Lys | Glu | His | Lys | Pro | Pro | Lys | Glu | His | Gly | Pro | Lys |  |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |  |
| Pro | Glu | Lys | Pro | Pro | Lys | Glu | His | Lys | Pro | Thr | Pro | Pro | Thr | Tyr | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro | Ser | Pro | Lys | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro | Thr | Pro | Thr | Pro |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |  |
| Pro | Lys | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro | Ala | Pro | Thr | Pro | His | Lys |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Pro | Thr | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro |     |     |     |     |     |     |  |
| 145 |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Gly | Gly | Ser | Gly | Arg | Ala | Ala | Leu | Leu | Leu | Ala | Leu | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Leu | Ala | Val | Glu | Ile | Gln | Ala | Asp | Ala | Gly | Tyr | Gly | Tyr | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Thr | Pro | Thr | Pro | Ala | Thr | Pro | Thr | Pro | Lys | Pro | Glu | Lys | Pro | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Lys | Gly | Pro | Lys | Pro | Glu | Lys | Pro | Pro | Lys | Glu | His | Lys | Pro | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Glu | His | Gly | Pro | Lys | Pro | Glu | Lys | Pro | Pro | Lys | Glu | His | Lys | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Pro | Pro | Thr | Tyr | Thr | Pro | Ser | Pro | Lys | Pro | Thr | Pro | Pro | Thr | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Pro | Thr | Pro | Thr | Pro | Pro | Lys | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Pro | Thr | Pro | His | Lys | Pro | Thr | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:2073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Gly | Ser | Gly | Arg | Ala | Ala | Leu | Leu | Leu | Ala | Leu | Val | Ala | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Leu | Ala | Val | Glu | Ile | Gln | Ala | Asp | Ala | Gly | Tyr | Gly | Tyr | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Pro | Thr | Pro | Ala | Thr | Pro | Thr | Pro | Lys | Pro | Glu | Lys | Pro | Pro | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Gly | Pro | Lys | Pro | Glu | Lys | Pro | Pro | Lys | Glu | His | Lys | Pro | Pro | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | His | Gly | Pro | Lys | Pro | Glu | Lys | Pro | Pro | Lys | Glu | His | Lys | Pro | Thr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Pro | Thr | Tyr | Thr | Pro | Ser | Pro | Lys | Pro | Thr | Pro | Pro | Thr | Tyr | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Thr | Pro | Thr | Pro | Pro | Lys | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Pro | His | Lys | Pro | Thr | Pro | Thr | Pro | Pro | Thr | Tyr | Thr | Pro |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502086

```

(ii) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..121
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502087

```

(2) INFORMATION FOR SEQ ID NO:2076:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..97
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502088

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076: |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                                        | Tyr | Gln | Arg | Pro | Asp | Met | Ile | Thr | Pro | Gly | Val | Asp | Ala | Gln | Gly |
| 1                                          |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn                                        | Pro | Ile | Asp | Pro | Glu | Arg | Ile | Gln | Glu | Asp | Phe | Glu | Asp | Phe | Tyr |
|                                            |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu                                        | Asp | Ile | Phe | Val | Glu | Leu | Ser | Lys | His | Gly | Glu | Ile | Glu | Ser | Leu |
|                                            |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His                                        | Val | Cys | Asp | Asn | Leu | Ala | Asp | His | Met | Ile | Gly | Asn | Val | Tyr | Val |
|                                            | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu                                        | Phe | Arg | Glu | Glu | Glu | Gln | Ala | Xaa | Arg | Ala | Leu | Xaa | Ala | Leu | Xaa |
| 65                                         |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |



Gly Arg Leu Leu Leu Gly Pro Pro His His Arg Arg Val Leu Ala Gly  
85 90 95  
Asp

(2) INFORMATION FOR SEQ ID NO:2077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ile | Thr | Pro | Gly | Val | Asp | Ala | Gln | Gly | Asn | Pro | Ile | Asp | Pro | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Arg | Ile | Gln | Glu | Asp | Phe | Glu | Asp | Phe | Tyr | Glu | Asp | Ile | Phe | Val | Glu |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Ser | Lys | His | Gly | Glu | Ile | Glu | Ser | Leu | His | Val | Cys | Asp | Asn | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Asp | His | Met | Ile | Gly | Asn | Val | Tyr | Val | Glu | Phe | Arg | Glu | Glu | Glu |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gln | Ala | Xaa | Arg | Ala | Leu | Xaa | Ala | Leu | Xaa | Gly | Arg | Leu | Leu | Leu | Gly |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Pro | Pro | His | His | Arg | Arg | Val | Leu | Ala | Gly | Asp |     |     |     |     |     |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..314
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aaccatttgg | acaccgatcc | atccatccat | ccagccccgt | acgtgtctcg | ctggccgtcc  | 60  |
| gtatatatag | agagaggcat | cggagattrg | ccgccacgtt | gccatcgcg  | gcr gcgccc  | 120 |
| ccggccaagg | ccaaccatgc | tggcgagggc | tctctcgccg | cggccgtgct | ccagcggcgt  | 180 |
| ttgcatcgcc | cgcgcacatc | caagarcmgc | cgcgcgtcgc | gccaggccgg | nggacgacga  | 240 |
| ggacgacgac | gacggtcgcg | gcggcggcgg | cagaggccgc | tntctaacgg | gtc arcggcg | 300 |
| gcggccgtcg | cagg       |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | His | Leu | Asp | Thr | Asp | Pro | Ser | Ile | His | Pro | Ala | Pro | Tyr | Val | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Trp | Pro | Ser | Val | Tyr | Ile | Glu | Arg | Gly | Ile | Gly | Asp | Xaa | Pro | Pro |  |

20 25 30  
Arg Cys His Arg Ala Xaa Arg Pro Ala Lys Ala Asn His Ala Gly  
35 40 45  
Glu Gly Ser Ser Ala Ala Ala Val Leu Gln Arg Arg Leu His Arg Pro  
50 55 60  
Arg Thr Ser Lys Xaa Xaa Arg Arg Arg Gly Gln Ala Xaa Gly Arg Arg  
65 70 75 80  
Gly Arg Arg Arg Arg Ser Arg Arg Arg Arg Gln Arg Pro Xaa Ser Asn  
85 90 95  
Gly Ser Xaa Ala Ala Val Ala  
100

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

Pro Phe Gly His Arg Ser Ile His Pro Ser Ser Pro Val Arg Val Ser  
1 5 10 15  
Leu Ala Val Arg Ile Tyr Arg Glu Arg His Arg Arg Xaa Ala Ala Thr  
20 25 30  
Leu Pro Ser Arg Xaa Ala Pro Ala Gly Gln Gly Gln Pro Cys Trp Arg  
35 40 45  
Gly Leu Leu Arg Arg Gly Arg Ala Pro Ala Ala Phe Ala Ser Pro Ala  
50 55 60  
His Ile Gln Xaa Xaa Pro Pro Ser Arg Pro Gly Arg Xaa Thr Thr Arg  
65 70 75 80  
Thr Thr Thr Thr Val Ala Ala Ala Ala Ala Glu Ala Ala Xaa  
85 90

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Met Leu Ala Arg Ala Pro Pro Pro Arg Pro Cys Ser Ser Gly Val Cys  
1 5 10 15  
Ile Ala Arg Ala His Pro Arg Xaa Ala Ala Val Ala Ala Arg Pro Xaa  
20 25 30  
Asp Asp Glu Asp Asp Asp Asp Gly Arg Gly Gly Gly Gly Arg Gly Arg  
35 40 45  
Xaa Leu Thr Gly Xaa Arg Arg Arg Pro Ser Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:2082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1036

(D) OTHER INFORMATION: / Ceres Seq. ID 1502094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| accctatggt | catgccacca | tggaagggt   | tcgtattgga | gcaccgatta | tgcagggtta  | 60   |
| tcatgagaaa | tcttttatct | tacctgatgt  | ttcaagggtg | cttgcttgcc | tttatgagaa  | 120  |
| ggatgtcaag | tttgagactc | acacagcctc  | atacaggagc | ctactcggat | tgcaggcatc  | 180  |
| atctcatgct | ccagttccat | tctatgaagg  | ccctactttt | ctagaagaat | ccagagaaat  | 240  |
| ctgccgttat | atagcagaaa | agtatgaaaa  | tcaaggatat | ccgttcctcc | ttggaaagga  | 300  |
| tgcccttgag | agggcttcaa | ttgaacaatg  | gctccacaac | gaggagcatg | ctttcaaccc  | 360  |
| tccgagccgg | gccttgttct | ttcatttggc  | ctttcccctg | ggtgaaggag | aagatgatga  | 420  |
| tattgatggt | catacaagga | agctagaaga  | ggttctggaa | gtttatgagc | aaaggctcag  | 480  |
| tgacagcgaa | ttccttggtg | gaaacaagtt  | cactcttgcc | gaccttgttc | acctgccaaa  | 540  |
| ttcccactat | atcaaagcat | ctaacaagtt  | tctttacctt | tatgattcga | ggaaaaatgt  | 600  |
| aaggagggtg | tgggatgcta | tttctgaccg  | gagttcttgg | aagaaagtgc | tgagggtatat | 660  |
| gaagagcgtg | gaggagaaga | acaaacaaga  | agaactcaag | aagcagcagc | agcagcagga  | 720  |
| agaggctcct | agaacctcca | ccgacccaac  | tcgggtagac | tcgagaaagc | agagcagaac  | 780  |
| agagcctcgg | acaatatgtg | ttcctcctgc  | tgataacgag | tcacagcgtt | cgatagttcc  | 840  |
| tcgaacaaag | aagcctcttc | ctgggtgatca | cttagtgtct | actcaacaaa | ttgatgggtg  | 900  |
| tggtatgcca | gccacaaatt | gatgggtgatg | gtcgtcttag | tggtgtttgt | cttgtctttt  | 960  |
| attgtttggt | tctttaacaa | gagttatat   | tttaccttct | gaccaaagag | ttgtttaaca  | 1020 |
| ggatagtcac | tgtacg     |             |            |            |             |      |

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1502095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Tyr | Val | His | Ala | Thr | Met | Glu | Gly | Leu | Arg | Ile | Gly | Ala | Pro | Ile |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |
| Met | Gln | Val | Tyr | His | Glu | Lys | Ser | Phe | Ile | Leu | Pro | Asp | Val | Ser | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Val | Leu | Ala | Cys | Leu | Tyr | Glu | Lys | Asp | Val | Lys | Phe | Glu | Thr | His | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Ser | Tyr | Arg | Ser | Leu | Leu | Gly | Leu | Gln | Ala | Ser | Ser | His | Ala | Pro |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Val | Pro | Phe | Tyr | Glu | Gly | Pro | Thr | Phe | Leu | Glu | Ser | Arg | Glu | Ile |     |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |     |  |
| Cys | Arg | Tyr | Ile | Ala | Glu | Lys | Tyr | Glu | Asn | Gln | Gly | Tyr | Pro | Phe | Leu |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |     |  |
| Leu | Gly | Lys | Asp | Ala | Leu | Glu | Arg | Ala | Ser | Ile | Glu | Gln | Trp | Leu | His |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |  |
| Asn | Glu | Glu | His | Ala | Phe | Asn | Pro | Pro | Ser | Arg | Ala | Leu | Phe | Phe | His |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Ala | Phe | Pro | Leu | Gly | Glu | Gly | Glu | Asp | Asp | Asp | Ile | Asp | Val | His |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Thr | Arg | Lys | Leu | Glu | Glu | Val | Leu | Glu | Val | Tyr | Glu | Gln | Arg | Leu | Ser |  |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |     |     |  |
| Asp | Ser | Glu | Phe | Leu | Val | Gly | Asn | Lys | Phe | Thr | Leu | Ala | Asp | Leu | Val |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |     |     |  |
| His | Leu | Pro | Asn | Ser | His | Tyr | Ile | Lys | Ala | Ser | Asn | Lys | Phe | Leu | Tyr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |     |  |
| Leu | Tyr | Asp | Ser | Arg | Lys | Asn | Val | Arg | Arg | Trp | Trp | Asp | Ala | Ile | Ser |  |

195 200 205  
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu  
210 215 220  
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Gln Glu  
225 230 235 240  
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys  
245 250 255  
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn  
260 265 270  
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly  
275 280 285  
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala  
290 295 300  
Thr Asn  
305

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..300

(D) OTHER INFORMATION: / Ceres Seq. ID 1502096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

Met Glu Gly Leu Arg Ile Gly Ala Pro Ile Met Gln Val Tyr His Glu  
1 5 10 15  
Lys Ser Phe Ile Leu Pro Asp Val Ser Arg Val Leu Ala Cys Leu Tyr  
20 25 30  
Glu Lys Asp Val Lys Phe Glu Thr His Thr Ala Ser Tyr Arg Ser Leu  
35 40 45  
Leu Gly Leu Gln Ala Ser Ser His Ala Pro Val Pro Phe Tyr Glu Gly  
50 55 60  
Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile Cys Arg Tyr Ile Ala Glu  
65 70 75 80  
Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu Leu Gly Lys Asp Ala Leu  
85 90 95  
Glu Arg Ala Ser Ile Glu Gln Trp Leu His Asn Glu Glu His Ala Phe  
100 105 110  
Asn Pro Pro Ser Arg Ala Leu Phe Phe His Leu Ala Phe Pro Leu Gly  
115 120 125  
Glu Gly Glu Asp Asp Asp Ile Asp Val His Thr Arg Lys Leu Glu Glu  
130 135 140  
Val Leu Glu Val Tyr Glu Gln Arg Leu Ser Asp Ser Glu Phe Leu Val  
145 150 155 160  
Gly Asn Lys Phe Thr Leu Ala Asp Leu Val His Leu Pro Asn Ser His  
165 170 175  
Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr Leu Tyr Asp Ser Arg Lys  
180 185 190  
Asn Val Arg Arg Trp Trp Asp Ala Ile Ser Asp Arg Ser Ser Trp Lys  
195 200 205  
Lys Val Leu Arg Tyr Met Lys Ser Val Glu Glu Lys Asn Lys Gln Glu  
210 215 220  
Glu Leu Lys Lys Gln Gln Gln Gln Glu Glu Ala Pro Arg Thr Ser  
225 230 235 240  
Thr Asp Pro Thr Arg Val Asp Ser Arg Lys Gln Ser Arg Thr Glu Pro  
245 250 255  
Arg Thr Ile Leu Val Pro Pro Ala Asp Asn Glu Ser Ser Ala Ser Ile  
260 265 270

Val Pro Arg Thr Lys Lys Pro Leu Pro Gly Asp His Leu Val Ser Thr  
275 280 285  
Gln Gln Ile Asp Gly Val Gly Met Pro Ala Thr Asn  
290 295 300

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

Met Gln Val Tyr His Glu Lys Ser Phe Ile Leu Pro Asp Val Ser Arg  
1 5 10 15  
Val Leu Ala Cys Leu Tyr Glu Lys Asp Val Lys Phe Glu Thr His Thr  
20 25 30  
Ala Ser Tyr Arg Ser Leu Leu Gly Leu Gln Ala Ser Ser His Ala Pro  
35 40 45  
Val Pro Phe Tyr Glu Gly Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile  
50 55 60  
Cys Arg Tyr Ile Ala Glu Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu  
65 70 75 80  
Leu Gly Lys Asp Ala Leu Glu Arg Ala Ser Ile Glu Gln Trp Leu His  
85 90 95  
Asn Glu Glu His Ala Phe Asn Pro Pro Ser Arg Ala Leu Phe Phe His  
100 105 110  
Leu Ala Phe Pro Leu Gly Glu Gly Glu Asp Asp Asp Ile Asp Val His  
115 120 125  
Thr Arg Lys Leu Glu Glu Val Leu Glu Val Tyr Glu Gln Arg Leu Ser  
130 135 140  
Asp Ser Glu Phe Leu Val Gly Asn Lys Phe Thr Leu Ala Asp Leu Val  
145 150 155 160  
His Leu Pro Asn Ser His Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr  
165 170 175  
Leu Tyr Asp Ser Arg Lys Asn Val Arg Arg Trp Trp Asp Ala Ile Ser  
180 185 190  
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu  
195 200 205  
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Gln Glu  
210 215 220  
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys  
225 230 235 240  
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn  
245 250 255  
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly  
260 265 270  
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala  
275 280 285  
Thr Asn  
290

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..833

(D) OTHER INFORMATION: / Ceres Seq. ID 1502100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| atcctagaag  | gaaacaggaa | caggcagctc | tgaaagactg | aaactcacgg | ccatggccat | 60  |
| cctggggcgcc | ctcaggctcg | cgccgtctcc | acccgccctc | gccggcgctg | cgccaccggc | 120 |
| tacgtcgccg  | tctgcggctg | tacgtctctc | cgtgcacttc | cacctcgcca | atgccggcgc | 180 |
| cgccgcgctc  | ngtcgccgcc | tcgtctctcg | ccgccgaccc | cgccgtggct | ttcattggag | 240 |
| gaggaccgta  | cgggaagcag | gtgacgcggg | ggcaggacct | caccggcaag | gacttcagcg | 300 |
| gccagacact  | catcaagcag | gacttcaaga | cgtctatact | gaggcaggcg | aacttcaaag | 360 |
| gcgcgaacct  | gctcggcgcg | agcttcttcg | atgcagacct | cacaagcgct | gatctctctg | 420 |
| acgctgatct  | tagaggcgct | gatttgtcgc | tggcgaattt | aacgaaggca | aacttatcaa | 480 |
| atgccaaactt | agaaggggca | cttgccactg | ggaacacttc | tttcaaaggt | gccgacataa | 540 |
| ctggggcaga  | ttttaccgat | gtgccgctgc | gagatgatca | acgggagtac | ctctgcaaaa | 600 |
| tcgctgacgg  | agtaaattca | accactggaa | acccaacaaa | ggagactctg | ttctgcagct | 660 |
| gatcgacgga  | aggacctggg | acttgtgact | tattcaacgt | cttgataaac | ttgcatctgc | 720 |
| tgctgtaagc  | acgtgaggaa | tgtaaattga | gttatagagg | gttcctagaa | ataataactg | 780 |
| gtaattacgt  | gtaaataaac | caacaataaa | agtgtgtgct | gccctttgaa | tgt        |     |

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1502101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Leu | Gly | Ala | Leu | Arg | Leu | Ala | Pro | Ser | Pro | Pro | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Gly | Ala | Ala | Pro | Pro | Ala | Thr | Ser | Pro | Ser | Ala | Ala | Val | Arg | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Val | His | Phe | His | Leu | Ala | Asn | Ala | Gly | Ala | Ala | Ala | Leu | Xaa | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Arg | Leu | Ala | Pro | Arg | Arg | Arg | Pro | Arg | Arg | Gly | Phe | His | Trp | Arg | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Val | Arg | Glu | Ala | Gly | Asp | Ala | Gly | Ala | Gly | Pro | His | Arg | Gln | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gln | Arg | Pro | Asp | Thr | His | Gln | Ala | Gly | Leu | Gln | Asp | Val | Tyr | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ala | Gly | Glu | Leu | Gln | Arg | Arg | Glu | Pro | Ala | Arg | Arg | Glu | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Cys | Arg | Pro | His | Lys | Arg |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1502102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Ala | Pro | Pro | Arg | Xaa | Val | Ala | Ala | Ser | Leu | Leu | Ala | Ala | Asp |
| 1   |     |     |     | 5   |     |     |     |     |     |     | 10  |     |     |     | 15  |

Pro Ala Val Ala Phe Ile Gly Gly Gly Pro Tyr Gly Lys Gln Val Thr  
20 25 30  
Arg Gly Gln Asp Leu Thr Gly Lys Asp Phe Ser Gly Gln Thr Leu Ile  
35 40 45  
Lys Gln Asp Phe Lys Thr Ser Ile Leu Arg Gln Ala Asn Phe Lys Gly  
50 55 60  
Ala Asn Leu Leu Gly Ala Ser Phe Phe Asp Ala Asp Leu Thr Ser Ala  
65 70 75 80  
Asp Leu Ser Asp Ala Asp Leu Arg Gly Ala Asp Leu Ser Leu Ala Asn  
85 90 95  
Leu Thr Lys Ala Asn Leu Ser Asn Ala Asn Leu Glu Gly Ala Leu Ala  
100 105 110  
Thr Gly Asn Thr Ser Phe Lys Gly Ala Asp Ile Thr Gly Ala Asp Phe  
115 120 125  
Thr Asp Val Pro Leu Arg Asp Asp Gln Arg Glu Tyr Leu Cys Lys Ile  
130 135 140  
Ala Asp Gly Val Asn Ser Thr Thr Gly Asn Pro Thr Lys Glu Thr Leu  
145 150 155 160  
Phe Cys Ser

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| atctctatct catcgtcadc attagaaagg ccgaagcctt ctccgttcct cctcgacgcg | 60  |
| tctcttccac agccgcaacc tctatccctc gtctggtatc gtctctccca caccctctg  | 120 |
| ccccaaccca gaaaaaccct cgaaaagcgg cggcggcgcg acatggcgga ggtcgaggct | 180 |
| ccagctgctg cggttgcggc ggcgaccctt gaggtggcga cggtgaccga gggcggagcc | 240 |
| gctacggagg cgaagggtcc gcataagctg caccgccagt ggaccttctg gtacgacatc | 300 |
| cagtccaagc ccaagcccgg cgtgcgtggg ggcacctccc tcaaaaaggc gtacacctc  | 360 |
| gacaccgtcg aggagtgttg gggcttgat gatcatgtt tccgtccaag caagttgcct   | 420 |
| ggaactgctg attttcacct attcaaggct ggagtagagc caaaatgg              |     |

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

Ile Ser Ile Ser Ser Ser Ser Leu Glu Arg Pro Lys Pro Ser Pro Phe  
1 5 10 15  
Leu Leu Asp Ala Ser Leu Pro Gln Pro Gln Pro Leu Ser Leu Val Trp  
20 25 30  
Tyr Arg Leu Ser His Thr Pro Leu Pro Gln Pro Arg Lys Thr Leu Glu  
35 40 45  
Lys Arg Arg Arg Arg Asp Met Ala Glu Val Glu Ala Pro Ala Ala Ala  
50 55 60  
Val Ala Ala Ala Thr Pro Glu Val Ala Thr Val Thr Glu Gly Gly Ala

(2) INFORMATION FOR SEQ ID NO:2091:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

(2) INFORMATION FOR SEQ ID NO:2092:

(A) LENGTH: 513 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..513

(D) OTHER INFORMATION: / Ceres Seq. ID 1502133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

(2) INFORMATION FOR SEQ ID NO:2093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..132
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | Asn | His | Phe | Ile | Pro | Gly | Thr | Gly | Arg | Arg | Thr | Ala | Val | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Lys | Ser | Gly | Gln | Ser | Ser | Arg | Arg | Pro | Pro | His | Pro | Ile | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gln | Ala | Cys | Cys | Arg | Pro | Leu | Pro | Ser | Pro | Ala | Pro | Ser | Pro | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Thr | Pro | Gly | Pro | Thr | Arg | Trp | Thr | Gln | Arg | Ala | Pro | Leu | His | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Ala | Pro | Pro | Pro | Ser | Arg | Val | Glu | Ala | Glu | Val | Leu | Gly | Asp | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | Pro | Trp | Arg | Ala | Pro | Ala | Thr | Ala | Ala | Gly | Thr | Thr | Met | Gln |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Gly | Ser | Ser | Trp | Arg | Ile | Ala | Thr | Arg | Arg | Ala | Arg | Ser | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ala | Arg | Met | Glu | Ser | Ser | Ser | Arg | Pro | Ser | Thr | Pro | Arg | Leu | Glu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Gln | Ser | Arg |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2094:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..153
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502135
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Ile | Ile | Ser | Ser | Pro | Glu | Pro | Asp | Ala | Glu | Arg | Gln | Cys | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Pro | Asp | Lys | Ala | Arg | Ala | Ala | His | Arg | Thr | Arg | Ser | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | Arg | Ala | Ala | Val | Arg | Ser | Leu | Leu | Pro | Arg | Arg | Arg | Leu | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Arg | Pro | Gly | Arg | Pro | Ala | Gly | Pro | Ser | Val | Arg | Arg | Ser | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Arg | Arg | Arg | Pro | Leu | Gly | Leu | Arg | Arg | Arg | Cys | Leu | Gly | Thr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Pro | His | Gly | Glu | Arg | Arg | Gln | Gln | Arg | Gln | Arg | Gly | Arg | Arg | Cys | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Glu | Ala | Pro | Gly | Gly | Ser | Leu | Pro | Glu | Gly | Arg | Gly | Pro | Arg | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | His | Val | Trp | Ser | Arg | Leu | Gln | Gly | His | Arg | His | Gln | Asp | Trp | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Ser | Arg | Gly | Lys | Ala | Asn | Pro | Asp | Arg | Lys | Gly | Gln | Glu | Gly | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys | Gln | Leu | His | Cys | Val | Glu | Gly | Asn |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2095:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..89  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502136  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:  
Met Ala Ser Ala Gly Asn Ser Gly Ser Gly Asp Asp Asp Ala Gly Gly  
1 5 10 15  
Lys Leu Leu Ala Asp Arg Tyr Gln Lys Gly Glu Val Leu Gly Glu Gly  
20 25 30  
Thr Tyr Gly Val Val Phe Lys Ala Ile Asp Thr Lys Thr Gly Asn Thr  
35 40 45  
Val Ala Val Lys Arg Ile Arg Ile Gly Lys Asp Lys Lys Glu Gly Val  
50 55 60  
Asn Phe Thr Ala Leu Arg Glu Ile Lys Leu Leu Lys Glu Leu Lys Asp  
65 70 75 80  
Pro Asn Ile Ile Glu Leu Ile Asp Cys  
85

(2) INFORMATION FOR SEQ ID NO:2096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..522  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

aatccctccc gatcagatcc ctgcacaatg gcactccagg cagcctacga gtacctgcag 60  
caggccgctcg gccatggcgc gtggtcgctcc acgcagacgc tgacgctgct gctcatcgcc 120  
gtaccacccg tactactgct gtagcgctcc ctgcacaaga gcacgtcgct gtccggtagg 180  
ggcaagccgc cgtccctcc ctgcgcgcgc ggcaccctcc ccatcgctgg gcacctacac 240  
cacatcgggc cccagaccca catctcgctc caggagctgg tggccaagta cgggcacaac 300  
gggttcctgt tcctccgcgc cggcgccgtg cccaccctga tcgtgtcgct gccagcgcc 360  
gccgaggccg tgatgcgcac ccacgaccac atcttcgcgt cccggccgtg gtccatggcc 420  
tcccacatcc tccgtacaa cacctgcgac gtggccttct cgccgctcgg cgaatactgg 480  
cagcagacca ggaagctgat gaacacgcac ctgctcagca ac

(2) INFORMATION FOR SEQ ID NO:2097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..174  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

Asn Pro Ser Arg Ser Asp Pro Ser Thr Met Ala Leu Gln Ala Ala Tyr  
1 5 10 15  
Glu Tyr Leu Gln Gln Ala Val Gly His Gly Ala Trp Ser Ser Thr Gln  
20 25 30  
Thr Leu Thr Leu Leu Leu Ile Ala Val Pro Thr Val Leu Leu Leu  
35 40 45

Ala Ser Leu Ala Lys Ser Thr Ser Ser Ser Gly Arg Gly Lys Pro Pro  
50 55 60  
Leu Pro Pro Ser Pro Pro Gly Thr Leu Pro Ile Val Gly His Leu His  
65 70 75 80  
His Ile Gly Pro Gln Thr His Ile Ser Leu Gln Glu Leu Val Ala Lys  
85 90 95  
Tyr Gly His Asn Gly Phe Leu Phe Leu Arg Ala Gly Ala Val Pro Thr  
100 105 110  
Leu Ile Val Ser Ser Pro Ser Ala Ala Glu Ala Val Met Arg Thr His  
115 120 125  
Asp His Ile Phe Ala Ser Arg Pro Trp Ser Met Ala Ser His Ile Leu  
130 135 140  
Arg Tyr Asn Thr Cys Asp Val Ala Phe Ser Pro Leu Gly Glu Tyr Trp  
145 150 155 160  
Gln Gln Thr Arg Lys Leu Met Asn Thr His Leu Leu Ser Asn  
165 170

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1502155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Ala Leu Gln Ala Ala Tyr Glu Tyr Leu Gln Gln Ala Val Gly His  
1 5 10 15  
Gly Ala Trp Ser Ser Thr Gln Thr Leu Thr Leu Leu Leu Ile Ala Val  
20 25 30  
Pro Thr Val Leu Leu Leu Leu Ala Ser Leu Ala Lys Ser Thr Ser Ser  
35 40 45  
Ser Gly Arg Gly Lys Pro Pro Leu Pro Pro Ser Pro Pro Gly Thr Leu  
50 55 60  
Pro Ile Val Gly His Leu His His Ile Gly Pro Gln Thr His Ile Ser  
65 70 75 80  
Leu Gln Glu Leu Val Ala Lys Tyr Gly His Asn Gly Phe Leu Phe Leu  
85 90 95  
Arg Ala Gly Ala Val Pro Thr Leu Ile Val Ser Ser Pro Ser Ala Ala  
100 105 110  
Glu Ala Val Met Arg Thr His Asp His Ile Phe Ala Ser Arg Pro Trp  
115 120 125  
Ser Met Ala Ser His Ile Leu Arg Tyr Asn Thr Cys Asp Val Ala Phe  
130 135 140  
Ser Pro Leu Gly Glu Tyr Trp Gln Gln Thr Arg Lys Leu Met Asn Thr  
145 150 155 160  
His Leu Leu Ser Asn  
165

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..626
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| aaagccgaaa | aggagaaagt | accccggttcc | gtcggccgca | gtgccgcacc | tgcacccacc | 60  |
| gcacgccgag | tcacgcccc  | cctggaccag  | ccaacgtgac | actccaccgc | cgccggcgcc | 120 |
| gcggcagccc | gtagcaaccg | ccaccgctg   | cccattctct | ctctatcccg | cgccgcattg | 180 |
| ccgcgtactt | caaccactcc | tcgtcctacc  | cgccgcgcgc | tccccgcgcg | ggcacttccc | 240 |
| cgtacggcgc | gtaccgccac | gcctacccgc  | cgccgcgcgc | acccccggcc | gcttacggcg | 300 |
| cctactacga | ccgcgcagag | caggccctcc  | cgccgcggga | cgaggtcgcg | accctcttca | 360 |
| tcgctggcct | ccccgcccgc | gccaaagccg  | gcgaagtcta | caacctcttc | cgcgatttcc | 420 |
| ccgatacgt  | ctcctcccac | ctccgcacgg  | gcaaatcctc | tcaggcgat  | gcgtttgctg | 480 |
| tgtttgcaga | tcaacagtct | gcactagctg  | ccttgagtg  | cacaaatgga | atgggtattg | 540 |
| atcttgagaa | aaattgttct | cttcatgtag  | atctcgcaaa | atccaattcc | agatcaaagc | 600 |
| gcttgagatc | agatgatact | tcacct      |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1502166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Lys | Arg | Arg | Lys | Tyr | Pro | Val | Pro | Ser | Ala | Ala | Val | Pro | His |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | His | Pro | Pro | His | Ala | Glu | Ser | Arg | Pro | Pro | Trp | Thr | Ser | Gln | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Thr | Pro | Pro | Pro | Pro | Ala | Pro | Arg | Gln | Pro | Val | Ala | Thr | Ala | Thr |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Cys | Pro | Ser | Pro | Leu | Tyr | Pro | Ala | Pro | His | Gly | Arg | Val | Leu | Gln |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Pro | Leu | Leu | Val | Leu | Pro | Ala | Ala | Ala | Ser | Pro | Ala | Gly | His | Phe | Pro |
|     |     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Val | Arg | Arg | Val | Pro | Pro | Arg | Leu | Pro | Ala | Gly | Ala | Gly | Thr | Pro | Gly |
|     |     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     | 95  |
| Arg | Leu | Arg | Arg | Leu | Leu | Arg | Pro | Arg | Ala | Gly | Pro | Pro | Arg | Arg | Ala |
|     |     |     |     |     |     |     |     | 100 |     |     |     |     | 110 |     |     |
| Gly | Arg | Gly | Pro | His | Pro | Leu | His | Arg | Trp | Pro | Pro | Arg | Arg | Arg | Gln |
|     |     |     |     |     |     |     |     | 115 |     |     |     |     | 125 |     |     |
| Ala | Ala | Arg | Ser | Leu | Gln | Pro | Leu | Pro | Arg | Phe | Pro | Arg | Ile | Arg | Leu |
|     |     |     |     |     |     |     |     | 130 |     |     |     |     | 135 |     | 140 |
| Leu | Pro | Pro | Pro | His | Gly | Gln | Ile | Leu | Ser | Gly | Val | Cys | Val | Cys | Cys |
|     |     |     |     |     |     |     |     | 145 |     |     |     |     | 150 |     | 155 |
| Val | Cys | Arg | Ser | Thr | Val | Cys | Thr | Ser | Cys | Leu | Glu | Cys | His | Lys | Trp |
|     |     |     |     |     |     |     |     | 165 |     |     |     |     | 170 |     | 175 |
| Asn | Gly | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1502167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

Met Ala Ala Tyr Phe Asn His Ser Ser Ser Tyr Pro Pro Pro Pro Pro

1 5 10 15  
Pro Pro Gly Thr Ser Pro Tyr Gly Ala Tyr Arg His Ala Tyr Pro Pro  
20 25 30  
Ala Pro Ala Pro Pro Ala Ala Tyr Gly Ala Tyr Tyr Asp Arg Ala Glu  
35 40 45  
Gln Ala Leu Pro Ala Arg Asp Glu Val Arg Thr Leu Phe Ile Ala Gly  
50 55 60  
Leu Pro Ala Asp Ala Lys Pro Arg Glu Val Tyr Asn Leu Phe Arg Asp  
65 70 75 80  
Phe Pro Gly Tyr Val Ser Ser His Leu Arg Thr Gly Lys Ser Ser Gln  
85 90 95  
Ala Tyr Ala Phe Ala Val Phe Ala Asp Gln Gln Ser Ala Leu Ala Ala  
100 105 110  
Leu Ser Ala Thr Asn Gly Met Val Phe Asp Leu Glu Lys Asn Cys Ser  
115 120 125  
Leu His Val Asp Leu Ala Lys Ser Asn Ser Arg Ser Lys Arg Leu Arg  
130 135 140  
Ser Asp Asp Thr Ser Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| acgggaaagg agtacggagt accggagaca tcgtcaacgc catggccgga ggagggtgcaa  | 60  |
| cgggtgtgcgt gaccggagcc ggcgggttca tcgcctcgtg ggtagtgaag ctccctgctct | 120 |
| cccgcgggta caccgtgcac ggcaccgtcc gccacctcag tgacgagaag acaggccacc   | 180 |
| tgaagcgctt ggagaatgct gccggaaacc ttaggatctt caaggctgac ctgctggact   | 240 |
| acgacgccat ggcagctgcg gtcgtcgggt gccaggggggt tttccatgtg gccactcctg  | 300 |
| tgccttcgga ggacctgact gaccagagc tacaatgct gggtcctgct gttaccggca     | 360 |
| ccacgaatgt gctcaaagct gcctccagcg cgaacgtcca gcgagtgggt gtgggtgtcgt  | 420 |
| ccatggttgc cgtcgagatc agccccaaag attggcctga aggt                    |     |

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Gly Lys Gly Val Arg Ser Thr Gly Asp Ile Val Asn Ala Met Ala Gly  
1 5 10 15  
Gly Gly Ala Thr Val Cys Val Thr Gly Ala Gly Gly Phe Ile Ala Ser  
20 25 30  
Trp Val Val Lys Leu Leu Leu Ser Arg Gly Tyr Thr Val His Gly Thr  
35 40 45  
Val Arg His Leu Ser Asp Glu Lys Thr Gly His Leu Lys Arg Leu Glu  
50 55 60  
Asn Ala Ala Gly Asn Leu Arg Ile Phe Lys Ala Asp Leu Leu Asp Tyr  
65 70 75 80

Asp Ala Met Ala Ala Ala Val Val Gly Cys Gln Gly Val Phe His Val  
85 90 95  
Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu Leu Gln Met  
100 105 110  
Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys Ala Ala Ser  
115 120 125  
Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met Val Ala Val  
130 135 140  
Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly  
145 150

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

Met Ala Gly Gly Gly Ala Thr Val Cys Val Thr Gly Ala Gly Gly Phe  
1 5 10 15  
Ile Ala Ser Trp Val Val Lys Leu Leu Leu Ser Arg Gly Tyr Thr Val  
20 25 30  
His Gly Thr Val Arg His Leu Ser Asp Glu Lys Thr Gly His Leu Lys  
35 40 45  
Arg Leu Glu Asn Ala Ala Gly Asn Leu Arg Ile Phe Lys Ala Asp Leu  
50 55 60  
Leu Asp Tyr Asp Ala Met Ala Ala Ala Val Val Gly Cys Gln Gly Val  
65 70 75 80  
Phe His Val Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu  
85 90 95  
Leu Gln Met Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys  
100 105 110  
Ala Ala Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met  
115 120 125  
Val Ala Val Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..843
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tcttcaccca cattataaag atcctccact tcgcactttc gccgcgcgct ctctccttcc  | 60  |
| cgagcaggag gcggacaagg taagcagcaa tcgcaggaac cctagcgccg ccgcacccgc  | 120 |
| aggaatgggt atcgacctcg tcgccgttg gaggrkaag aagaccaagc gcactgcgcc    | 180 |
| caagtctgac gatgtctacc tcaagctcct cgtcaagctc taccgtttcn ttggtcagga  | 240 |
| ggaccaagag caatttcaac gctgtcattc tcaagaggct tttcatgagt aaaaccaacc  | 300 |
| gaccaccaat ctccatgcgc cgccttgatga agtttatgga aggaaaggag aagaacattg | 360 |
| ctgtcattgt tggcacagtc acagatgaca aaaggatcca ggagggtcca gcaatgaagg  | 420 |
| ttactgccct gaggttcacg gagacagcaa gggccaggat tgtcaatgct ggtggcgagt  | 480 |
| gcctcacatt tgaccagctt gctcttcgtg ctccacttgg cgagaacacg gtcctcttga  | 540 |

```
ggggccccc aa gaatgcccg gaggcagtga ggcactttgg caaggctcct ggagtgccgc 600
acagccacac caagccgtat gtgcgctcca aggggaaggaa gttcgagaag gctcgtggca 660
ggaggaacag ccgtggattc aaggtttaaa acaaattgtg gccctccgtg ttsccatcag 720
catmstgcaa ccgttggtgt tgatcagtcg acagtaatta gtcatcactc tgtaccgaga 780
ttmstaggac aatttggtgt cctggtytga attytsgaag atatttgatg tcgtctccyt 840
att
```

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1502190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

```
Met Ser Thr Ser Ser Ser Ser Ser Ser Ser Thr Val Xaa Leu Val Arg
1 5 10 15
Arg Thr Lys Ser Asn Phe Asn Ala Val Ile Leu Lys Arg Leu Phe Met
 20 25 30
Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys Phe
 35 40 45
Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val Thr
 50 55 60
Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala Leu
 65 70 75 80
Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly Glu
 85 90 95
Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu Asn
 100 105 110
Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg His
 115 120 125
Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr Val
 130 135 140
Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn Ser
 145 150 155 160
Arg Gly Phe Lys Val
 165
```

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1502191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

```
Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys
1 5 10 15
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val
 20 25 30
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala
 35 40 45
Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly
 50 55 60
Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu
```

```

65 70 75 80
Asn Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg
 85 90 95
His Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr
 100 105 110
Val Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn
 115 120 125
Ser Arg Gly Phe Lys Val
 130
```

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1502192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

```

Met Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala
1 5 10 15
Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro
 20 25 30
Ala Met Lys Val Thr Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg
 35 40 45
Ile Val Asn Ala Gly Gly Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu
 50 55 60
Arg Ala Pro Leu Gly Glu Asn Thr Val Leu Leu Arg Gly Pro Lys Asn
65 70 75 80
Ala Arg Glu Ala Val Arg His Phe Gly Lys Ala Pro Gly Val Pro His
 85 90 95
Ser His Thr Lys Pro Tyr Val Arg Ser Lys Gly Arg Lys Phe Glu Lys
 100 105 110
Ala Arg Gly Arg Arg Asn Ser Arg Gly Phe Lys Val
 115 120
```

(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..819

(D) OTHER INFORMATION: / Ceres Seq. ID 1502193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

```

aaatcccccac gaaaacccta aaccctcgct acccgggcggc ggctacaagc tcttcgtcgg 60
ttcagcacca tgargccacc ggctagagga ggacgtggtg ggaggggtgg cagggttcgat 120
ggcgggcgggc tctgtcgcgg cggcggttgc atcgtcccct gcctcaccgt tctcttcctt 180
ctcgcgctcg cgggcttcct cctctggccc gcggaaccgg acatctccct ggcccgctc 240
cacctagcgc acgtctccgt cgtggcacgc cctgccgtcg ccgtcactat atccgccacg 300
ctcaaggttc gcgttcgcaa tctgacctc ttccgcgtcg actacaccgg cctcgacgtc 360
gctatcgggct accgcggtgc ggggcttggc cgggtaacat ccggcgggcg acgggtccgg 420
gcgcgcgctg tctcgtacgt cgacgccaac ctgcagctcg acggcatacg cgtcgtcgag 480
gacgcgatgt acctgctcga ggacctcgcg caaggatccg tgcccttcga caccatcgcc 540
gaggtcgagg gccacctcca ctctcttttc ctcagcatcc cgggtcaaggg gagaatatct 600
tgcgtaaatgc atattaatcc acacaaccaa accatagtac atcaggactg ctatcctgag 660
tgaattgctt atggcggtgga aatgtggaag ggtgtaagct atgttgctt gcgaatggat 720
```



cgtttgattt gtttctaacc ttgtcttcca gtcgtggttg taaaagtaag aaccaactaa 780  
ggggtggttg aatgtaatta agctaatagt tagttcgct

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Xaa | Pro | Pro | Ala | Arg | Gly | Gly | Arg | Gly | Gly | Arg | Gly | Gly | Arg | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Gly | Gly | Gly | Leu | Cys | Arg | Gly | Gly | Arg | Cys | Ile | Val | Pro | Cys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Val | Leu | Phe | Leu | Leu | Ala | Leu | Ala | Gly | Phe | Leu | Leu | Trp | Pro | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Pro | Asp | Ile | Ser | Leu | Ala | Arg | Leu | His | Leu | Ala | His | Val | Ser | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Arg | Pro | Ala | Val | Ala | Val | Thr | Ile | Ser | Ala | Thr | Leu | Lys | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Val | Arg | Asn | Pro | Asp | Leu | Phe | Ala | Leu | Asp | Tyr | Thr | Arg | Leu | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Ala | Ile | Gly | Tyr | Arg | Gly | Ala | Gly | Leu | Gly | Arg | Val | Thr | Ser | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Gly | Arg | Val | Arg | Ala | Arg | Ala | Val | Ser | Tyr | Val | Asp | Ala | Asn | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Leu | Asp | Gly | Ile | Arg | Val | Val | Glu | Asp | Ala | Met | Tyr | Leu | Leu | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Leu | Ala | Gln | Gly | Ser | Val | Pro | Phe | Asp | Thr | Ile | Ala | Glu | Val | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gly | His | Leu | His | Phe | Leu | Phe | Leu | Ser | Ile | Pro | Val | Lys | Gly | Arg | Ile |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Cys | Val | Met | His | Ile | Asn | Pro | His | Asn | Gln | Thr | Ile | Val | His | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Asp | Cys | Tyr | Pro | Glu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ataaatcaac  | cgccggtgaa | gtctagtcgt | ctcgtcgctc | ggtccaccac | ctcagctccg  | 60  |
| ccgcttgccc  | gcttttgctc | tctccctccc | ggctctcggc | ttcttctaca | cgctaccgtc  | 120 |
| tcacagccgt  | aaacgcccct | cccggatccc | gctagttcgc | caccgcccgc | cgcccgcccg  | 180 |
| ccttttcgcct | catcatggcc | gcctcgtcga | ccgccacctc | cgtccacgac | ttcatcgctca | 240 |
| aggatgcgag  | cggcaaagac | gttgacctca | gcacctacaa | ggggaagggt | cttctcattg  | 300 |
| ttaacgtcgc  | atcccagtg  | ggcttaacca | actccaacta | cactgagctg | gcccagctct  | 360 |
| atgagaagta  | caaggaccaa | ggctttgaaa | tcctggcttt | cccatgcaac | cagtttggtg  | 420 |
| ggcaggagcc  | tggtaccaat | aaggagattg | tccagtttgc | ctgcacacgc | ttcaaggctg  | 480 |
| agtacccatc  | ttcgacaagg | ttgatgtc   |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

```
Met Ala Ala Ser Thr Ala Thr Ser Val His Asp Phe Ile Val Lys
1 5 10 15
Asp Ala Ser Gly Lys Asp Val Asp Leu Ser Thr Tyr Lys Gly Lys Val
 20 25 30
Leu Leu Ile Val Asn Val Ala Ser Gln Cys Gly Leu Thr Asn Ser Asn
 35 40 45
Tyr Thr Glu Leu Ala Gln Leu Tyr Glu Lys Tyr Lys Asp Gln Gly Phe
 50 55 60
Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Gly Gln Glu Pro Gly
65 70 75 80
Thr Asn Lys Glu Ile Val Gln Phe Ala Cys Thr Arg Phe Lys Ala Glu
 85 90 95
Tyr Pro Ser Ser Thr Arg Leu Met
100
```

(2) INFORMATION FOR SEQ ID NO:2113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..523
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

```
attggcacgt atgaatgctc agccacatgc gtatgtatac atcacggcca cggttcacgct 60
tcccccttct gcaagcaaac ctaaccaagc ctctgcggtc cttcttcgaa tccaactcct 120
ccccgatccc caaaatcgaa cccaagtcga aaccctaacc tcggccttct cgatgtcggc 180
cgccacaacc gccccaaacc ctgcggtggc caccocgatg gcgccgcctc cgtcgtaccc 240
ggcctcctcc acgatctccg cctocgtggc cgcgtcggtc gaggaagagg acgacctcta 300
tggccgcctc aagtcgctcc agcgccacat ggagttcgtc gagatccagg aggagtacgt 360
taaagacgaa cagaagaacc tcaagcgaga actcctccgt gcgcaggagg aggtcaagcg 420
gatccagttc gtaccgntcg tcatcggccg gtttatggag atggtcgacg gcaacaacgg 480
catcgtgggt tctactacgg gcagcaacta ctatgtgcgg atc
```

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

```
Leu Ala Arg Met Asn Ala Gln Pro His Ala Tyr Val Tyr Ile Thr Ala
1 5 10 15
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Thr | Phe | Thr | Leu | Pro | Pro | Ser | Ala | Ser | Lys | Pro | Asn | Gln | Ala | Ser | Ala |  |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |  |  |
| Ala | Leu | Leu | Arg | Ile | Gln | Leu | Leu | Pro | Asp | Pro | Gln | Asn | Arg | Thr | Gln |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Val | Glu | Thr | Leu | Thr | Ser | Ala | Phe | Ser | Met | Ser | Ala | Ala | Thr | Thr | Ala |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Pro | Thr | Pro | Ala | Val | Ala | Thr | Pro | Met | Ala | Pro | Pro | Pro | Ser | Tyr | Pro |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Ala | Ser | Ser | Thr | Ile | Ser | Ala | Ser | Val | Ala | Ala | Ser | Val | Glu | Glu | Glu |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Asp | Asp | Leu | Tyr | Gly | Arg | Leu | Lys | Ser | Leu | Gln | Arg | His | Met | Glu | Phe |  |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Val | Glu | Ile | Gln | Glu | Glu | Tyr | Val | Lys | Asp | Glu | Gln | Lys | Asn | Leu | Lys |  |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Arg | Glu | Leu | Leu | Arg | Ala | Gln | Glu | Glu | Val | Lys | Arg | Ile | Gln | Ser | Val |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Pro | Xaa | Val | Ile | Gly | Gln | Phe | Met | Glu | Met | Val | Asp | Gly | Asn | Asn | Gly |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Ile | Val | Gly | Ser | Thr | Gly | Ser | Asn | Tyr | Tyr | Val | Arg | Ile |     |     |     |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Asn | Ala | Gln | Pro | His | Ala | Tyr | Val | Tyr | Ile | Thr | Ala | Thr | Phe | Thr |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Leu | Pro | Pro | Ser | Ala | Ser | Lys | Pro | Asn | Gln | Ala | Ser | Ala | Ala | Leu | Leu |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Arg | Ile | Gln | Leu | Leu | Pro | Asp | Pro | Gln | Asn | Arg | Thr | Gln | Val | Glu | Thr |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Leu | Thr | Ser | Ala | Phe | Ser | Met | Ser | Ala | Ala | Thr | Thr | Ala | Pro | Thr | Pro |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Ala | Val | Ala | Thr | Pro | Met | Ala | Pro | Pro | Pro | Ser | Tyr | Pro | Ala | Ser | Ser |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |
| Thr | Ile | Ser | Ala | Ser | Val | Ala | Ala | Ser | Val | Glu | Glu | Glu | Asp | Asp | Leu |  |  |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Tyr | Gly | Arg | Leu | Lys | Ser | Leu | Gln | Arg | His | Met | Glu | Phe | Val | Glu | Ile |  |  |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Gln | Glu | Glu | Tyr | Val | Lys | Asp | Glu | Gln | Lys | Asn | Leu | Lys | Arg | Glu | Leu |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |  |
| Leu | Arg | Ala | Gln | Glu | Glu | Val | Lys | Arg | Ile | Gln | Ser | Val | Pro | Xaa | Val |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |  |
| Ile | Gly | Gln | Phe | Met | Glu | Met | Val | Asp | Gly | Asn | Asn | Gly | Ile | Val | Gly |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |  |
| Ser | Thr | Thr | Gly | Ser | Asn | Tyr | Tyr | Val | Arg | Ile |     |     |     |     |     |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

```
Met Ser Ala Ala Thr Thr Ala Pro Thr Pro Ala Val Ala Thr Pro Met
1 5 10 15
Ala Pro Pro Pro Ser Tyr Pro Ala Ser Ser Thr Ile Ser Ala Ser Val
20 25 30
Ala Ala Ser Val Glu Glu Glu Asp Leu Tyr Gly Arg Leu Lys Ser
35 40 45
Leu Gln Arg His Met Glu Phe Val Glu Ile Gln Glu Glu Tyr Val Lys
50 55 60
Asp Glu Gln Lys Asn Leu Lys Arg Glu Leu Leu Arg Ala Gln Glu Glu
65 70 75 80
Val Lys Arg Ile Gln Ser Val Pro Xaa Val Ile Gly Gln Phe Met Glu
85 90 95
Met Val Asp Gly Asn Asn Gly Ile Val Gly Ser Thr Thr Gly Ser Asn
100 105 110
Tyr Tyr Val Arg Ile
115
```

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1058
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

```
ctcacacgcc ggccgcgcgc caagagccgt ggccccgtcg acgtccgccc gcacaggact 60
ctccgagtgt gggattgagc cgtagttttt tttttttggt ggctcggggc gatatccggt 120
actgtatgag ggttgccaac tactagactt taagatcgct gattcaatgg aggcctccga 180
ggcagcacct gcagcggcgg ccaccgtcat ggaagcagag gatgtgagcg gcgggaaggg 240
cgaatggtag gtgcttgggg agcgggcgct gatggtgccg tacacgcggg agcacgtgcc 300
gcggtaccac gactggatgc aggaccgggc gctgctggag gccaccgcgt cggagcccct 360
ctccctctcg caggagttcg aggtccaccg ytcattggacc ctgcaccctc taaagcacac 420
cttcatagtg ttggataagg agctcataga gggagagttc gtgccgggca acccgcacat 480
tgaagctatg gktggkgatg tgaacatata tatgaatgac tctgatgatg tgcagatcgc 540
ggagatagag attatgatag ctgaacataa gasccgtggg aagggtattg gtcaagaagc 600
aatcttactg atgatggcat ttgcagtaga gaaatatgga attcacacgt tcaggggcaa 660
aattagcgaa tcaaatatgg catcgcttaa gctcttcagg aagttgggct tcaaggatgc 720
ttcatacagt gtggtgttca aggaggtgac tctggaggca cccgtgact cactcccgtt 780
gagatttcct ctgaccattg gagactggtg acgtttgaca tgccccaagt taattccatg 840
cagacgacac aagaagctaa tgctgtttgt ctgtactatc tgacccaaat ttactcgggc 900
tgatattgta tgaaaaaaat gaataaaaca gttgcacagt tgtgattcaa ttgcattaga 960
ccagtcgggt ttttcatgtc actattttga agacccata tcttataaac aaatgtagac 1020
aagttttatc tcataatttt tttatagtat ctcccgtc
```

(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1502225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

Met Glu Ala Ser Glu Ala Ala Pro Ala Ala Ala Thr Val Met Glu  
1 5 10 15  
Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu Gly Glu  
20 25 30  
Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His  
35 40 45  
Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro  
50 55 60  
Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp  
65 70 75 80  
Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly  
85 90 95  
Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val  
100 105 110  
Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu  
115 120 125  
Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly Gln Glu  
130 135 140  
Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His  
145 150 155 160  
Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu  
165 170 175  
Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys  
180 185 190  
Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro  
195 200 205  
Leu Thr Ile Gly Asp Trp  
210

(2) INFORMATION FOR SEQ ID NO:2119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1502226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:

Met Glu Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu  
1 5 10 15  
Gly Glu Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg  
20 25 30  
Tyr His Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser  
35 40 45  
Glu Pro Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr  
50 55 60  
Leu Asp Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile  
65 70 75 80  
Glu Gly Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa  
85 90 95  
Asp Val Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu  
100 105 110  
Ile Glu Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly  
115 120 125  
Gln Glu Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly  
130 135 140  
Ile His Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu

(2) INFORMATION FOR SEQ ID NO:2120:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1502227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

(2) INFORMATION FOR SEQ ID NO:2121:

(A) LENGTH: 640 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..640

(D) OTHER INFORMATION: / Ceres Seq. ID 1502228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

| (X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1 |             |            |            |            |            |  |     |  |
|-----------------------------------------|-------------|------------|------------|------------|------------|--|-----|--|
| acatccatcc                              | atccatccat  | ccatccatcc | ctaaaaatca | aggctacaca | ccaacttact |  | 60  |  |
| ttctaggtct                              | caaattaaat  | ggcctcctcg | tctcctcct  | tgctgctggc | gtcgatggcg |  | 120 |  |
| gtggcggcac                              | tctttgtcgt  | cggtcctgtt | ggcggcgcgc | tcaccttcac | gatcggaag  |  | 180 |  |
| gactccagct                              | ccacccaaact | atccctcgtc | actaacgttg | ccatctccga | gggtgcggtc |  | 240 |  |
| aaggagaagg                              | gcgccttggg  | ctggtcggat | gatctcaagg | agtcgcaagc | caaaaccttc |  | 300 |  |
| accctcgata                              | gcaaggagcc  | gattaagggc | cccatctccg | tccgcttcgc | tgtgaaaggt |  | 360 |  |

```
ggtggctacc gcgtcgtcga tgacgtcatc cctgcgcact tcaagcctgg ctctgtttac 420
cagacaggcg aacaaatctg agtaatggat tctgctgcgt gcagattata ttgatctcta 480
aaataaatgt ttgacagaga ctaattaagc acmcaaacia agcaaggcmc taattcattt 540
cctatgttta ctttgtggta ggcaactgca aaacaatgta ttgtatgcat gttctcctct 600
cacatatgtt gbtgggtgtgc tgtatatata attaattycc
```

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

```
Ile His Pro Ser Ile His Pro Ser Ile Pro Lys Asn Gln Gly Tyr Thr
1 5 10 15
Pro Thr Tyr Phe Leu Gly Leu Lys Leu Asn Gly Leu Leu Val Leu Leu
20 25 30
Leu Ala Ala Gly Val Asp Gly Gly Gly Gly Thr Leu Cys Arg Arg Leu
35 40 45
Val Trp Arg Arg Ala His Leu His Asp Arg Gln Gly Leu Gln Leu His
50 55 60
Gln Thr Ile Pro Arg His
65 70
```

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1502230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

```
Met Ala Ser Ser Ser Ser Ser Leu Leu Leu Ala Ser Met Ala Val Ala
1 5 10 15
Ala Leu Phe Val Val Gly Ser Cys Gly Gly Ala Leu Thr Phe Thr Ile
20 25 30
Gly Lys Asp Ser Ser Ser Thr Lys Leu Ser Leu Val Thr Asn Val Ala
35 40 45
Ile Ser Glu Val Ser Val Lys Glu Lys Gly Ala Leu Asp Trp Ser Asp
50 55 60
Asp Leu Lys Glu Ser Pro Ala Lys Thr Phe Thr Leu Asp Ser Lys Glu
65 70 75 80
Pro Ile Lys Gly Pro Ile Ser Val Arg Phe Ala Val Lys Gly Gly Gly
85 90 95
Tyr Arg Val Val Asp Asp Val Ile Pro Ala Asp Phe Lys Pro Gly Ser
100 105 110
Val Tyr Gln Thr Gly Glu Gln Ile
115 120
```

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Ala | Ala | Leu | Phe | Val | Val | Gly | Ser | Cys | Gly | Gly | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Phe | Thr | Ile | Gly | Lys | Asp | Ser | Ser | Ser | Thr | Lys | Leu | Ser | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Thr | Asn | Val | Ala | Ile | Ser | Glu | Val | Ser | Val | Lys | Glu | Lys | Gly | Ala | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Trp | Ser | Asp | Asp | Leu | Lys | Glu | Ser | Pro | Ala | Lys | Thr | Phe | Thr | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Lys | Glu | Pro | Ile | Lys | Gly | Pro | Ile | Ser | Val | Arg | Phe | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Gly | Gly | Gly | Tyr | Arg | Val | Val | Asp | Asp | Val | Ile | Pro | Ala | Asp | Phe |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Pro | Gly | Ser | Val | Tyr | Gln | Thr | Gly | Glu | Gln | Ile |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1502270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

|             |             |             |             |            |            |     |
|-------------|-------------|-------------|-------------|------------|------------|-----|
| cggggtgcctc | gcttcgcttt  | gsscgcgatt  | cgatccaggc  | tttggttgga | ggcatggcct | 60  |
| cgtcgcccgc  | gagcagctac  | gactgctcct  | tcaaggctcct | gcttatcggg | gattcggccg | 120 |
| tgggcaagag  | cagcctcctc  | gtcagcttcg  | tctcgcgcgc  | tcacatcgac | gacgacatcg | 180 |
| cgccaacccat | aggggtggat  | tttaaaatca  | aattttctcag | tgtgggtggg | aagaaactaa | 240 |
| aactgacaat  | atgggacact  | gccggtcaag  | agagggttcag | gacaattacc | agctcttact | 300 |
| acaggggtgc  | tcattgggatt | atttttagttt | atgacgttac  | aaagagggag | agtttcacaa | 360 |
| atttggtctga | tgtgtggacc  | aaggaaatag  | agttacactc  | aacaaataag | gaatgcacat | 420 |
| aaatgcttgt  | tggaaataaa  | gtggacaagg  | atgaggacag  | aatggtgaca | aaagaagaag | 480 |

g

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ala | Ser | Leu | Arg | Phe | Xaa | Arg | Asp | Ser | Ile | Gln | Ala | Leu | Val | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Met | Ala | Ser | Ser | Pro | Ala | Ser | Ser | Tyr | Asp | Cys | Ser | Phe | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Ile | Gly | Asp | Ser | Ala | Val | Gly | Lys | Ser | Ser | Leu | Leu | Val | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Val | Ser | Ala | Ala | His | Ile | Asp | Asp | Asp | Ile | Ala | Pro | Thr | Ile | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |



Val Asp Phe Lys Ile Lys Phe Leu Ser Val Gly Gly Lys Lys Leu Lys  
65 70 75 80  
Leu Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr  
85 90 95  
Ser Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Leu Val Tyr Asp Val  
100 105 110  
Thr Lys Arg Glu Ser Phe Thr Asn Leu Ala Asp Val Trp Thr Lys Glu  
115 120 125  
Ile Glu Leu His Ser Thr Asn Lys Glu Cys Ile Lys Met Leu Val Gly  
130 135 140  
Asn Lys Val Asp Lys Asp Glu Asp Arg Met Val Thr Lys Glu Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met Ala Ser Ser Pro Ala Ser Ser Tyr Asp Cys Ser Phe Lys Val Leu  
1 5 10 15  
Leu Ile Gly Asp Ser Ala Val Gly Lys Ser Ser Leu Leu Val Ser Phe  
20 25 30  
Val Ser Ala Ala His Ile Asp Asp Ile Ala Pro Thr Ile Gly Val  
35 40 45  
Asp Phe Lys Ile Lys Phe Leu Ser Val Gly Gly Lys Lys Leu Lys Leu  
50 55 60  
Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser  
65 70 75 80  
Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Leu Val Tyr Asp Val Thr  
85 90 95  
Lys Arg Glu Ser Phe Thr Asn Leu Ala Asp Val Trp Thr Lys Glu Ile  
100 105 110  
Glu Leu His Ser Thr Asn Lys Glu Cys Ile Lys Met Leu Val Gly Asn  
115 120 125  
Lys Val Asp Lys Asp Glu Asp Arg Met Val Thr Lys Glu Glu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

gaccgcgcgg caggggaagc ttagcacgga cgggaccagc tgacgaccag gccatggggga 60  
agtacatgcg caagggcaag atgtccgggg aggtggccgt catggagggtc cccggcgggcg 120  
cgctgctkkg tgtccgcacc gctccgcac gctcgcgctg cagagggcgc agaggccgct 180  
cgacaagggg gacgcggatg acgccgccg acagtacctc gagctcagga gccggangna 240  
gaagcctcat aaggaccatc agccgctgcc gctgccgccg cccgcccccg cagccaagag 300  
gggcgcgggg aggaaggccg cctccgccgc cgccgcgccg cacg

(2) INFORMATION FOR SEQ ID NO:2129:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 114 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..114  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Arg | Gly | Arg | Gly | Ser | Leu | Ala | Arg | Thr | Gly | Pro | Ala | Asp | Asp | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Met | Gly | Lys | Tyr | Met | Arg | Lys | Gly | Lys | Met | Ser | Gly | Glu | Val | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Met | Glu | Val | Pro | Gly | Gly | Ala | Leu | Xaa | Xaa | Val | Arg | Thr | Ala | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Ser | Arg | Cys | Arg | Gly | Arg | Arg | Gly | Arg | Ser | Thr | Arg | Gly | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Arg | Met | Thr | Pro | Pro | Asp | Ser | Thr | Ser | Ser | Ser | Gly | Ala | Gly | Xaa | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Ile | Arg | Thr | Ile | Ser | Arg | Cys | Arg | Cys | Arg | Arg | Pro | Pro | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gln | Pro | Arg | Gly | Ala | Pro | Gly | Gly | Arg | Pro | Pro | Pro | Pro | Pro | Pro | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Arg Thr

(2) INFORMATION FOR SEQ ID NO:2130:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 97 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..97  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Tyr | Met | Arg | Lys | Gly | Lys | Met | Ser | Gly | Glu | Val | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Glu | Val | Pro | Gly | Gly | Ala | Leu | Xaa | Xaa | Val | Arg | Thr | Ala | Pro | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ser | Arg | Cys | Arg | Gly | Arg | Arg | Gly | Arg | Ser | Thr | Arg | Gly | Thr | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Met | Thr | Pro | Pro | Asp | Ser | Thr | Ser | Ser | Ser | Gly | Ala | Gly | Xaa | Arg | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Ile | Arg | Thr | Ile | Ser | Arg | Cys | Arg | Cys | Arg | Arg | Pro | Pro | Pro | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Arg | Gly | Ala | Pro | Gly | Gly | Arg | Pro | Pro | Pro | Pro | Pro | Pro | Arg | Arg |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |

Thr

(2) INFORMATION FOR SEQ ID NO:2131:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 93 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1502288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

```
Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala Val Met Glu Val Pro
1 5 10 15
Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro Ala Arg Ser Arg Cys
20 25 30
Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr Arg Met Thr Pro Pro
35 40 45
Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg Ser Leu Ile Arg Thr
50 55 60
Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro Gln Pro Arg Gly Ala
65 70 75 80
Pro Gly Gly Arg Pro Pro Pro Pro Pro Arg Arg Thr
85 90
```

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1502297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

```
ctcacgcaag kntntgcctc cggttaagcc acaaacacac agacaccatg gccttcccag 60
ggactccggc gaggaagatc gtaccaggcg gcttcaccgc agcacgaacc gccgtggcca 120
gcgssgcgct cttagcttcg acctggacgg cgccggcgac tttttctggg gccgtgtggca 180
gctcatcaag gcgaaggccg ccgaggcagc ggcctacctc gctgccctct tcgcggcgct 240
ggcggagaag gcggacgaga tcttcccgcg ggagaccgcg tcggagacgc tccggcagtg 300
gatgcgcgct gccgtcaccg tgggtattcc cggccctagt ggtcgccctc gtgctttgct 360
gctgctggcg ctgctgctgc t
```

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1502298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

```
Ser Arg Lys Xaa Xaa Pro Pro Val Lys Pro Gln Thr His Arg His His
1 5 10 15
Gly Leu Pro Arg Asp Ser Gly Glu Glu Asp Arg Thr Arg Arg Leu His
20 25 30
Arg Ser Thr Asn Arg Arg Gly Gln Xaa Xaa Ala Leu Ser Phe Asp Leu
35 40 45
Asp Gly Ala Gly Asp Phe Phe Trp Gly Leu Trp Gln Leu Ile Lys Ala
50 55 60
Lys Ala Ala Glu Ala Ala Ala Tyr Leu Ala Ala Leu Phe Ala Ala Leu
65 70 75 80
Ala Glu Lys Ala Asp Glu Ile Phe Pro Pro Glu Thr Arg Ser Glu Thr
85 90 95
Leu Arg Gln Trp Met Arg Val Ala Val Thr Val Val Ile Pro Gly Pro
100 105 110
```

Ser Gly Arg Pro Arg Ala Leu Leu Leu Ala Leu Leu Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1502299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ala | Xaa | Xaa | Cys | Leu | Arg | Leu | Ser | His | Lys | His | Thr | Asp | Thr | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Phe | Pro | Gly | Thr | Pro | Ala | Arg | Lys | Ile | Val | Pro | Gly | Gly | Phe | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Arg | Thr | Ala | Val | Ala | Ser | Xaa | Ala | Leu | Leu | Ala | Ser | Thr | Trp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Pro | Ala | Thr | Phe | Ser | Gly | Ala | Cys | Gly | Ser | Ser | Ser | Arg | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Pro | Pro | Arg | Gln | Arg | Pro | Thr | Ser | Leu | Pro | Ser | Ser | Arg | Arg | Trp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Arg | Arg | Arg | Thr | Arg | Ser | Ser | Arg | Arg | Arg | Pro | Ala | Arg | Arg | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Gly | Ser | Gly | Cys | Ala | Ser | Pro | Ser | Pro | Trp |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1502300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Phe | Pro | Gly | Thr | Pro | Ala | Arg | Lys | Ile | Val | Pro | Gly | Gly | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ala | Ala | Arg | Thr | Ala | Val | Ala | Ser | Xaa | Ala | Leu | Leu | Ala | Ser | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Thr | Ala | Pro | Ala | Thr | Phe | Ser | Gly | Ala | Cys | Gly | Ser | Ser | Ser | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Pro | Pro | Arg | Gln | Arg | Pro | Thr | Ser | Leu | Pro | Ser | Ser | Arg | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Trp | Arg | Arg | Arg | Arg | Thr | Arg | Ser | Ser | Arg | Arg | Arg | Pro | Ala | Arg | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Gly | Ser | Gly | Cys | Ala | Ser | Pro | Ser | Pro | Trp |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1502315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cttgtttcaa | atcctgggtc | cgccattggg | ggcgggtgag | ccaccctagt | agaggctaga | 60  |
| ggatgatata | cacggcgatc | gacacgttct | acctgacaga | tgagcagctc | cgtgactcgc | 120 |
| catcacggaa | ggatgggatc | gacgaggcca | ccgagactgc | gcttcssstc | tatggctgtg | 180 |
| acctcatcca | ggagagcggc | atcctcctca | ggctaccaca | agcagtgatg | gccacggcac | 240 |
| aagtattgtt | ccatcgcttt | tactgcaaga | aatcatttgt | tcgatttagt | gcaaagagag | 300 |
| ttgctgctag | ctgtgtttgg | ctggcaggga | agttggagga | gagtcccagg | aatcaaggc  | 360 |
| atattatatt | tgtcttccac | agaatggaat | gtaggagaga | aaacttgcca | attgaatttt | 420 |
| tagatgtttt | ttcaaagaaa | tattcggaac | tgaggc     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1502316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ile | Tyr | Thr | Ala | Ile | Asp | Thr | Phe | Tyr | Leu | Thr | Asp | Glu | Gln | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg | Asp | Ser | Pro | Ser | Arg | Lys | Asp | Gly | Ile | Asp | Glu | Ala | Thr | Glu | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Leu | Xaa | Xaa | Tyr | Gly | Cys | Asp | Leu | Ile | Gln | Glu | Ser | Gly | Ile | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Leu | Arg | Leu | Pro | Gln | Ala | Val | Met | Ala | Thr | Ala | Gln | Val | Leu | Phe | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Phe | Tyr | Cys | Lys | Lys | Ser | Phe | Val | Arg | Phe | Ser | Ala | Lys | Arg | Val |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Ala | Ser | Cys | Val | Trp | Leu | Ala | Gly | Lys | Leu | Glu | Glu | Ser | Pro | Arg |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Lys | Ser | Arg | His | Ile | Ile | Phe | Val | Phe | His | Arg | Met | Glu | Cys | Arg | Arg |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Glu | Asn | Leu | Pro | Ile | Glu | Phe | Leu | Asp | Val | Phe | Ser | Lys | Lys | Tyr | Ser |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Glu | Leu | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Ala | Gln | Val | Leu | Phe | His | Arg | Phe | Tyr | Cys | Lys | Lys | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Val | Arg | Phe | Ser | Ala | Lys | Arg | Val | Ala | Ala | Ser | Cys | Val | Trp | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Ala | Gly | Lys | Leu | Glu | Glu | Ser | Pro | Arg | Lys | Ser | Arg | His | Ile | Ile | Phe |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Val | Phe | His | Arg | Met | Glu | Cys | Arg | Arg | Glu | Asn | Leu | Pro | Ile | Glu | Phe |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |

Leu Asp Val Phe Ser Lys Lys Tyr Ser Glu Leu Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| gatttggctc ttgccatgga ggtgcccgtc tccccaccgc gtgcccacgc cggcctcctc  | 60  |
| tgctgcagct ccaactccgt cgtcctcggc ctccgctccc gctccgccac cgtcccgagc  | 120 |
| cgccgcgcaa ggccactcct tgcccgcaga accgggacag ccggagcgac gaggagaccg  | 180 |
| cggcggassc aagatcatca cggtcgggcg gccgggggnak agcgggcggc ggcgcaacag | 240 |
| gaagcagcag cagcagcagc agcagacggc ggcgaaggaa gaagaagaag aggaggagga  | 300 |
| agatgaggac gacgaggagg agcgtgacgc gacgatcccg gagtggtagc gaaccggatg  | 360 |
| atgcggcggg gtgggcgcgt cgggtggggt tccgctggcg ctgggcgtgg ggttttcttc  | 420 |
| cgggtgttcta ctacctgaag gcgktggcga aggtggacgt gccgacgtgg atccccctt  |     |

(2) INFORMATION FOR SEQ ID NO:2140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Asp Leu Ala Leu Ala Met Glu Val Pro Leu Ser Pro Pro Arg Ala His |  |
| 1 5 10 15                                                       |  |
| Ala Gly Leu Leu Cys Cys Ser Ser Thr Pro Val Val Leu Gly Leu Arg |  |
| 20 25 30                                                        |  |
| Ser Arg Ser Ala Thr Ala Pro Ser Arg Arg Ala Arg Pro Leu Leu Ala |  |
| 35 40 45                                                        |  |
| Arg Arg Thr Gly Thr Ala Gly Ala Thr Arg Arg Pro Arg Arg Xaa Gln |  |
| 50 55 60                                                        |  |
| Asp His His Gly Arg Ala Ala Gly Xaa Xaa Arg Ala Ala Ala Gln Gln |  |
| 65 70 75 80                                                     |  |
| Glu Ala Ala Ala Ala Ala Ala Asp Gly Gly Glu Gly Arg Arg Arg     |  |
| 85 90 95                                                        |  |
| Arg Gly Gly Gly Arg                                             |  |
| 100                                                             |  |

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

Ile Trp Leu Leu Pro Trp Arg Cys Arg Ser Pro His Arg Val Pro Thr

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttaacttgat | tgatttagct | gggagtgagc | gtcttgctaa | aagtggctcc | acaggtgatc | 60  |
| gcttgaagga | aactcaqtca | atcaataaaa | gcttgctggc | tttgagcgat | gtaatcttcg | 120 |

cgatcgcaaa aggagatgac cacgttccgt tcagaaattc aaaacttaca tacctattgc 180  
agccttgcc tggaggtgac tcgaaagctc tcatgtttgt caacatttca ccggagcatc 240  
ctccgttggt gagacgatat ghtcgttgag gtttgcttca aggggtgaatg cttgtgagat 300  
tggaatacca agacgtcaca cataagcccg tcccttcgtt ctaggctgaa ttatgggtga 360  
aggtagctgt agggatcatg ataatgtgat atataatgtg ttggtttgtg ccgcatttgg 420  
ccacaaaggt gatgcccaac aaaattcttg taacttgtac agtgtagggtg atgggtg

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Asn Leu Ile Asp Leu Ala Gly Ser Glu Arg Leu Ala Lys Ser Gly Ser  
1 5 10 15  
Thr Gly Asp Arg Leu Lys Glu Thr Gln Ser Ile Asn Lys Ser Leu Ser  
20 25 30  
Ala Leu Ser Asp Val Ile Phe Ala Ile Ala Lys Gly Asp Asp His Val  
35 40 45  
Pro Phe Arg Asn Ser Lys Leu Thr Tyr Leu Leu Gln Pro Cys Leu Gly  
50 55 60  
Gly Asp Ser Lys Ala Leu Met Phe Val Asn Ile Ser Pro Glu His Pro  
65 70 75 80  
Pro Leu Val Arg Arg Tyr Xaa Arg  
85

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..388
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

attaacagcc aggaagctgg cgtcttgctt gtccttggtc ttttcccacc cggtacccc 60  
cgctgctgcc gccgctttcc ccgtggtntc agagctcgag tcggctagct aggcgcctg 120  
gctaattctc ctgccttcta taagtacaga gatcaggag gcggcacact ccatccactg 180  
accgctcatg gcgaaggtcc acctctacgt cgccgcggcc tgcgccgtcg tcctcgcgct 240  
cgccgccccg gccctgcgcc gcgaccccg catgctgcag gacgtctgcc cggtgacta 300  
cgccctccccg gtgaagctga acgggttcgc gtgcaaggcg aacttttcgg cggacgactt 360  
cttcttcgac gggctgagga acnccggc

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:



Leu Thr Ala Arg Lys Leu Ala Ser Cys Leu Ser Leu Phe Phe Ser His  
1 5 10 15  
Pro Ala Thr Pro Val Val Ala Ala Ala Phe Pro Val Xaa Ser Glu Leu  
20 25 30  
Glu Ser Ala Ser  
35

(2) INFORMATION FOR SEQ ID NO:2147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

Met Ala Lys Val His Leu Tyr Val Ala Ala Cys Ala Val Val Leu  
1 5 10 15  
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp  
20 25 30  
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala  
35 40 45  
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg  
50 55 60  
Asn Xaa Gly  
65

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu  
1 5 10 15  
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe  
20 25 30  
Asp Gly Leu Arg Asn Xaa Gly  
35

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..397
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttaactgttg | ctgtcaagac | actcaaccat | gatgggttgc | aggggcataa | agagtgggtg | 60  |
| gcagaagttg | attttcttgg | aaaccttcag | catccacatc | tagtgaaatt | ggttggtac  | 120 |
| tgcatgaag  | atgaccagag | gttgcttgtg | tatgaattta | tgccccgtgg | aagtttgag  | 180 |

aatcatcttt ttagaaagtc attgcctcta ccatgggcca ttagaatgaa aattgctctt 240  
ggtgctgcga aaggcctcgc ttttcttcat gaagaagctg aaagaccagt aatctatcgg 300  
gacttcaaaa cctccaatat tcttttagat gcggactata acgcaaaact ctctgatattt 360  
ggacttgcta aagatggccc tgagggtgat aaaacac

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

Leu Thr Val Ala Val Lys Thr Leu Asn His Asp Gly Leu Gln Gly His  
1 5 10 15  
Lys Glu Trp Val Ala Glu Val Asp Phe Leu Gly Asn Leu Gln His Pro  
20 25 30  
His Leu Val Lys Leu Val Gly Tyr Cys Ile Glu Asp Asp Gln Arg Leu  
35 40 45  
Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe  
50 55 60  
Arg Lys Ser Leu Pro Leu Pro Trp Ala Ile Arg Met Lys Ile Ala Leu  
65 70 75 80  
Gly Ala Ala Lys Gly Leu Ala Phe Leu His Glu Glu Ala Glu Arg Pro  
85 90 95  
Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn Ile Leu Leu Asp Ala Asp  
100 105 110  
Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Glu  
115 120 125  
Gly Asp Lys Thr  
130

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe Arg Lys Ser Leu Pro  
1 5 10 15  
Leu Pro Trp Ala Ile Arg Met Lys Ile Ala Leu Gly Ala Ala Lys Gly  
20 25 30  
Leu Ala Phe Leu His Glu Glu Ala Glu Arg Pro Val Ile Tyr Arg Asp  
35 40 45  
Phe Lys Thr Ser Asn Ile Leu Leu Asp Ala Asp Tyr Asn Ala Lys Leu  
50 55 60  
Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Glu Gly Asp Lys Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..480
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aagacctagg gttgcttctt tccttttaac ctgcgcgcgc catccgacgc ccatctcctc  | 60  |
| cacccagccg cngccgcgcg ctaaggagaa gaggtgccg ccgtctcctt gccccgatgg   | 120 |
| cgtccgagaa gaagcagtc aacccgatgc gggagatcaa ggtgcagaag ctggtcctca   | 180 |
| acatatccgt agggagagcg ggcaccgcct caccgcgcgc gccaaaggtgc tggagcagct | 240 |
| cagcggccag acccccgtct tctccaaggc gaggtacacg gtgcgctcgt tcggcatccg  | 300 |
| gcgtaacgag aagatcgctt gctacgtcac ggtcaggggc gacaaggcca tgcagctgct  | 360 |
| tgagagcggc ctcaagggtca aggagtacga gctgctcagg aggaacttca gcgacaccgg | 420 |
| ctgcttcggg ttccggcatcc aagagcacat cgaccttggt atcaagtatg atccatcaac | 480 |

(2) INFORMATION FOR SEQ ID NO:2153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 159 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..159
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Pro | Arg | Val | Ala | Ser | Phe | Leu | Leu | Thr | Ser | Arg | Arg | His | Pro | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ile | Ser | Ser | Thr | Gln | Pro | Xaa | Pro | Pro | Pro | Lys | Glu | Lys | Arg | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Arg | Pro | Ser | Pro | Cys | Pro | Asp | Gly | Val | Arg | Glu | Glu | Ala | Val | Gln | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Gly | Asp | Gln | Gly | Ala | Glu | Ala | Gly | Pro | Gln | His | Ile | Arg | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ser | Gly | Asp | Arg | Leu | Thr | Arg | Ala | Ala | Lys | Val | Leu | Glu | Gln | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gly | Gln | Thr | Pro | Val | Phe | Ser | Lys | Ala | Arg | Tyr | Thr | Val | Arg | Ser |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gly | Ile | Arg | Arg | Asn | Glu | Lys | Ile | Ala | Cys | Tyr | Val | Thr | Val | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gly | Asp | Lys | Ala | Met | Gln | Leu | Leu | Glu | Ser | Gly | Leu | Lys | Val | Lys | Glu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Tyr | Glu | Leu | Leu | Arg | Arg | Asn | Phe | Ser | Asp | Thr | Gly | Cys | Phe | Gly | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ile | Gln | Glu | His | Ile | Asp | Leu | Gly | Ile | Lys | Tyr | Asp | Pro | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..121
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val

1 5 10 15  
Gln Lys Leu Val Leu Asn Ile Ser Val Gly Arg Ala Ala Thr Ala Ser  
20 25 30  
Pro Ala Pro Pro Arg Cys Trp Ser Ser Ala Ala Arg Pro Pro Ser  
35 40 45  
Ser Pro Arg Arg Gly Thr Arg Cys Ala Arg Ser Ala Ser Gly Val Thr  
50 55 60  
Arg Arg Ser Pro Ala Thr Ser Arg Ser Gly Ala Thr Arg Pro Cys Ser  
65 70 75 80  
Cys Leu Arg Ala Ala Ser Arg Ser Arg Ser Thr Ser Cys Ser Gly Gly  
85 90 95  
Thr Ser Ala Thr Pro Ala Ala Ser Gly Ser Ala Ser Lys Ser Thr Ser  
100 105 110  
Thr Leu Val Ser Ser Met Ile His Gln  
115 120

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly  
1 5 10 15  
Arg Ala Ala Thr Ala Ser Pro Ala Pro Pro Arg Cys Trp Ser Ser  
20 25 30  
Ala Ala Arg Pro Pro Ser Ser Pro Arg Arg Gly Thr Arg Cys Ala Arg  
35 40 45  
Ser Ala Ser Gly Val Thr Arg Arg Ser Pro Ala Thr Ser Arg Ser Gly  
50 55 60  
Ala Thr Arg Pro Cys Ser Cys Leu Arg Ala Ala Ser Arg Ser Arg Ser  
65 70 75 80  
Thr Ser Cys Ser Gly Gly Thr Ser Ala Thr Pro Ala Ala Ser Gly Ser  
85 90 95  
Ala Ser Lys Ser Thr Ser Thr Leu Val Ser Ser Met Ile His Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

attcagccca tcgctagctc tcgcgtctcg cctgtctcct ctagtagcac aagaccacga 60  
gggattaagc gatgacaacc tctaagctcg ctgtcctcac tctgtttgcc ctgctcggct 120  
ccgtgtcatg ccagtcagggt ggctactact tctacccaac cccgcagcaa ccatctccaa 180  
caccagccc tccttctagt ccgcaactca tggtcggata ctacaaggac aagtgtgccg 240  
cttacgtgga tggtgaagct attgtcaaga agcacgtcaa ggccaccgat gctggcatgc 300  
aggccgggct tgctcgtctc ttattccacg actgcttcgt ccgtggatgc gacggctccg 360  
tcctcctcga caggttcagc aacgacacca gcctgacccc agagaagttc ggcgtgccca 420  
acttccccag cctgcggggc ttcgaggtga tcgacgcggc caaggccgag atcgaggc

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

```
Met Thr Thr Ser Lys Leu Ala Val Leu Thr Leu Phe Ala Leu Leu Gly
1 5 10 15
Ser Val Ser Cys Gln Ser Gly Gly Tyr Tyr Phe Tyr Pro Thr Pro Gln
 20 25 30
Gln Pro Ser Pro Thr Pro Ser Pro Pro Ser Ser Pro Gln Leu Met Val
 35 40 45
Gly Tyr Tyr Lys Asp Lys Cys Ala Ala Tyr Val Asp Val Glu Ala Ile
50 55 60
Val Lys Lys His Val Lys Ala Thr Asp Ala Gly Met Gln Ala Gly Leu
65 70 75 80
Val Arg Leu Leu Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser
 85 90 95
Val Leu Leu Asp Thr Phe Ser Asn Asp Thr Ser Leu Thr Pro Glu Lys
 100 105 110
Phe Gly Val Pro Asn Phe Pro Ser Leu Arg Gly Phe Glu Val Ile Asp
 115 120 125
Ala Ala Lys Ala Glu Ile Glu
130 135
```

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

```
Met Val Gly Tyr Tyr Lys Asp Lys Cys Ala Ala Tyr Val Asp Val Glu
1 5 10 15
Ala Ile Val Lys Lys His Val Lys Ala Thr Asp Ala Gly Met Gln Ala
 20 25 30
Gly Leu Val Arg Leu Leu Phe His Asp Cys Phe Val Arg Gly Cys Asp
 35 40 45
Gly Ser Val Leu Leu Asp Thr Phe Ser Asn Asp Thr Ser Leu Thr Pro
50 55 60
Glu Lys Phe Gly Val Pro Asn Phe Pro Ser Leu Arg Gly Phe Glu Val
65 70 75 80
Ile Asp Ala Ala Lys Ala Glu Ile Glu
 85
```

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aacccttttcg cctccgcgcg cgcctgatag ctccagcgcc ctcgccgtcg gctgcccggc | 60  |
| tgccgtccctc ccgctacgag ctaggcatct ctttcgccga tccagcatgg gtaagacacg | 120 |
| tggtatggga gctgggcgca asstcaagac ccacaggagg aaccagaggt ggtgctgaca  | 180 |
| aagcctacaa gaagagccat cttggcaacg agtggaagaa accctttgct ggatcatctc  | 240 |
| acgcaaaggg gatcgctctc gaaaagatcg gcatcgaggc caagcagcct aactctgcta  | 300 |
| ttcgtaagtg tgctcgtgtt cagctgggtga agaacggtaa gaagattgcc gcctttgtgc | 360 |
| cgaacgacgg ctgcttgaac tacatcgagg aaaacgatga ggtgctgac gcgggggttcg  | 420 |
| gtcgtaaggg ccacgct                                                 |     |

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Pro Phe Arg Leu Arg Arg Arg Leu Ile Ala Pro Ala Pro Ser Pro Ser |  |
| 1 5 10 15                                                       |  |
| Ala Ala Arg Leu Pro Ser Ser Arg Tyr Glu Leu Gly Ile Ser Phe Ala |  |
| 20 25 30                                                        |  |
| Asp Pro Ala Trp Val Arg His Val Trp Glu Leu Gly Ala Xaa Ser     |  |
| 35 40 45                                                        |  |
| Arg Pro Thr Gly Gly Thr Arg Gly Gly Ala Asp Lys Ala Tyr Lys Lys |  |
| 50 55 60                                                        |  |
| Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His |  |
| 65 70 75 80                                                     |  |
| Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro |  |
| 85 90 95                                                        |  |
| Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly |  |
| 100 105 110                                                     |  |
| Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile |  |
| 115 120 125                                                     |  |
| Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His |  |
| 130 135 140                                                     |  |
| Ala                                                             |  |
| 145                                                             |  |

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaagtgaata cagaaacctc cagccccagg ccaattcctc gaccgcatcg ccaccacccc | 60  |
| catctccatg gctacctccg cgacctcacc gcggggaaga aggtggtgct cttcgccgtg | 120 |
| cccgsscggt tcacgcccac ctgaccccag aagcacctcc cggggttcgt ggccaaggcc | 180 |
| ggggagctcc gcgccaaggg ctcgacaccg tggcctgcgt ctccgtcaac gacgccttcg | 240 |

tgatgcgcgc gtggaaggag agtctgggga tcggggacga ggtgctgctc ctgtcggacg 300  
gcaacggcga gctggcgcgc gcatgggctc gagctogacc tctccgacaa gcccgtaggg 360  
tcggcgctccg gtcccgcgcg tacgsgctgc tcgcgaggga cggcgtaggtc aaggtgatca 420  
acctcgagga gggcggcgcg ttcaccaaca gcagcgccga ggacatgctc aacgcgctct 480  
gaactcgca cgccatggtt g

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Val | Asn | Thr | Glu | Thr | Ser | Ser | Pro | Arg | Pro | Ile | Pro | Arg | Pro | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | His | Pro | Pro | His | Leu | His | Gly | Tyr | Leu | Arg | Asp | Leu | Thr | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Lys | Val | Val | Leu | Phe | Ala | Val | Pro | Xaa | Xaa | Phe | Thr | Pro | Thr | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gln | Lys | His | Leu | Pro | Gly | Phe | Val | Ala | Lys | Ala | Gly | Glu | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Lys | Gly | Ser | Thr | Pro | Trp | Pro | Ala | Ser | Pro | Ser | Thr | Thr | Pro | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Tyr | Arg | Asn | Leu | Gln | Pro | Gln | Ala | Asn | Ser | Ser | Thr | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Thr | Pro | Ser | Pro | Trp | Leu | Pro | Pro | Arg | Pro | His | Arg | Gly | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Gly | Ala | Leu | Arg | Arg | Ala | Arg | Xaa | Val | His | Ala | His | Leu | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Pro | Glu | Ala | Pro | Pro | Gly | Val | Arg | Gly | Gln | Gly | Arg | Gly | Ala | Pro | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Gly | Leu | Asp | Thr | Val | Ala | Cys | Val | Ser | Val | Asn | Asp | Ala | Phe | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Arg | Ala | Trp | Lys | Glu | Ser | Leu | Gly | Ile | Gly | Asp | Glu | Val | Leu | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Ser | Asp | Gly | Asn | Gly | Glu | Leu | Ala | Arg | Ala | Trp | Ala | Arg | Ala | Arg |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Leu | Arg | Gln | Ala | Arg | Gly | Val | Gly | Val | Arg | Ser | Arg | Arg | Tyr | Xaa |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Ala | Glu | Asp | Gly | Val | Val | Lys | Val | Ile | Asn | Leu | Glu | Glu | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ala | Phe | Thr | Asn | Ser | Ser | Ala | Glu | Asp | Met | Leu | Asn | Ala | Leu |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

```
Met Ala Thr Ser Ala Thr Ser Pro Arg Gly Arg Arg Trp Cys Ser Ser
1 5 10 15
Pro Cys Pro Xaa Arg Ser Arg Pro Pro Ala Pro Arg Ser Thr Ser Arg
 20 25 30
Gly Ser Trp Pro Arg Pro Gly Ser Ser Ala Pro Arg Ala Arg His Arg
 35 40 45
Gly Leu Arg Leu Arg Gln Arg Arg Leu Arg Asp Ala Arg Val Glu Gly
 50 55 60
Glu Ser Gly Asp Arg Gly Arg Gly Ala Ala Pro Val Gly Arg Gln Arg
65 70 75 80
Arg Ala Gly Ala Arg Met Gly Ser Ser Ser Thr Ser Pro Thr Ser Pro
 85 90 95
Trp Gly Arg Arg Pro Val Pro Pro Leu Xaa Ala Ala Arg Gly Gly Arg
 100 105 110
Arg Gly Gln Gly Asp Gln Pro Arg Gly Gly Arg Arg Val His Gln Gln
 115 120 125
Gln Arg Arg Gly His Ala Gln Arg Ala Leu Asn Ser Arg Arg His Gly
 130 135 140
```

(2) INFORMATION FOR SEQ ID NO:2165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

```
acgatcacac accactccac agcagtagca agaggtag agcaaggcca cacacacaca 60
caccactagg ctaggttagc ctttttagtcg tcgtcgagga gcaagaaggg cgcgcacgca 120
agcaggcaag caagaagaga gccgatcgac cgagagctag cacgcgatgg cgaggtcttc 180
caagatgatg gttgcggcas stctgctggc cctggccctg gccgtgtcga ccgccgaggg 240
gaggaacatc aagacgacga cgacggagaa gaaggacgac gcggtggtgc agccgcagac 300
attcccgccc ttcgaccgcc tcggcgggcg gcgtccccgg cgttcggcgg cctccccggc 360
ggcagcattc ctggcagcag cattccccgg ttcagcat
```

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77



(D) OTHER INFORMATION: / Ceres Seq. ID 1502430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

Met Ala Arg Ser Ser Lys Met Met Val Ala Ala Xaa Leu Leu Ala Leu  
1 5 10 15  
Ala Leu Ala Val Ser Thr Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr  
20 25 30  
Thr Glu Lys Lys Asp Asp Ala Val Val Gln Pro Gln Thr Phe Pro Pro  
35 40 45  
Phe Asp Arg Leu Gly Gly Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro  
50 55 60  
Ala Ala Ala Phe Leu Ala Ala Ala Phe Pro Gly Ser Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

Met Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Leu Ala Val Ser Thr  
1 5 10 15  
Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Glu Lys Lys Asp Asp  
20 25 30  
Ala Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly  
35 40 45  
Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Ala Phe Leu Ala  
50 55 60  
Ala Ala Phe Pro Gly Ser Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:2168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Leu Ala Val Ser Thr Ala  
1 5 10 15  
Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Glu Lys Lys Asp Asp Ala  
20 25 30  
Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly Ala  
35 40 45  
Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Ala Phe Leu Ala Ala  
50 55 60  
Ala Phe Pro Gly Ser Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..362  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502441  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:  
aggttcacgg gaggcgagga ccttgccccc ctgcattcct ccggtcgctg gacctccggc 60  
acaaccagct gacgggcccc atcccggcgg gctgggtgcag gggcagttcc ggctcgctggt 120  
cctgtcctac aaccagctca cgggcccacat ccgcgcgcac gacgcgnanc gagatcaaca 180  
ccgtcgacct ctcccacaac aggctcaccg ggcacccctc ccacctgttt cgccgcccggc 240  
cggcccattc ggcaagggtg acctgtcgtg gaactacctc aacttcgacc tcagcaggct 300  
ggtgttcccg ccggagctca cgtacctgga cctgtcccac aacctcatcc gcggcaccgt 360  
gc

(2) INFORMATION FOR SEQ ID NO:2170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Arg | Glu | Ala | Arg | Thr | Leu | Pro | Pro | Cys | Ile | Pro | Pro | Val | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Pro | Pro | Ala | Gln | Pro | Ala | Asp | Gly | Pro | His | Pro | Gly | Gly | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gly | Gln | Phe | Arg | Ser | Leu | Val | Leu | Ser | Tyr | Asn | Gln | Leu | Thr | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ile | Pro | Arg | Asp | Asp | Ala | Xaa | Arg | Asp | Gln | His | Arg | Arg | Pro | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Gln | Gln | Ala | His | Arg | Arg | Pro | Leu | Pro | Pro | Val | Ser | Pro | Pro | Ala |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Pro | Phe | Gly | Lys | Val | Asp | Leu | Ser | Trp | Asn | Tyr | Leu | Asn | Phe | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Ser | Arg | Leu | Val | Phe | Pro | Pro | Glu | Leu | Thr | Tyr | Leu | Asp | Leu | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Asn | Leu | Ile | Arg | Gly | Thr | Val |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Gly | Arg | Arg | Gly | Pro | Cys | Pro | Pro | Ala | Phe | Leu | Arg | Ser | Leu |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asp | Leu | Arg | His | Asn | Gln | Leu | Thr | Gly | Pro | Ile | Pro | Ala | Gly | Trp | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Gly | Ser | Ser | Gly | Arg | Trp | Ser | Cys | Pro | Thr | Thr | Ser | Ser | Arg | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ser | Arg | Ala | Thr | Thr | Xaa | Xaa | Glu | Ile | Asn | Thr | Val | Asp | Leu | Ser |

50 55 60  
His Asn Arg Leu Thr Gly Asp Pro Ser His Leu Phe Arg Arg Arg Pro  
65 70 75 80  
Ala His Ser Ala Arg Trp Thr Cys Arg Gly Thr Thr Ser Thr Ser Thr  
85 90 95  
Ser Ala Gly Trp Cys Ser Arg Arg Ser Ser Arg Thr Trp Thr Cys Pro  
100 105 110  
Thr Thr Ser Ser Ala Ala Pro Cys  
115 120

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..396
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

aaaaccctag ccaaccctag tccgccgans stntcgcgcg ccgcacctcc tcccgctgcc 60  
ccctcctccg gcggcgccat ccacgcgggc cgtctccgcg cgcaaccacg gggggcgcac 120  
ggcntgagct ctcgggcccc accccgcgcg tgggtgncgt cacctccggc aaggkcgcg 180  
tcggaaagas saccaccacc gccaacctcg ccgcctctct cgcgcgcctc ggccctccag 240  
ccgtcgccgt cgacgcgat gctggcctcc gcaacctcga cctcctgctc ggccctcgaga 300  
accgcgtoca cctcaccgcc gccgacdtcc tcgcgggaga ctgccgactc gaccaggcgc 360  
tcgtccgcca ccgcgcgctt ccacgacctc cacctc

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

Lys Thr Leu Ala Asn Pro Ser Pro Pro Xaa Xaa Ser Arg Ala Ala Pro  
1 5 10 15  
Pro Pro Ala Ala Pro Ser Ser Gly Gly Gly Ile His Ala Gly Arg Leu  
20 25 30  
Arg Ala Gln Pro Arg Gly Ala His Gly Xaa Ser Ser Arg Ala Arg Pro  
35 40 45  
Arg Ala Trp Trp Xaa Ser Pro Pro Ala Arg Xaa Ala Ser Glu Arg Xaa  
50 55 60  
Pro Pro Pro Pro Thr Ser Pro Pro Leu Ser Arg Ala Ser Ala Ser Gln  
65 70 75 80  
Pro Ser Pro Ser Thr Pro Met Leu Ala Ser Ala Thr Ser Thr Ser Cys  
85 90 95  
Ser Ala Ser Arg Thr Ala Ser Thr Ser Pro Pro Pro Xaa Ser Ser Arg  
100 105 110  
Glu Thr Ala Asp Ser Thr Arg Arg Ser Ser Ala Thr Ala Arg Phe His  
115 120 125  
Asp Leu His Leu  
130

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..497
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502479
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| caaaggatgt | caagaaggag | gctccaaagg | aggcccccaa | gccaaaggtg | ggtgaggcac | 60  |
| cagcagaaga | ggaagcacca | aagccaaagc | caaagaatcc | tcttgacttg | ctgccaccaa | 120 |
| gcaagatggt | ccttgatgac | tggagaggc  | tatactcaaa | cacaaagact | aacttcggg  | 180 |
| aggttgccat | caaagggttc | tgggacatgt | acgaccaga  | ggctactctt | tgtggttctg | 240 |
| tgactacaag | tacaatgatg | agaacaccgt | ctcctttgtg | accctgaaca | aggttggttg | 300 |
| attcctgcag | cggatggacc | tgtgccgcaa | gtacgccttt | gggaagatgc | tcgtgatagg | 360 |
| ctctgagcca | cccttcaagc | tgaagggcct | ttggtctctc | cgtggccagg | atgttcccaa | 420 |
| gtttgtaatg | gacgaggtct | atgacatgga | gctctacgag | tgggaccaag | gtggacatct | 480 |
| ctgatgaggc | cagaagg    |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 80 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..80
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502480
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Arg | Met | Ser | Arg | Arg | Arg | Leu | Gln | Arg | Arg | Pro | Pro | Ser | Gln | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Trp | Leu | Arg | His | Gln | Gln | Lys | Arg | Lys | His | Gln | Ser | Gln | Ser | Gln | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Leu | Leu | Thr | Cys | Cys | His | Gln | Ala | Arg | Trp | Ser | Leu | Met | Thr | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Gly | Tyr | Thr | Gln | Thr | Gln | Arg | Leu | Thr | Ser | Gly | Arg | Leu | Pro | Ser |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Lys | Val | Ser | Gly | Thr | Cys | Thr | Thr | Gln | Arg | Leu | Leu | Phe | Val | Val | Leu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |

(2) INFORMATION FOR SEQ ID NO:2176:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..92
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502481
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Asp | Val | Lys | Lys | Glu | Ala | Pro | Lys | Glu | Ala | Pro | Lys | Pro | Lys | Val |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Val | Glu | Ala | Pro | Ala | Glu | Glu | Glu | Ala | Pro | Lys | Pro | Lys | Pro | Lys | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |  |
| Pro | Leu | Asp | Leu | Leu | Pro | Pro | Ser | Lys | Met | Val | Leu | Asp | Asp | Trp | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Leu | Tyr | Ser | Asn | Thr | Lys | Thr | Asn | Phe | Arg | Glu | Val | Ala | Ile | Lys |  |

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| 50                                                              | 55 | 60 |
| Gly Phe Trp Asp Met Tyr Asp Pro Glu Ala Thr Leu Cys Gly Ser Val |    |    |
| 65                                                              | 70 | 75 |
| Thr Thr Ser Thr Met Met Arg Thr Pro Ser Pro Leu                 |    | 80 |
| 85                                                              | 90 |    |

(2) INFORMATION FOR SEQ ID NO:2177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Ser Arg Arg Arg Leu Gln Arg Arg Pro Pro Ser Gln Arg Trp Leu |    |    |
| 1                                                               | 5  | 10 |
| Arg His Gln Gln Lys Arg Lys His Gln Ser Gln Ser Gln Arg Ile Leu |    | 15 |
| 20                                                              | 25 | 30 |
| Leu Thr Cys Cys His Gln Ala Arg Trp Ser Leu Met Thr Gly Arg Gly |    |    |
| 35                                                              | 40 | 45 |
| Tyr Thr Gln Thr Gln Arg Leu Thr Ser Gly Arg Leu Pro Ser Lys Val |    |    |
| 50                                                              | 55 | 60 |
| Ser Gly Thr Cys Thr Thr Gln Arg Leu Leu Phe Val Val Leu         |    |    |
| 65                                                              | 70 | 75 |

(2) INFORMATION FOR SEQ ID NO:2178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2178:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tttgatgttt tcctattaat ttgacttga tccaaaaggc cggatacatc ttttatcaga   | 60  |
| tttggtgaat cccctcccc tctcacgctc caccactgat catggggcta ctcagcatta   | 120 |
| tccgcaagat caagcgcaag gagaaggaga tgcgcacccat catggttggc ctggacaact | 180 |
| caggaagac aaccatcggt ctcaagatca atggggaggga caccagcgctc attagcccaa | 240 |
| cccttggtt caacatcaag accatcaagt accacaaata ctctttgaac atatgggatg   | 300 |
| ttggaggaca gaagacaatc aggtcttact ggagaaacta ctttgagcag actgatggat  | 360 |
| tagtttgggt tggtgatagt tcagacataa ggaggcttga tgattgccgt gctgaactcc  | 420 |
| acaatctctt gaaagaagag agactagttg gagct                             |     |

(2) INFORMATION FOR SEQ ID NO:2179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

|                                                                 |   |    |
|-----------------------------------------------------------------|---|----|
| Met Gly Leu Leu Ser Ile Ile Arg Lys Ile Lys Arg Lys Glu Lys Glu |   |    |
| 1                                                               | 5 | 10 |
|                                                                 |   | 15 |

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile  
20 25 30  
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu  
35 40 45  
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile  
50 55 60  
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr  
65 70 75 80  
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile  
85 90 95  
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu  
100 105 110  
Glu Arg Leu Val Gly Ala  
115

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile  
1 5 10 15  
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu  
20 25 30  
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile  
35 40 45  
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr  
50 55 60  
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile  
65 70 75 80  
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu  
85 90 95  
Glu Arg Leu Val Gly Ala  
100

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile Val Leu Lys Ile  
1 5 10 15  
Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu Gly Phe Asn Ile  
20 25 30  
Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile Trp Asp Val Gly  
35 40 45  
Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr Phe Glu Gln Thr  
50 55 60  
Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile Arg Arg Leu Asp

(2) INFORMATION FOR SEQ ID NO:2182:

(A) LENGTH: 462 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1502514

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| aacctcctaa  | tcgaaaaaaa | gctctctgct | tccctctcca | ttttttcatc  | tcattcggcg | 60  |
| ccgcggcacc  | ccctgctcgt | cactcgcgat | ggcccggatc | aaggtgcacg  | agctgcgcgg | 120 |
| aaagagcaag  | acggatctgc | aagcgcmsst | caaggagctt | aaatcggagc  | tctccctcct | 180 |
| acgcgtcgc   | awggtcaccg | gcggggctcc | caacaagctc | tccaaaaatca | agattgtgcg | 240 |
| cacctccatc  | gctcgcgtgc | tcaccgttat | ctcgcagaag | cagaagtcgg  | cgctgcgtga | 300 |
| ggcgatacaag | aagaagaagc | ttctcccgtc | cgatctccgc | cccaagaaga  | ccgcgcgcct | 360 |
| tcgcaggcgc  | ctcaccaagc | accagctctc | cttgaagacc | gagagggaaa  | agaagcgtga | 420 |
| gaagtatttt  | cccatgcgga | agtacgctat | caaggcctag | at          |            |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2183:

(2) INFORMATION FOR SEQ ID NO:2184:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1502516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

```
Met Ala Arg Ile Lys Val His Glu Leu Arg Gly Lys Ser Lys Thr Asp
1 5 10 15
Leu Gln Ala Xaa Xaa Lys Glu Leu Lys Ser Glu Leu Ser Leu Leu Arg
20 25 30
Val Ala Xaa Val Thr Gly Gly Ala Pro Asn Lys Leu Ser Lys Ile Lys
35 40 45
Ile Val Arg Thr Ser Ile Ala Arg Val Leu Thr Val Ile Ser Gln Lys
50 55 60
Gln Lys Ser Ala Leu Arg Glu Ala Tyr Lys Lys Lys Lys Leu Leu Pro
65 70 75 80
Leu Asp Leu Arg Pro Lys Lys Thr Arg Ala Ile Arg Arg Arg Leu Thr
85 90 95
Lys His Gln Leu Ser Leu Lys Thr Glu Arg Glu Lys Lys Arg Glu Lys
100 105 110
Tyr Phe Pro Met Arg Lys Tyr Ala Ile Lys Ala
115 120
```

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1502517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

```
tccattgcag tgcaggaatc ggaaggactg gtacttacat cacaatccat actacaattg 60
agcgaattct tcttgagat aaaagctctt acgatcttgc caaaactgta aagaatttta 120
gatcccaacg acctgggatg gtccaaacag aggaacaata caagttctgc tacagggcaa 180
ttgctgtacg agctgaaaga cctgctaaat tcagatcatt gaggtgggtc acatgagacg 240
gacagcaacg ckkctagcat ttattacgtt tttttagaca tttctatgtg aaggaacact 300
tacccttttag aggagtgaat tagtcaatct cagttctctt taaactatgt ttgttctagt 360
caaaatctat gtaataaaaa atctatcata tgtgaagcta tgctatgttt ttgactaatc 420
gttgctatta ctaccgt
```

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1502518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

```
His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Tyr Ile Thr Ile His
1 5 10 15
Thr Thr Ile Glu Arg Ile Leu Leu Gly Asp Lys Ser Ser Tyr Asp Leu
20 25 30
Ala Lys Thr Val Lys Asn Phe Arg Ser Gln Arg Pro Gly Met Val Gln
35 40 45
Thr Glu Glu Gln Tyr Lys Phe Cys Tyr Arg Ala Ile Ala Val Arg Ala
```



50 55 60  
Glu Arg Pro Ala Lys Phe Arg Ser Leu Arg Trp Val Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| attctcccag ccacaaatcg atcggaacg cagccccctt tctcttcgcc ttttcgcgtc    | 60  |
| gtccagatct cagtcgttct tcgctccatg agctaggaat ccgagggtgc ctctaggcta   | 120 |
| agcgaagtgt gccggcgccg gctaggatgg ggttgatata cgggatgatg atgggggtca   | 180 |
| ttgttggcgt cgcacatcatg ccggtctggag ccgcgtcatg cgccgacgca gcacgaagcg | 240 |
| catcgccaag gctgcggata tcaaggtgct tgggtctctc agcagggacg acctcaggaa   | 300 |
| gctgtgcgnt gataacttcc cggagtggat atccttcccg cagtttgagc aggttaaatg   | 360 |
| gttgaacaag catctgagca aactttggcc ttttggtgta gaagctgcaa cagtagtggt   | 420 |
| taagggaatc cgttgaacca ctgctagatg attaccggcc tccaggaat               |     |

(2) INFORMATION FOR SEQ ID NO:2188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Gly Leu Ile Ser Gly Met Met Met Gly Val Ile Val Gly Val Ala |  |
| 1 5 10 15                                                       |  |
| Ser Trp Pro Ala Gly Ala Ala Ser Cys Ala Asp Ala Ala Arg Ser Ala |  |
| 20 25 30                                                        |  |
| Ser Pro Arg Leu Arg Ile Ser Arg Cys Leu Gly Leu Ser Ala Gly Thr |  |
| 35 40 45                                                        |  |
| Thr Ser Gly Ser Cys Ala Xaa Ile Thr Ser Arg Ser Gly Tyr Pro Ser |  |
| 50 55 60                                                        |  |
| Arg Ser Leu Ser Arg Leu Asn Gly                                 |  |
| 65 70                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Gly Trp Ser Arg Val Met Arg Arg Arg Ser Thr Lys Arg Ile |  |
| 1 5 10 15                                                       |  |
| Ala Lys Ala Ala Asp Ile Lys Val Leu Gly Ser Leu Ser Arg Asp Asp |  |
| 20 25 30                                                        |  |

Leu Arg Lys Leu Cys Xaa Asp Asn Phe Pro Glu Trp Ile Ser Phe Pro  
35 40 45  
Gln Phe Glu Gln Val Lys Trp Leu Asn Lys His Leu Ser Lys Leu Trp  
50 55 60  
Pro Phe Val Val Glu Ala Ala Thr Val Val Val Lys Gly Ile Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1502522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

Met Arg Arg Arg Ser Thr Lys Arg Ile Ala Lys Ala Ala Asp Ile Lys  
1 5 10 15  
Val Leu Gly Ser Leu Ser Arg Asp Asp Leu Arg Lys Leu Cys Xaa Asp  
20 25 30  
Asn Phe Pro Glu Trp Ile Ser Phe Pro Gln Phe Glu Gln Val Lys Trp  
35 40 45  
Leu Asn Lys His Leu Ser Lys Leu Trp Pro Phe Val Val Glu Ala Ala  
50 55 60  
Thr Val Val Val Lys Gly Ile Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1502527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atagacagga agattgaatt tccaaatcct aacgaggatt cacgtttcga tatcttgaag  | 60  |
| atccattcaa gaaaaatgaa cttgatgcgt ggcattgatc tgaaaaagat cgcggaaaag  | 120 |
| atgaatgggg cctcaggagc tgagctcaag gccgtctgca cagaggctgg aatgtttgct  | 180 |
| cttcgtgaga gaagggtgca cgttacccag gaggacttcg agatggcagt ggccaagggtg | 240 |
| atgaagaaag acacggagaa gaacatgtcc ctgcgcaass tctggaagtg aggctcgtgc  | 300 |
| ccacctttca cggcctcccc gaagctagtgc gcagtgcctt catatccata tcttttacca | 360 |
| aagcagtgga atggtgtaac ggcattgctt ggacaatggt atctcaagtt gcgccgcgc   |     |

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1502528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe  
1 5 10 15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Ile | Leu | Lys | Ile | His | Ser | Arg | Lys | Met | Asn | Leu | Met | Arg | Gly | Ile |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |
| Asp | Leu | Lys | Lys | Ile | Ala | Glu | Lys | Met | Asn | Gly | Ala | Ser | Gly | Ala | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Lys | Ala | Val | Cys | Thr | Glu | Ala | Gly | Met | Phe | Ala | Leu | Arg | Glu | Arg |  |
|     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Arg | Val | His | Val | Thr | Gln | Glu | Asp | Phe | Glu | Met | Ala | Val | Ala | Lys | Val |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Met | Lys | Lys | Asp | Thr | Glu | Lys | Asn | Met | Ser | Leu | Arg | Xaa | Xaa | Trp | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |

(2) INFORMATION FOR SEQ ID NO:2193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Leu | Met | Arg | Gly | Ile | Asp | Leu | Lys | Lys | Ile | Ala | Glu | Lys | Met |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asn | Gly | Ala | Ser | Gly | Ala | Glu | Leu | Lys | Ala | Val | Cys | Thr | Glu | Ala | Gly |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Met | Phe | Ala | Leu | Arg | Glu | Arg | Arg | Val | His | Val | Thr | Gln | Glu | Asp | Phe |  |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |  |
| Glu | Met | Ala | Val | Ala | Lys | Val | Met | Lys | Lys | Asp | Thr | Glu | Lys | Asn | Met |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Leu | Arg | Xaa | Xaa | Trp | Lys |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1502530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Gly | Ile | Asp | Leu | Lys | Lys | Ile | Ala | Glu | Lys | Met | Asn | Gly | Ala |  |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Gly | Ala | Glu | Leu | Lys | Ala | Val | Cys | Thr | Glu | Ala | Gly | Met | Phe | Ala |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Leu | Arg | Glu | Arg | Arg | Val | His | Val | Thr | Gln | Glu | Asp | Phe | Glu | Met | Ala |  |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |  |
| Val | Ala | Lys | Val | Met | Lys | Lys | Asp | Thr | Glu | Lys | Asn | Met | Ser | Leu | Arg |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Xaa | Xaa | Trp | Lys |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..511  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502542  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| gcaccgcggc  | cacagcctcg  | cgtcgtcgcc  | ccacagccac | gcgagcssnc | gccgatccgc | 60  |
| gagcgcagat  | cgcggaagcca | ggcggcgcnag | agggagctcg | aggcggcgga | ggaaggcggt | 120 |
| cgcacagtcg  | ctgatttccc  | tggggaagag  | atggggctct | cctttggtaa | gctgttcagc | 180 |
| cgctcttcg   | ccaagaagga  | gatgaggatt  | ctcatggtcg | ggctcgatgc | cgccggtaa  | 240 |
| accaccatcc  | tctacaagct  | caagctcggc  | gagatcgta  | ccaccatccc | cactatcgga | 300 |
| ttcaatgttg  | aaactgttga  | gtataagaac  | attagcttca | ctgtttggga | tgttggtggc | 360 |
| caggacaaga  | tcaggccctt  | gtggaggcac  | tactttcaga | acacacaggg | acttattttt | 420 |
| gtttagagaca | gcaacgacag  | ggaacgtgtt  | gttgaggcta | gagatgagct | ccacaggatg | 480 |
| ctgaatgagg  | atgagctgcg  | tgacgtgtg   | c          |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2196:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 170 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..170  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Arg | Pro | Gln | Pro | Arg | Val | Val | Ala | Pro | Gln | Pro | Arg | Glu | Xaa |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Xaa | Pro | Ile | Arg | Glu | Arg | Arg | Ser | Arg | Ser | Gln | Ala | Ala | Xaa | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Ala | Ala | Glu | Glu | Gly | Val | Arg | Thr | Val | Ala | Asp | Phe | Pro | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Met | Gly | Leu | Ser | Phe | Gly | Lys | Leu | Phe | Ser | Arg | Leu | Phe | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Lys | Glu | Met | Arg | Ile | Leu | Met | Val | Gly | Leu | Asp | Ala | Ala | Gly | Lys |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Thr | Ile | Leu | Tyr | Lys | Leu | Lys | Leu | Gly | Glu | Ile | Val | Thr | Thr | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Thr | Ile | Gly | Phe | Asn | Val | Glu | Thr | Val | Glu | Tyr | Lys | Asn | Ile | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Thr | Val | Trp | Asp | Val | Gly | Gly | Gln | Asp | Lys | Ile | Arg | Pro | Leu | Trp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | His | Tyr | Phe | Gln | Asn | Thr | Gln | Gly | Leu | Ile | Phe | Val | Val | Asp | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asn | Asp | Arg | Glu | Arg | Val | Val | Glu | Ala | Arg | Asp | Glu | Leu | His | Arg | Met |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Leu | Asn | Glu | Asp | Glu | Leu | Arg | Asp | Ala | Val |     |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2197:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 120 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys  
1 5 10 15  
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
20 25 30  
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
35 40 45  
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr  
50 55 60  
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His  
65 70 75 80  
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp  
85 90 95  
Arg Glu Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn  
100 105 110  
Glu Asp Glu Leu Arg Asp Ala Val  
115 120

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:

Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile  
1 5 10 15  
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile  
20 25 30  
Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val  
35 40 45  
Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr  
50 55 60  
Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg  
65 70 75 80  
Glu Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu  
85 90 95  
Asp Glu Leu Arg Asp Ala Val  
100

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..488
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:

aggaggagcg cgccatggag cggggggcatc ctgccgctgc tccgcccgcg cacgctgggtg 60  
cagacgttcg gccagcgcaa ccacgtgtgc ctgcaggacg gctccatcac cgtcccgccc 120  
tacgccgacc cgggcaagat gcaggcgcac ctcatcagcc ccggcacgcc gcgctccatc 180  
ttcgtctact tcaggggcct cttctacgac atgggcaacg acccgaggg cggtactac 240  
gccaggggcc tcgcgcgtcg gtgtgggaga acttcaagga caaccgcgtg ttgcacatct 300  
cgacggagca cccgtcgacg tactacgagg acatgcagcg cgccatcttc tgccgtgtgcc 360

cgctgggggtg ggcgccttg agccccggc tggaggaggc ggtggtgttc ggggtgcatcc 420  
ccgtcatcat cgccgacgac atcgtgtgc cgttcgcgga cgccatcccc tgggaggaca 480  
tcagcgtg

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Ser | Ala | Pro | Trp | Ser | Gly | Gly | Ile | Leu | Pro | Leu | Leu | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Thr | Leu | Val | Gln | Thr | Phe | Gly | Gln | Arg | Asn | His | Val | Cys | Leu | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Gly | Ser | Ile | Thr | Val | Pro | Pro | Tyr | Ala | Asp | Pro | Gly | Lys | Met | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | His | Leu | Ile | Ser | Pro | Gly | Thr | Pro | Arg | Ser | Ile | Phe | Val | Tyr | Phe |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Gly | Leu | Phe | Tyr | Asp | Met | Gly | Asn | Asp | Pro | Glu | Gly | Gly | Tyr | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Arg | Gly | Leu | Ala | Arg | Arg | Cys | Gly | Arg | Thr | Ser | Arg | Thr | Thr | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |
| Cys | Ser | Thr | Ser | Arg | Arg | Ser | Thr | Arg | Arg | Arg | Thr | Thr | Arg | Thr | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ala | Pro | Ser | Ser | Ala | Cys | Ala | Arg | Trp | Gly | Gly | Arg | Pro | Gly | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Gly | Trp | Trp | Arg | Arg | Trp | Cys | Ser | Gly | Ala | Ser | Pro | Ser | Ser | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Pro | Thr | Thr | Ser | Cys | Cys | Arg | Ser | Arg | Thr | Pro | Ser | Pro | Gly | Arg | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Ala | Arg | His | Gly | Ala | Gly | Ala | Ser | Cys | Arg | Cys | Ser | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Trp | Cys | Arg | Arg | Ser | Ala | Ser | Ala | Thr | Thr | Cys | Ala | Cys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Pro | Ser | Pro | Ser | Arg | Pro | Thr | Pro | Thr | Arg | Ala | Arg | Cys | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Thr | Ser | Ser | Ala | Pro | Ala | Arg | Arg | Ala | Pro | Ser | Ser | Ser | Thr | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Gly | Ala | Ser | Ser | Thr | Thr | Trp | Ala | Thr | Thr | Pro | Arg | Ala | Ala | Thr | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Gly | Ala | Ser | Arg | Val | Gly | Val | Gly | Glu | Leu | Gln | Gly | Gln | Pro | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Val Arg His Leu Asp Gly Ala Pro Val Asp Val Leu Arg Gly His Ala  
100 105 110  
Ala Arg His Leu Leu Pro Val Pro Ala Gly Val Gly Ala Leu Glu Pro  
115 120 125  
Pro Ala Gly Gly Gly Gly Gly Val Arg Val His Pro Arg His His Arg  
130 135 140  
Arg Arg His Arg Ala Ala Val Arg Gly Arg His Pro Leu Gly Gly His  
145 150 155 160  
Gln Arg

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

Glu Glu Arg Ala Met Glu Arg Gly His Pro Ala Ala Ala Pro Pro Arg  
1 5 10 15  
His Ala Gly Ala Asp Val Arg Pro Ala Gln Pro Arg Val Pro Ala Gly  
20 25 30  
Arg Leu His His Arg Pro Ala Leu Arg Arg Pro Gly Gln Asp Ala Gly  
35 40 45  
Ala Pro His Gln Pro Arg His Ala Ala Leu His Leu Arg Leu Leu Gln  
50 55 60  
Gly Pro Leu Leu Arg His Gly Gln Arg Pro Arg Gly Arg Leu Leu Arg  
65 70 75 80  
Gln Gly Pro Arg Ala Ser Val Trp Glu Asn Phe Lys Asp Asn Pro Leu  
85 90 95  
Phe Asp Ile Ser Thr Glu His Pro Ser Thr Tyr Tyr Glu Asp Met Gln  
100 105 110  
Arg Ala Ile Phe Cys Leu Cys Pro Leu Gly Trp Ala Pro Trp Ser Pro  
115 120 125  
Arg Leu Val Glu Ala Val Val Phe Gly Cys Ile Pro Val Ile Ile Ala  
130 135 140  
Asp Asp Ile Val Leu Pro Phe Ala Asp Ala Ile Pro Trp Glu Asp Ile  
145 150 155 160  
Ser Val

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1502613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctctccgtct | cgggtotcca | gtctcgtcgc | ttccacaagt | ccacaaccgt | accagcacca | 60  |
| ccgcgccatg | gcgtcctccg | ccgatccmga | tgccgccacg | ccaccatccg | cncgcagcc  | 120 |
| ggagcccgcg | cggaaggcag | tccgcgtggt | ggtgaagggg | cgcgtcacgg | gggtgggggt | 180 |
| ccgcgactgg | actgcgtcac | ggccgagtcg | ctcggtctgc | cggctgggtc | cgcaaccgcc | 240 |
| gtgacggcag | tgtggaggcc | ctcctctccg | gagaccccg  | gaagatcgaa | gacatgataa | 300 |

```
ccccgccgct ccccgctcggc cccccagccg ccaccgtcac cgccgctcgtc ccgtccackg 360
ccgagcccggt ggtatccgtc caccggcttc ggagatcaag ttcaccgtct gaccccccg 420
tcccgcgaca ggttcgcgtc tcgcccgcgcg ggtcttgaac ggtctattcg tgcactacta 480
ctgcgaatct gcg
```

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

```
Leu Ser Val Ser Gly Leu Gln Ser Arg Cys Phe His Lys Ser Thr Thr
1 5 10 15
Val Pro Ala Pro Pro Arg His Gly Val Leu Arg Arg Ser Xaa Cys Arg
 20 25 30
His Ala Thr Ile Arg Xaa Ala Ala Gly Ala Arg Thr Glu Gly Ser Pro
 35 40 45
Arg Gly Gly Glu Gly Ala Arg His Gly Gly Gly Val Pro Arg Leu Asp
 50 55 60
Cys Val Thr Ala Glu Ser Leu Gly Ser Pro Ala Gly Ser Ala Thr Ala
 65 70 75 80
Val Thr Ala Val Trp Arg Pro Ser Ser Pro Glu Thr Pro Arg Arg Ser
 85 90 95
Lys Thr
```

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

```
Ser Pro Ser Pro Val Ser Ser Leu Ala Ala Ser Thr Ser Pro Gln Pro
1 5 10 15
Tyr Gln His His Arg Ala Met Ala Ser Ser Ala Asp Xaa Asp Ala Ala
 20 25 30
Thr Pro Pro Ser Xaa Pro Gln Pro Glu Pro Ala Arg Lys Ala Val Arg
 35 40 45
Val Val Val Lys Gly Arg Val Thr Gly Val Gly Phe Arg Asp Trp Thr
 50 55 60
Ala Ser Arg Pro Ser Arg Ser Ala Arg Arg Leu Gly Pro Gln Pro Pro
 65 70 75 80
```

(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1502616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

Met Ala Ser Ser Ala Asp Xaa Asp Ala Ala Thr Pro Pro Ser Xaa Pro  
1 5 10 15  
Gln Pro Glu Pro Ala Arg Lys Ala Val Arg Val Val Val Lys Gly Arg  
20 25 30  
Val Thr Gly Val Gly Phe Arg Asp Trp Thr Ala Ser Arg Pro Ser Arg  
35 40 45  
Ser Ala Arg Arg Leu Gly Pro Gln Pro Pro  
50 55

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1502621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

aagatcaagc caccaccacc gccagcaaga gcagagaggc gagaccgcga gagtgtacgt 60  
gccaccagca gcagcagcaa tggccgccgc cgccaccacc tcctcatcct cccacctgct 120  
cctcctctcc cgccagcagg sscctcccta cgatgccgcc tctccttctt cggccagccc 180  
agaaggcccg gc

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1502622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

Lys Ile Lys Pro Pro Pro Pro Pro Ala Arg Ala Glu Arg Arg Asp Arg  
1 5 10 15  
Glu Ser Val Arg Ala Thr Ser Ser Ser Ser Asn Gly Arg Arg Arg His  
20 25 30  
His Leu Leu Ile Leu Pro Pro Ala Pro Pro Leu Pro Pro Ala Xaa Xaa  
35 40 45  
Ser Leu Arg Cys Arg Leu Ser Phe Leu Gly Gln Pro Arg Arg Pro Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

Arg Ser Ser His His Arg Gln Gln Glu Gln Arg Gly Glu Thr Ala  
1 5 10 15  
Arg Val Tyr Val Pro Pro Ala Ala Ala Ala Met Ala Ala Ala Ala Thr  
20 25 30  
Thr Ser Ser Ser Ser His Leu Leu Leu Leu Ser Arg Gln Gln Xaa Pro  
35 40 45  
Pro Tyr Asp Ala Ala Ser Pro Ser Ser Ala Ser Pro Glu Gly Pro  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Asp Gln Ala Thr Thr Thr Ala Ser Lys Ser Arg Glu Ala Arg Pro Arg  
1 5 10 15  
Glu Cys Thr Cys His Gln Gln Gln Gln Gln Trp Pro Pro Pro Pro Pro  
20 25 30  
Pro Pro His Pro Pro Thr Cys Ser Ser Ser Pro Ala Ser Arg Xaa Leu  
35 40 45  
Pro Thr Met Pro Pro Leu Leu Pro Arg Pro Ala Gln Lys Ala Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1502635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| agtgttggtgt cctagcgccg ccgcccgcctt gcgtgactga aagctcgctcg          | 60  |
| gcttccgctcc acgcgagaag cgagagcatg gacaccagc tgaagcttgc tgttggtggtg | 120 |
| aaggtgatgg gcaggaccgg ctccaggggt caggbgacct aggtcagagt taagttcttg  | 180 |
| gatgaccaga accggctcat catgaggaat gtcaaggggc ccgtccgcga gggtgacatc  | 240 |
| ctcaccctgc tcgagtccga gatggatgcc akgaggctgc gctgaagccc tagcgttctt  | 300 |
| ggtcacatccaa gaacttaact ctgacct                                    |     |

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1502636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

Met Asp Thr Gln Val Lys Leu Ala Val Val Val Lys Val Met Gly Arg

1 5 10 15  
Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys Phe Leu Asp  
20 25 30  
Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro Val Arg Glu  
35 40 45  
Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala Xaa Arg Leu  
50 55 60  
Arg  
65

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

Met Gly Arg Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys  
1 5 10 15  
Phe Leu Asp Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro  
20 25 30  
Val Arg Glu Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala  
35 40 45  
Xaa Arg Leu Arg  
50

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

Met Ser Arg Gly Pro Ser Ala Arg Val Thr Ser Ser Pro Cys Ser Ser  
1 5 10 15  
Pro Arg Trp Met Pro Xaa Gly Cys Ala Glu Ala Leu Ala Phe Leu Val  
20 25 30  
Ile Gln Glu Leu Asn Ser Asp  
35

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

gctgttgcaa attacgttcc ctctagtctc tactctagcc ccctctctct ctcacacaca 60  
cacacacccc tatcacttgg actgtgctag tataggtagc cgccgtgtaa tggagcagga 120

```
gctcagcctt gagctcacc ctttccacc ctcggtctcg ccggaaccgc cgggctattt 180
cgtctgcacg tactgcgacc gcaagttctt cacctcgag gctctcggtg gccaccagaa 240
cgcgacacaag tacgagcgcm sctgggcaa ggcgcggcg agatcgccac cgccctgcgc 300
gcgcacgggg cgcccgccac cgccacgggc gtccaggacg cgccgctatg ggctctcgcg 360
atgtccccgc cagccccaa gacgggtag cgggtgccgac aagagcgcaa caaggatgga 420
taagcacaag gcgcctgctg atgatgccgc tccc
```

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1502644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

```
Leu Leu Gln Ile Thr Phe Pro Leu Val Ser Thr Leu Ala Pro Ser Leu
1 5 10 15
Ser His Thr His Thr His Pro Tyr His Leu Asp Cys Ala Ser Ile Gly
20 25 30
Ser Arg Arg Val Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe
35 40 45
His Pro Ser Val Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr
50 55 60
Cys Asp Arg Lys Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn
65 70 75 80
Ala His Lys Tyr Glu Arg Xaa Leu Ala Lys Arg Arg Arg Arg Ser Pro
85 90 95
Pro Pro Cys Ala Arg Thr Gly Arg Pro Pro Pro Pro Arg Ala Ser Arg
100 105 110
Thr Arg Arg Tyr Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr
115 120 125
Gly Ser Gly Ala Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala
130 135 140
Pro Ala Asp Asp Ala Ala Pro
145 150
```

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1502645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

```
Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe His Pro Ser Val
1 5 10 15
Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr Cys Asp Arg Lys
20 25 30
Phe Phe Thr Ser Gln Ala Leu Gly His Gln Asn Ala His Lys Tyr
35 40 45
Glu Arg Xaa Leu Ala Lys Arg Arg Arg Arg Ser Pro Pro Pro Cys Ala
50 55 60
Arg Thr Gly Arg Pro Pro Pro Pro Arg Ala Ser Arg Thr Arg Arg Tyr
65 70 75 80
Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr Gly Ser Gly Ala
```

85 90 95  
Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala Pro Ala Asp Asp  
100 105 110  
Ala Ala Pro  
115

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| atcagcagac caccacccaa tcacaccagc tctctctaga gctagccctc tcttctctcca  | 60  |
| acacttggtg atccccctccc atctcctcaa gccttcttca ctgaatttct ggccgggtcga | 120 |
| tcgtcatgca cagctacaga gccatgcacc cgtacactca tcaactgtac cagcaccaca   | 180 |
| ccgcggccgn gcgcccacca agcacggcca cggccacgga catggacatg gccatggcga   | 240 |
| cgaggaggac gaccagtcac gctgctcctc tccctctggc ctcttgccac caccacggca   | 300 |
| acgcgtgct tcacggcgt gctcgtctcc cccgatctgc gccassgcca ccaccacctc     | 360 |
| tatggcagcc gctgctcct ccccgcttc ttacccttg gctcaccac caaagccttt       | 420 |
| acaataatgc cggctgcggc ggtaggggag c                                  |     |

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Ala Asp His Pro Ile Thr Pro Ala Leu Ser Arg Ala Ser Pro     |  |
| 1 5 10 15                                                       |  |
| Leu Phe Leu Gln His Leu Leu Ile Pro Ser His Leu Leu Lys Pro Ser |  |
| 20 25 30                                                        |  |
| Ser Leu Asn Phe Trp Pro Val Asp Arg His Ala Gln Leu Gln Ser His |  |
| 35 40 45                                                        |  |
| Ala Pro Val His Ser Ser Leu Val Pro Ala Pro His Arg Gly Xaa Ala |  |
| 50 55 60                                                        |  |
| Pro Thr Lys His Gly His Gly His Gly His Gly His Gly Asp         |  |
| 65 70 75 80                                                     |  |
| Glu Glu Asp Asp Gln Ser Cys Cys Ser Ser Pro Ser Gly Leu Leu Ala |  |
| 85 90 95                                                        |  |
| Pro Pro Arg Gln Arg Ala Ala Ser Ser Ala Cys Ser Ser Pro Pro Ile |  |
| 100 105 110                                                     |  |
| Cys Ala Xaa Ala Thr Thr Thr Ser Met Ala Ala Ala Ser Ser Pro     |  |
| 115 120 125                                                     |  |
| Ala Ser Tyr Pro Trp Ala His Pro Pro Lys Pro Leu Gln             |  |
| 130 135 140                                                     |  |

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

```
Met His Ser Tyr Arg Ala Met His Pro Tyr Thr His His Ser Tyr Gln
1 5 10 15
His His Thr Ala Ala Xaa Arg Pro Pro Ser Thr Ala Thr Ala Thr Asp
20 25 30
Met Asp Met Ala Met Ala Thr Arg Arg Thr Thr Ser His Ala Ala Pro
35 40 45
Leu Pro Leu Ala Ser Trp His His His Gly Asn Ala Leu Leu His Arg
50 55 60
Arg Ala Arg Leu Pro Arg Ser Ala Pro Xaa Pro Pro Pro Pro Leu Trp
65 70 75 80
Gln Pro Leu Pro Pro Pro Pro Leu Leu Thr Leu Gly Leu Thr His Gln
85 90 95
Ser Leu Tyr Asn Asn Ala Gly Cys Gly Gly Arg Gly
100 105
```

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

```
Met His Pro Tyr Thr His His Ser Tyr Gln His His Thr Ala Ala Xaa
1 5 10 15
Arg Pro Pro Ser Thr Ala Thr Ala Thr Asp Met Asp Met Ala Met Ala
20 25 30
Thr Arg Arg Thr Thr Ser His Ala Pro Leu Pro Leu Ala Ser Trp
35 40 45
His His His Gly Asn Ala Leu Leu His Arg Arg Ala Arg Leu Pro Arg
50 55 60
Ser Ala Pro Xaa Pro Pro Pro Pro Leu Trp Gln Pro Leu Pro Pro Pro
65 70 75 80
Pro Leu Leu Thr Leu Gly Leu Thr His Gln Ser Leu Tyr Asn Asn Ala
85 90 95
Gly Cys Gly Gly Arg Gly
100
```

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1502653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

```
ggggaggttag tggatatcaa gggtgataat ccagatgctg ttgttcctgg tctaatggct 60
gctggtgaag casstgtgca tctgttcatt gtgcgaatag gctaggcgca aattcgcttc 120
ttgacatagt tgtttttggc agagcttgtg caaacagggt agcagatatt tctaaaccag 180
```

gtgagaagca gaaacctctg gaaaaagatg ctggagaaaa gaccatagcc tggttggaca 240  
agctgaggaa tgcgaatggg tcattgccaa cttccaagat ccgtctcaac atgcagcgtg 300  
ttatgcaaaa taatgctgct gtattccgta cacaagaata cacttgaaga aggttgtgag 360  
ctgattagca aaacatggga aagttttcca tgatgtgaag ctgagttgac cggagtctca 420  
tttggaactc tgacctgata gag

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Gly Glu Val Val Asp Ile Lys Gly Asp Asn Pro Asp Ala Val Val Pro  
1 5 10 15  
Gly Leu Met Ala Ala Gly Glu Ala Xaa Val His Leu Phe Met Val Arg  
20 25 30  
Ile Gly

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Met Arg Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser  
1 5 10 15  
Val Leu Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu  
20 25 30  
Glu Glu Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser Val Leu  
1 5 10 15  
Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu Glu Glu  
20 25 30  
Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..386  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502682  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ttccccctcc | ctctgccaat | ctggccagct | agccagccca | gtccccacgc | ccatcccatc | 60  |
| ccatctaaaa | actgcatcga | atcctcgccg | ccgcaccgct | agactcagcc | gacgssatgc | 120 |
| cgccgcccac | ctccgctccc | cgctcgcgc  | ttcccgaat  | ggcccgatcc | cagacccaga | 180 |
| cccagtccca | gggagacctc | gacttcccg  | ccctcatctc | cgacctcacc | tccttgcctc | 240 |
| tccactcccc | cgccagcgcc | ggcgccggtg | gctccggacc | cgtcttctcc | tcctcctccc | 300 |
| tttccatccc | cactcccaaa | cccaagccga | accccagtc  | cacatcagca | gcgcgcgcga | 360 |
| ccccgctggc | gcgcgcggcc | atcggg     |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Pro | Ser | Leu | Cys | Gln | Ser | Gly | Gln | Leu | Ala | Ser | Pro | Val | Pro | Thr |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Pro | Ile | Pro | Ser | His | Leu | Lys | Thr | Ala | Ser | Asn | Pro | Arg | Arg | Arg | Thr |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Arg | Leu | Ser | Arg | Xaa | Xaa | Ala | Ala | Ala | Gln | Leu | Arg | Ser | Pro | Pro |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Arg | Ala | Ser | Arg | Asn | Gly | Pro | Ile | Pro | Asp | Pro | Asp | Pro | Val | Pro | Gly |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Arg | Pro | Arg | Leu | Pro | Val | Pro | His | Leu | Arg | Pro | His | Leu | Pro | Ala | Pro |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |  |
| Pro | Leu | Pro | Arg | Gln | Arg | Arg | Arg | Arg | Trp | Leu | Arg | Thr | Arg | Leu | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Leu | Leu | Pro | Phe | His | Pro | His | Ser | Gln | Thr | Gln | Ala | Glu | Pro | Gln |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | His | Ile | Ser | Ser | Ala | Ala | Asp | Pro | Ala | Gly | Ala | Arg | Gly | His | Arg |  |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..90  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Pro | Pro | Asn | Ser | Ala | Pro | Arg | Leu | Ala | Leu | Pro | Ala | Met | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |



Arg Ser Gln Thr Gln Thr Gln Ser Gln Gly Asp Leu Asp Phe Pro Ser  
20 25 30  
Leu Ile Ser Asp Leu Thr Ser Leu Leu His Ser Pro Ala Ser Ala  
35 40 45  
Gly Ala Gly Gly Ser Gly Pro Val Phe Ser Ser Ser Ser Leu Ser Ile  
50 55 60  
Pro Thr Pro Lys Pro Lys Pro Asn Pro Ser Pro Thr Ser Ala Ala Pro  
65 70 75 80  
Pro Thr Pro Leu Ala Arg Ala Ala Ile Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

Met Ala Arg Ser Gln Thr Gln Thr Gln Ser Gln Gly Asp Leu Asp Phe  
1 5 10 15  
Pro Ser Leu Ile Ser Asp Leu Thr Ser Leu Leu Leu His Ser Pro Ala  
20 25 30  
Ser Ala Gly Ala Gly Gly Ser Gly Pro Val Phe Ser Ser Ser Ser Leu  
35 40 45  
Ser Ile Pro Thr Pro Lys Pro Lys Pro Asn Pro Ser Pro Thr Ser Ala  
50 55 60  
Ala Pro Pro Thr Pro Leu Ala Arg Ala Ala Ile Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1502713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

ttgatgatga ggagaggccc tatttaccta agcacattct ctacaggcaa aaggaacagt 60  
tcagtgatgg tgttggttat agttggatcg atggattgaa ggaccatgcc agccaacatg 120  
tctccgattc catgatgatg aatgctggct ttgtttaccc agagaacaca cccacaacaa 180  
aagaagggta ctactacaga atgatattcg agaaattctt tccaagcct gcagcaaggt 240  
caactgttcc tggaggtcct agtgtggcct gcagcactgc caaagctgtt gaatgggatg 300  
catcctggtc caagaacctt gatccttctg ggcgtgctgc tttgggtgtt cacgatgctg 360  
cgtatgaaga cactgcaggg gaaactcctg cctctgctga tcctgtctca gacaagggcc 420  
ttcgtccagc tattggcgaa asstagggac acccgttgct tcagccacag ctgtctaacc 480  
ttatgtttat c

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asp | Glu | Glu | Arg | Pro | Tyr | Leu | Pro | Lys | His | Ile | Leu | Tyr | Arg | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Gln | Phe | Ser | Asp | Gly | Val | Gly | Tyr | Ser | Trp | Ile | Asp | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asp | His | Ala | Ser | Gln | His | Val | Ser | Asp | Ser | Met | Met | Met | Asn | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Phe | Val | Tyr | Pro | Glu | Asn | Thr | Pro | Thr | Thr | Lys | Glu | Gly | Tyr | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Arg | Met | Ile | Phe | Glu | Lys | Phe | Phe | Pro | Lys | Pro | Ala | Ala | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Val | Pro | Gly | Gly | Pro | Ser | Val | Ala | Cys | Ser | Thr | Ala | Lys | Ala | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Trp | Asp | Ala | Ser | Trp | Ser | Lys | Asn | Leu | Asp | Pro | Ser | Gly | Arg | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Leu | Gly | Val | His | Asp | Ala | Ala | Tyr | Glu | Asp | Thr | Ala | Gly | Glu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Ala | Ser | Ala | Asp | Pro | Val | Ser | Asp | Lys | Gly | Leu | Arg | Pro | Ala | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Glu | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 104 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..104
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Met | Asn | Ala | Gly | Phe | Val | Tyr | Pro | Glu | Asn | Thr | Pro | Thr | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Gly | Tyr | Tyr | Tyr | Arg | Met | Ile | Phe | Glu | Lys | Phe | Phe | Pro | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ala | Ala | Arg | Ser | Thr | Val | Pro | Gly | Gly | Pro | Ser | Val | Ala | Cys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Lys | Ala | Val | Glu | Trp | Asp | Ala | Ser | Trp | Ser | Lys | Asn | Leu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Gly | Arg | Ala | Ala | Leu | Gly | Val | His | Asp | Ala | Ala | Tyr | Glu | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ala | Gly | Glu | Thr | Pro | Ala | Ser | Ala | Asp | Pro | Val | Ser | Asp | Lys | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Arg | Pro | Ala | Ile | Gly | Glu | Xaa |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..103
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

```
Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys
1 5 10 15
Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro
20 25 30
Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr
35 40 45
Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro
50 55 60
Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Tyr Glu Asp Thr
65 70 75 80
Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu
85 90 95
Arg Pro Ala Ile Gly Glu Xaa
100
```

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

```
atcatctaca ccgccgaggg gccgacaacc acttggcgac catgagcacg ggcacggacg 60
ccgtccgggtc gccgtggssc cggcgaassc ccgcccatca acaagtacgc cttcgccctgc 120
gccctgctcg cctccatgaa ctccgtcctc ctcggtatg acatctcggg gatgagcggc 180
gcgcassgtg ttcatagaag aggacctcaa gatcacggac acgctagatc gagatcctcg 240
ccggcgctcat caacatctac tcgctcttcg gmtccctcgc cgcggggcyc acctccgamt 300
ggytcggccg ccgtacacc atggtgctgg cgcccgccat cttcttcacg ggcgcgctcc 360
tcatgggctt cgcccgggac tacg
```

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

```
Met Asn Ser Val Leu Gly Tyr Asp Ile Ser Val Met Ser Gly Ala
1 5 10 15
Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly His Ala Arg Ser
20 25 30
Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser Ser Xaa Pro Ser
35 40 45
Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala Thr Pro Trp Cys
50 55 60
Trp Arg Pro Pro Ser Ser Arg Ala Arg Ser Ser Trp Ala Ser Pro
65 70 75 80
Gly Thr Thr
```

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..71  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502719  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:  
Met Ser Gly Ala Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly  
1 5 10 15  
His Ala Arg Ser Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser  
20 25 30  
Ser Xaa Pro Ser Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala  
35 40 45  
Thr Pro Trp Cys Trp Arg Pro Pro Ser Ser Ser Arg Ala Arg Ser Ser  
50 55 60  
Trp Ala Ser Pro Gly Thr Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:2237:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

Met Lys Glu Asp Leu Lys Ile Thr Asp Thr Leu Asp Arg Asp Pro Arg  
1 5 10 15  
Arg Arg His Gln His Leu Leu Ala Leu Arg Xaa Pro Arg Arg Gly Xaa  
20 25 30  
His Leu Arg Xaa Xaa Arg Pro Pro Leu His His Gly Ala Gly Gly Arg  
35 40 45  
His Leu Leu His Gly Arg Ala Pro His Gly Pro Arg Pro Gly Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2238:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 484 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1502721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| tatgcaatca gagagaacat tgagaaggat attgagaggg aaaggcggag aaaggacaac   | 60  |
| cctgaggcga tggaggaaga tgaagtggat gagatcgccg agatcagggc ccctcacttc   | 120 |
| gaggagtcca tgaagtatgc tcggcgtagt gtcagtgatg ctgatatccg caagtaccag   | 180 |
| gcgtttgccc agactttgca gcagtcgccg gggtttgcca gtgagttccg cttctcggat   | 240 |
| cagccggcga casstggtgc tgctgctgca sscgatccgt ttgcttctgc ggggtgctgc   | 300 |
| gctgatgacg acgatctata cagctagttg gggtgtctcaa tatcagtcgc gtcactcatc  | 360 |
| tgttttaaac tgatcatact aaacacgcat gtcattgcaat gatattttatt tgccgtacat | 420 |
| ttggacgtcg ctgagatgat gcaactctcg ccttcgggta ccttttcatt ccatattctc   | 480 |
| catg                                                                |     |

(2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 108 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..108  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502722  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:  
Tyr Ala Ile Arg Glu Asn Ile Glu Lys Asp Ile Glu Arg Glu Arg Arg  
1                    5                    10                    15  
Arg Lys Asp Asn Pro Glu Ala Met Glu Glu Asp Glu Val Asp Glu Ile  
                    20                    25                    30  
Ala Glu Ile Arg Ala Pro His Phe Glu Glu Ser Met Lys Tyr Ala Arg  
                    35                    40                    45  
Arg Ser Val Ser Asp Ala Asp Ile Arg Lys Tyr Gln Ala Phe Ala Gln  
50                    55                    60  
Thr Leu Gln Gln Ser Arg Gly Phe Gly Ser Glu Phe Arg Phe Ser Asp  
65                    70                    75                    80  
Gln Pro Ala Thr Xaa Gly Ala Ala Ala Ala Xaa Asp Pro Phe Ala Ser  
                    85                    90                    95  
Ala Gly Ala Ala Ala Asp Asp Asp Asp Leu Tyr Ser  
                    100                    105

(2) INFORMATION FOR SEQ ID NO:2240:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..85  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502723  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:  
Met Glu Glu Asp Glu Val Asp Glu Ile Ala Glu Ile Arg Ala Pro His  
1                    5                    10                    15  
Phe Glu Glu Ser Met Lys Tyr Ala Arg Arg Ser Val Ser Asp Ala Asp  
                    20                    25                    30  
Ile Arg Lys Tyr Gln Ala Phe Ala Gln Thr Leu Gln Gln Ser Arg Gly  
35                    40                    45  
Phe Gly Ser Glu Phe Arg Phe Ser Asp Gln Pro Ala Thr Xaa Gly Ala  
50                    55                    60  
Ala Ala Ala Xaa Asp Pro Phe Ala Ser Ala Gly Ala Ala Ala Asp Asp  
65                    70                    75                    80  
Asp Asp Leu Tyr Ser  
                    85

(2) INFORMATION FOR SEQ ID NO:2241:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 76 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502724  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

Met Leu Gly Val Val Ser Val Met Leu Ile Ser Ala Ser Thr Arg Arg  
1 5 10 15  
Leu Pro Arg Leu Cys Ser Ser Pro Gly Gly Leu Ala Val Ser Ser Ala  
20 25 30  
Ser Arg Ile Ser Arg Arg Xaa Xaa Val Leu Leu Leu Xaa Xaa Ile Arg  
35 40 45  
Leu Leu Leu Arg Val Leu Arg Leu Met Thr Thr Ile Tyr Thr Ala Ser  
50 55 60  
Trp Val Ala Gln Tyr Gln Ser Arg His Ser Ser Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| gaagcgagcc aaccagcca tggagaaggc gatcgatcgg cagcgggtcc tcctggcgca  | 60  |
| cctcctcccc tccccctccg ccgcctcctc gcagcctcag cttgcggcgt cggcgtgcgc | 120 |
| ggccggggac agcgccgcct accagaggtc ctcctccttc ggggacgatg tcgtcgtcgt | 180 |
| cgctgcctac aggacgccga tatgcaaggc caagcgagga ggcttcaagg acacctaccc | 240 |
| agaggacctc ctcactgttg ttctcaaggc tgttctggac aacactagaa tcaatccagc | 300 |
| tgacatcgg                                                         |     |

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Lys Arg Ala Asn Pro Ala Met Glu Lys Ala Ile Asp Arg Gln Arg Val  
1 5 10 15  
Leu Leu Ala His Leu Leu Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro  
20 25 30  
Gln Leu Ala Ala Ser Ala Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln  
35 40 45  
Arg Ser Ser Ser Phe Gly Asp Asp Val Val Val Val Ala Ala Tyr Arg  
50 55 60  
Thr Pro Ile Cys Lys Ala Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro  
65 70 75 80  
Glu Asp Leu Leu Thr Val Val Leu Lys Ala Val Leu Asp Asn Thr Arg  
85 90 95  
Ile Asn Pro Ala Asp Ile  
100

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

```
Ser Glu Pro Thr Gln Pro Trp Arg Arg Arg Ser Ile Gly Ser Gly Ser
1 5 10 15
Ser Trp Arg Thr Ser Ser Pro Pro Pro Pro Pro Pro Arg Ser Leu
20 25 30
Ser Leu Arg Arg Arg Arg Ala Arg Pro Gly Thr Ala Pro Pro Thr Arg
35 40 45
Gly Pro Pro Pro Ser Gly Thr Met Ser Ser Ser Ser Leu Pro Thr Gly
50 55 60
Arg Arg Tyr Ala Arg Pro Ser Glu Glu Ala Ser Arg Thr Pro Thr Gln
65 70 75 80
Arg Thr Ser Ser Leu Leu Phe Ser Arg Leu Phe Trp Thr Thr Leu Glu
85 90 95
Ser Ile Gln Leu Thr Ser
100
```

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1502729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

```
Met Glu Lys Ala Ile Asp Arg Gln Arg Val Leu Leu Ala His Leu Leu
1 5 10 15
Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro Gln Leu Ala Ala Ser Ala
20 25 30
Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln Arg Ser Ser Ser Phe Gly
35 40 45
Asp Asp Val Val Val Val Ala Ala Tyr Arg Thr Pro Ile Cys Lys Ala
50 55 60
Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro Glu Asp Leu Leu Thr Val
65 70 75 80
Val Leu Lys Ala Val Leu Asp Asn Thr Arg Ile Asn Pro Ala Asp Ile
85 90 95
```

(2) INFORMATION FOR SEQ ID NO:2246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 1502730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

```
gagaatcgag cagagccacc gatcgctcct gagcactttc cacattccag ttccactccg 60
cctccgctgc cggtcgccgt ctccgagact ccgacagtcc gaccgcaaga aggatgagtg 120
aagaggataa gactgctgct tctgctgagc agccgaagag ggcccctaag ctcaatgaaa 180
ggatcctctc ttctctgtcc aggaggtccg tagctgctca tccatggcat gatcttgaga 240
```

```
tcggtcctga tgctcctgct gttttcaatg ttgtaagtac cagcattacc ttagaaccgt 300
ttgatgtggtt atatgttcgg tgctgtgggg acttaggttg tctggaacca tctacgggaa 360
ggttgttgag atcacaaagg gaagcaaagt taaatatgag cttgacaaga aaactggact 420
gattaaggtt gatcgagtcg tgttactcat cagttgtata ccctcacaat tatggtttcg 480
ttccaaagga ctcttt
```

(2) INFORMATION FOR SEQ ID NO:2247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

```
Met Ser Glu Glu Asp Lys Thr Ala Ala Ser Ala Glu Gln Pro Lys Arg
1 5 10 15
Ala Pro Lys Leu Asn Glu Arg Ile Leu Ser Ser Leu Ser Arg Arg Ser
20 25 30
Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Asp Ala Pro
35 40 45
Ala Val Phe Asn Val Val Ser Thr Ser Ile Thr Leu Glu Pro Phe Asp
50 55 60
Val Leu Tyr Val Arg Cys Cys Gly Asp Leu Gly Cys Leu Glu Pro Ser
65 70 75 80
Thr Gly Arg Leu Leu Arg Ser Gln Arg Glu Ala Lys Leu Asn Met Ser
85 90 95
Leu Thr Arg Lys Leu Asp
100
```

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

```
acatcaatcc attccctttc ctctcccgtc ccacttccat gggcaagggt cggtccttct 60
tctcgcgctc ccgcagcggc aagcgcggca gscggagag caggctcgtc ctgcgcgcac 120
tcttcgcggg ccagcgcgcc gccgtcccgc tcccactcc cgaggaggtc achgtcgtcg 180
tcgtcaacca caaccagggg acgagacgga gcgcgtgttc cgcaagttcg acgcgaacgg 240
cgacgggcag atctcgcggt ccgagc
```

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

```
Thr Ser Ile His Ser Leu Ser Ser Pro Ala Pro Leu Pro Trp Ala Arg
```



1 5 10 15  
Phe Gly Pro Ser Ser Arg Ala Pro Ala Ala Ser Ala Ala Xaa Arg  
20 25 30  
Arg Ala Gly Ser Ser Ser Pro His Ser Ser Ala Ala Ser Ala Pro Pro  
35 40 45  
Ser Pro Ser Pro Leu Pro Arg Arg Ser Xaa Ser Ser Ser Ser Thr Thr  
50 55 60  
Thr Arg Gly Arg Asp Gly Ala Arg Val Pro Gln Val Arg Arg Glu Arg  
65 70 75 80  
Arg Arg Ala Asp Leu Ala Val Arg  
85

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

His Gln Ser Ile Pro Phe Pro Leu Pro Leu His Phe His Gly Gln Gly  
1 5 10 15  
Ser Val Leu Leu Leu Ala Leu Pro Gln Arg Gln Ala Arg Gln Xaa Gly  
20 25 30  
Glu Gln Ala Arg Pro Arg Arg Thr Pro Pro Arg Pro Ala Arg Arg Arg  
35 40 45  
Pro Arg Pro His Ser Arg Gly Gly His Xaa Arg Arg Arg Gln Pro Gln  
50 55 60  
Pro Gly Asp Glu Thr Glu Arg Val Phe Arg Lys Phe Asp Ala Asn Gly  
65 70 75 80  
Asp Gly Gln Ile Ser Arg Ser Glu  
85

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Ile Asn Pro Phe Pro Phe Leu Ser Arg Ser Thr Ser Met Gly Lys Val  
1 5 10 15  
Arg Ser Phe Phe Ser Arg Ser Arg Ser Gly Lys Arg Gly Xaa Pro Glu  
20 25 30  
Ser Arg Leu Val Leu Ala Ala Leu Arg Gly Gln Arg Ala Ala Val  
35 40 45  
Pro Val Pro Thr Pro Glu Glu Val Xaa Val Val Val Asn His Asn  
50 55 60  
Gln Gly Thr Arg Arg Ser Ala Cys Ser Ala Ser Ser Thr Arg Thr Ala  
65 70 75 80  
Thr Gly Arg Ser Arg Gly Pro Ser  
85

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:



(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

```
Met Leu Cys Asp Ser Arg Arg Gly Val Ala Leu Val Ala Leu Leu Val
1 5 10 15
Gly Thr Asn Asn Asn Leu Gly Asn Ile Thr Asn Lys Gly Ser Val Arg
 20 25 30
Lys Gly Phe Glu Glu Ile Asn Phe Phe Leu Phe
 35 40
```

(2) INFORMATION FOR SEQ ID NO:2256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

```
agatcagatg gcagacaaaa taaggatcac ggakttgacg agatatccaa tccaagcaca 60
tcggagggtgc tcattgaaga gagaagatcc ttgggtcccg aaaaggagac gagatcctgt 120
cctgggcagc gcaggagggg aggagttaat acctgcgtcc cctggcacgt gtgggtcgcc 180
ctgccccgcc ccgcaagaag cgcgcccccc gcsstggtat ataagcgcgc mssaccggcc 240
caaggctggg caagacggcg ggctcgtcgga gtcgacaggg gagtccaagc ttcagatggc 300
cagcgctcgtt ggagcagtg cggggggcgt gggggcgccg acgcgcacgt cctcgcggtg 360
gacgacagct ccgtcgaccg cgccatcatc gccgccatac tccggagctc ccggtttcgt 420
gtgactgcgg tggaaagtgg gaagagggcc ctggaactgt taggcacgga gccgaacg
```

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

```
Arg Ser Asp Gly Arg Gln Asn Lys Asp His Gly Xaa Ala Glu Ile Ser
1 5 10 15
Asn Pro Ser Thr Ser Glu Val Leu Ile Glu Glu Arg Arg Ser Leu Gly
 20 25 30
Pro Glu Lys Glu Thr Arg Ser Cys Pro Gly Gln Arg Arg Arg Gly Gly
 35 40 45
Val Asn Thr Cys Val Pro Trp His Val Trp Val Ala Leu Pro Arg Pro
 50 55 60
Ala Arg Ser Ala Pro Pro Xaa Xaa Val Tyr Lys Arg Xaa Xaa Pro Ala
 65 70 75 80
```

Gln Gly Trp Ala Arg Arg Arg Val Val Gly Val Asp Arg Gly Val Gln  
85 90 95  
Ala Ser Asp Gly Gln Arg Arg Trp Ser Ser Gly Arg Gly Arg Gly Gly  
100 105 110  
Ala Asp Ala His Val Leu Ala Val Asp Asp Ser Ser Val Asp Arg Ala  
115 120 125  
Ile Ile Ala Ala Ile Leu Arg Ser Ser Arg Phe Arg Val Thr Ala Val  
130 135 140  
Glu Ser Gly Lys Arg Ala Leu Glu Leu Leu Gly Thr Glu Pro Asn  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1502765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

Asp Gln Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro  
1 5 10 15  
Ile Gln Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val  
20 25 30  
Arg Lys Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu  
35 40 45  
Leu Ile Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro  
50 55 60  
Gln Glu Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro  
65 70 75 80  
Lys Ala Gly Gln Asp Gly Gly Ser Ser Glu Ser Thr Gly Glu Ser Lys  
85 90 95  
Leu Gln Met Ala Ser Val Gly Gly Ala Val Ala Gly Gly Val Gly Ala  
100 105 110  
Pro Thr Arg Thr Ser Ser Arg Trp Thr Thr Ala Pro Ser Thr Ala Pro  
115 120 125  
Ser Ser Pro Pro Tyr Ser Gly Ala Pro Gly Phe Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1502766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro Ile Gln  
1 5 10 15  
Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val Arg Lys  
20 25 30  
Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu Leu Ile  
35 40 45  
Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro Gln Glu  
50 55 60  
Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro Lys Ala

(2) INFORMATION FOR SEQ ID NO:2260:

(A) LENGTH: 459 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1502767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

|             |             |             |            |             |            |     |
|-------------|-------------|-------------|------------|-------------|------------|-----|
| atcgcaccgcg | tctcccgcgtt | ctgactccgc  | cckgcgcgc  | dctcccgcac  | gccccaggc  | 60  |
| tctcatctccg | ccgcgcgtcg  | cgccgcctcg  | ctccgatcga | cccccgaaac  | tccggaaacc | 120 |
| gtgggcttcg  | cgagatggat  | ctcaaggata  | gcctctccaa | atttaagcaa  | cagcaggaga | 180 |
| gatgccagtc  | atcactggcg  | agcatagctg  | cttcgacctc | aaagccaaag  | cacagggcc  | 240 |
| aaccagcgca  | tgtctcccaac | gtcccagcaa  | gaccatcaca | acctattaag  | ttttcfaatg | 300 |
| atacagaaag  | gctgcagcac  | atcaatttcga | ttaggaaatc | tcctgtttgga | gcacagatca | 360 |
| agcttgctcat | cgaactctctt | tacaagacaa  | gacaagcttt | tactgcagag  | cagantaaat | 420 |
| gaagcaactt  | atgttgatat  | tcatggtaat  | aaagctgtc  |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2261:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1502768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Arg | Leu | Pro | Val | Leu | Thr | Pro | Pro | Xaa | Pro | Xaa | Leu | Pro | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Pro | Arg | Leu | His | Leu | Arg | Arg | Arg | Arg | Arg | Arg | Ile | Ala | Pro | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Pro | Arg | Asn | Ser | Gly | Asn | Arg | Gly | Leu | Arg | Glu | Met | Asp | Leu | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Ser | Leu | Ser | Lys | Phe | Lys | Gln | Gln | Gln | Glu | Arg | Cys | Gln | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Ser | Ile | Ala | Ala | Ser | Thr | Ser | Lys | Pro | Lys | His | Arg | Ala | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Ala | His | Ala | Pro | Asn | Val | Pro | Ala | Arg | Pro | Ser | Gln | Pro | Ile | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ser | Asn | Asp | Thr | Glu | Arg | Leu | Gln | His | Ile | Asn | Ser | Ile | Arg | Lys |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Val | Gly | Ala | Gln | Ile | Lys | Leu | Val | Ile | Glu | Leu | Leu | Tyr | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Arg | Gln | Ala | Phe | Thr | Ala | Glu | Gln | Xaa | Lys |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..95  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502769  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:  
Met Asp Leu Lys Asp Ser Leu Ser Lys Phe Lys Gln Gln Gln Arg  
1 5 10 15  
Cys Gln Ser Ser Leu Ala Ser Ile Ala Ala Ser Thr Ser Lys Pro Lys  
20 25 30  
His Arg Ala Gln Pro Ala His Ala Pro Asn Val Pro Ala Arg Pro Ser  
35 40 45  
Gln Pro Ile Lys Phe Ser Asn Asp Thr Glu Arg Leu Gln His Ile Asn  
50 55 60  
Ser Ile Arg Lys Ser Pro Val Gly Ala Gln Ile Lys Leu Val Ile Glu  
65 70 75 80  
Leu Leu Tyr Lys Thr Arg Gln Ala Phe Thr Ala Glu Gln Xaa Lys  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..70  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

Met Leu Pro Thr Ser Gln Gln Asp His His Asn Leu Leu Ser Phe Gln  
1 5 10 15  
Met Ile Gln Lys Gly Cys Ser Thr Ser Ile Arg Leu Gly Asn Leu Leu  
20 25 30  
Leu Glu His Arg Ser Ser Leu Ser Ser Asn Phe Phe Thr Arg Gln Asp  
35 40 45  
Lys Leu Leu Leu Gln Ser Arg Xaa Asn Glu Ala Thr Tyr Val Asp Ile  
50 55 60  
His Gly Asn Lys Ala Val  
65 70

(2) INFORMATION FOR SEQ ID NO:2264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 486 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..486  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

gtgggacgag aacaagttca cagctgatga gctgcagact ctgacaaaca acctatgcta 60  
cacgtacgct aggtgcaccc gtcctgtgtc aattgtgccc ccggcatact atgctcatct 120  
ggcagccttc cgagctcgct tctacatgga gccagatacc tctgacagtg gctcaatggc 180  
cagtgggtgcc cgtggccctc caccaggtgc ggcacssagc atgagaggag cggggagtgt 240  
tgcggtcagg cccctacctg ctctcaagga aaacgtgaag cgtgtcatgt tttactgctg 300

agatgctgag ctaccttcac caagaaaata tcctgacttg ttccatgtac ccgcactggt 360  
tcggtgatac tatctgacac cgaatttatg cattaagtct tccagtggtc tggagatttt 420  
aagtaacgcc tgtttttatt cgtgagttgt aacgctgcag ttcgaggagc ttcagtgctg 480  
tatgat

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Trp | Asp | Glu | Asn | Lys | Phe | Thr | Ala | Asp | Glu | Leu | Gln | Thr | Leu | Thr | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Asn | Leu | Cys | Tyr | Thr | Tyr | Ala | Arg | Cys | Thr | Arg | Ser | Val | Ser | Ile | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Pro | Ala | Tyr | Tyr | Ala | His | Leu | Ala | Ala | Phe | Arg | Ala | Arg | Phe | Tyr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Glu | Pro | Asp | Thr | Ser | Asp | Ser | Gly | Ser | Met | Ala | Ser | Gly | Ala | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Pro | Pro | Pro | Gly | Ala | Ala | Xaa | Ser | Met | Arg | Gly | Ala | Gly | Ser | Val |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ala | Val | Arg | Pro | Leu | Pro | Ala | Leu | Lys | Glu | Asn | Val | Lys | Arg | Val | Met |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Phe | Tyr | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Pro | Asp | Thr | Ser | Asp | Ser | Gly | Ser | Met | Ala | Ser | Gly | Ala | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Gly | Pro | Pro | Pro | Gly | Ala | Ala | Xaa | Ser | Met | Arg | Gly | Ala | Gly | Ser | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Val | Arg | Pro | Leu | Pro | Ala | Leu | Lys | Glu | Asn | Val | Lys | Arg | Val | Met |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Tyr | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:  
atcagyaaya acttcaggct tggagaaaga agaaaggcat agcagcgggc agcggcatgg 60  
gcaccakccc cgtcatccct gcgacgatgc tcttcgtcgc tcttcttgtn nctgtctgct 120  
tc

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Xaa | Xaa | Thr | Ser | Gly | Leu | Glu | Lys | Glu | Glu | Arg | His | Ser | Ser | Gly |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Gln | Arg | His | Gly | His | Xaa | Pro | Arg | His | Pro | Cys | Asp | Asp | Ala | Leu | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Ser | Ser | Cys | Xaa | Cys | Leu | Leu |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Xaa | Xaa | Leu | Gln | Ala | Trp | Arg | Lys | Lys | Lys | Gly | Ile | Ala | Ala | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Gly | Met | Gly | Thr | Xaa | Pro | Val | Ile | Pro | Ala | Thr | Met | Leu | Phe | Val |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Leu | Leu | Xaa | Xaa | Val | Cys | Phe |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

accttactas sagcagacgg tatcggttcaa ggtccccata ctgctacaga agacgcaggt 60  
ssaccttctg tttcgccata ctaccgccgg cacaggtaca gatctgtctc caagtcatcc 120  
agttcatctc c

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..43  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502785  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:  
Thr Leu Leu Xaa Ala Asp Gly Ile Val Gln Gly Pro His Thr Ala Thr  
1                    5                    10                    15  
Glu Asp Ala Gly Xaa Pro Ser Val Ser Pro Tyr Tyr Arg Arg His Arg  
                    20                    25                    30  
Tyr Arg Ser Val Ser Lys Ser Ser Ser Ser Ser  
                    35                    40  
(2) INFORMATION FOR SEQ ID NO:2272:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 43 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..43  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502786  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:  
Pro Tyr Xaa Xaa Gln Thr Val Ser Phe Lys Val Pro Ile Leu Leu Gln  
1                    5                    10                    15  
Lys Thr Gln Xaa Xaa Leu Leu Phe Arg His Thr Thr Ala Gly Thr Gly  
                    20                    25                    30  
Thr Asp Leu Ser Pro Ser His Pro Val His Leu  
                    35                    40  
(2) INFORMATION FOR SEQ ID NO:2273:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 43 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..43  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502787  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:  
Leu Thr Xaa Ser Arg Arg Tyr Arg Ser Arg Ser Pro Tyr Cys Tyr Arg  
1                    5                    10                    15  
Arg Arg Arg Xaa Thr Phe Cys Phe Ala Ile Leu Pro Pro Ala Gln Val  
                    20                    25                    30  
Gln Ile Cys Leu Gln Val Ile Gln Phe Ile Ser  
                    35                    40  
(2) INFORMATION FOR SEQ ID NO:2274:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 473 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..473  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502805  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:  
agatttccttt ccctttccgt tagcaggata gagagggaga ggagcagaag atagcagagg

gccagaggcg cagaaggcag tcgcgacag gaggaagagg aagaagaagc ggcavsgcga 120  
ggatgccgtg cctgaacgtg tcgaccaacg tgaacctgga ggggggtggac acctccgcca 180  
tcctcgccga agcctccaag tccgtcgcca acatcatcgg caagcccgag gcctacgtga 240  
tggttgttct caagggttcg gtgcctatgg catttgaggg taccagaggag ccagcagctt 300  
acggtagagct gggttccatc ggaggcctga accctgatgt gaacaagaag cttagtgtctg 360  
gcacgccttc taccctggag tcaaagctgt ctgttcccaa gtcacgcttc tacctcaagt 420  
tctatgactc gaaggctcat cctgcacaag aaaatgctca atgtttgcat gct

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1502806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Met Pro Cys Leu Asn Val Ser Thr Asn Val Asn Leu Gly Val Asp  
1 5 10 15  
Thr Ser Ala Ile Leu Ala Glu Ala Ser Lys Ser Val Ala Asn Ile Ile  
20 25 30  
Gly Lys Pro Glu Ala Tyr Val Met Val Val Leu Lys Gly Ser Val Pro  
35 40 45  
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val  
50 55 60  
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly  
65 70 75 80  
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe  
85 90 95  
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala  
100 105 110  
Gln Cys Leu His Ala  
115

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1502807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

Met Val Val Leu Lys Gly Ser Val Pro Met Ala Phe Gly Gly Thr Gln  
1 5 10 15  
Glu Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Pro  
20 25 30  
Asp Val Asn Lys Lys Leu Ser Ala Gly Ile Ala Ser Ile Leu Glu Ser  
35 40 45  
Lys Leu Ser Val Pro Lys Ser Arg Phe Tyr Leu Lys Phe Tyr Asp Ser  
50 55 60  
Lys Ala His Pro Ala Gln Glu Asn Ala Gln Cys Leu His Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502808  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:  
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val  
1 5 10 15  
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly  
20 25 30  
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe  
35 40 45  
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala  
50 55 60  
Gln Cys Leu His Ala  
65

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..410  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

agactgtctg ccagtgagcg cgagggagcg cctccgcctc agatccaacc cccaccgatg 60  
cgagctccgg cgatgctccg ctgggcccgc gggssctcg cggggctcct cgccgctcac 120  
cggccgcccgc gttttacctt cccggcgctg cgccaacga cttccataag aaagatccac 180  
ttttggtgaa ggtgaataag ctgacatcca cgaagacgca acttccctac tcatattact 240  
ctcttccttt ctgtaaacca aacacgatag ttgacagtgc agagaatctt ggagaagtgc 300  
tgcgtggtga tcgcattgag aactctcctt atgtggtcag tactagatta ctgcttgta 360  
catattcagc attgtaattt gtaatgtacc aaatcactta gtcgtcatgc

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

Arg Leu Ser Ala Ser Gly Arg Glu Gly Ala Pro Pro Pro Gln Ile Gln  
1 5 10 15  
Pro Pro Pro Met Arg Ala Pro Ala Met Leu Arg Trp Ala Ala Xaa  
20 25 30  
Leu Ala Gly Leu Leu Ala Ala His Arg Pro Pro Arg Phe Thr Tyr Pro  
35 40 45  
Ala Trp Arg Pro Thr Thr Ser Ile Arg Lys Ile His Phe Trp  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..124
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502811
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

```
Thr Val Cys Gln Trp Thr Arg Gly Ser Ala Ser Ala Ser Asp Pro Thr
1 5 10 15
Pro Thr Asp Ala Ser Ser Gly Asp Ala Pro Leu Gly Arg Gly Xaa Xaa
20 25 30
Arg Gly Ala Pro Arg Arg Ser Pro Ala Ala Ala Phe Tyr Leu Pro Gly
35 40 45
Val Ala Pro Asn Asp Phe His Lys Lys Asp Pro Leu Leu Val Lys Val
50 55 60
Asn Lys Leu Thr Ser Thr Lys Thr Gln Leu Pro Tyr Ser Tyr Tyr Ser
65 70 75 80
Leu Pro Phe Cys Lys Pro Asn Thr Ile Val Asp Ser Ala Glu Asn Leu
85 90 95
Gly Glu Val Leu Arg Gly Asp Arg Ile Glu Asn Ser Pro Tyr Val Val
100 105 110
Ser Thr Arg Leu Leu Leu Val Thr Tyr Ser Ala Leu
115 120
```

(2) INFORMATION FOR SEQ ID NO:2281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 443 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..443
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502820
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

```
aacatcctaa tcgaaaaacg gaagtttcgg cggcgssgcg tgctcgtgat ctcaacccaa 60
ggcgtgcctc cgctccggtc acccgctcgt ccacgcaacc atgtcgagga ggaagaccag 120
ggagcccaag gaggagaacg tcacccttgg acccactgtc cgtgaaggag agtatgtctt 180
tgggtgctcg caccatctttg catccttcaa tgacaccttc attcatatca ctgatttgctc 240
tgaggaggaa actctggttc ggatcacccg tggtcatgaag gtgaaggctg accgtgacga 300
gtcgtcacct tacgtgtgta tgcttgctgc tcaagacgtc gcacagcgct gcaaggagct 360
tggcattact gcaactgcaca ttaagcttcg cgccaccgga gcaacaagac caagaccctt 420
ggacctgggtg cccagtctgc cct
```

(2) INFORMATION FOR SEQ ID NO:2282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..91
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1502821
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

```
His Pro Asn Arg Lys Thr Glu Val Ser Ala Ala Xaa Arg Ala Arg Asp
1 5 10 15
Leu Asn Pro Arg Arg Ala Ser Ala Pro Val Thr Arg Arg Ser Thr Gln
20 25 30
Pro Cys Arg Gly Gly Arg Pro Gly Ser Pro Arg Arg Arg Thr Ser Pro
```

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| 35                                                              | 40 | 45 |
| Leu Asp Pro Leu Ser Val Lys Glu Ser Met Ser Leu Val Ser Leu Thr |    |    |
| 50                                                              | 55 | 60 |
| Ser Leu His Pro Ser Met Thr Pro Ser Phe Ile Ser Leu Ile Cys Leu |    |    |
| 65                                                              | 70 | 75 |
| Gly Gly Lys Leu Trp Phe Gly Ser Pro Val Ala                     |    | 80 |
| 85                                                              | 90 |    |

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1502822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu |     |     |
| 1                                                               | 5   | 10  |
| Gly Pro Thr Val Arg Glu Gly Glu Tyr Val Phe Gly Val Ala His Ile |     |     |
| 20                                                              | 25  | 30  |
| Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly |     |     |
| 35                                                              | 40  | 45  |
| Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp |     |     |
| 50                                                              | 55  | 60  |
| Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val |     |     |
| 65                                                              | 70  | 75  |
| Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu |     |     |
| 85                                                              | 90  | 95  |
| Arg Ala Thr Gly Ala Thr Arg Pro Arg Pro Leu Asp Leu Val Pro Ser |     |     |
| 100                                                             | 105 | 110 |
| Leu Pro                                                         |     |     |

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1502834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| ttaactcgag aggaggtgaa gcatcccgga atggagatcc tgatgctttg gcaacaatga   | 60  |
| acgcaactgc agaagctctt gaagcaaaag awaagcaaaa gccatcgttt gaattgtctg   | 120 |
| gaaagcttgc tgaggagacc aacagagttg caggtgtaaa tctattatat tcagaacccc   | 180 |
| cagaggctcg aaagtcagag attagatgga ggctctatgt atttaaagat ggtgaaccac   | 240 |
| tgaatgaacc actgtatggt catcggtatga cctgctacct ttttgggaaga gaaakgaaag | 300 |
| ttgcagatgt cccacagat catccctcct gcagcaagca acatgcagtt cttcaatata    | 360 |
| gacttgtgga gaaggagcaa ctgatggca tactgacgaa gagaataagg ccttawctga    | 420 |
| tgatcttga tagtacaat gg                                              |     |

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1502835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

```
Asn Ser Arg Gly Gly Glu Ala Ser Arg Asn Gly Asp Pro Asp Ala Leu
1 5 10 15
Ala Thr Met Asn Ala Thr Ala Glu Ala Leu Glu Ala Lys Xaa Lys Gln
 20 25 30
Lys Pro Ser Phe Glu Leu Ser Gly Lys Leu Ala Glu Glu Thr Asn Arg
 35 40 45
Val Ala Gly Val Asn Leu Leu Tyr Ser Glu Pro Pro Glu Ala Arg Lys
 50 55 60
Ser Glu Ile Arg Trp Arg Leu Tyr Val Phe Lys Asp Gly Glu Pro Leu
65 70 75 80
Asn Glu Pro Leu Tyr Val His Arg Met Thr Cys Tyr Leu Phe Gly Arg
 85 90 95
Glu Xaa Lys Val Ala Asp Val Pro Thr Asp His Pro Ser Cys Ser Lys
 100 105 110
Gln His Ala Val Leu Gln Tyr Arg Leu Val Glu Lys Glu Gln Leu Asp
 115 120 125
Gly Ile Leu Thr Lys Arg Ile Arg Pro Xaa Leu Met Asp Leu Asp Ser
130 135 140
Thr Asn
145
```

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

```
Met Asn Ala Thr Ala Glu Ala Leu Glu Ala Lys Xaa Lys Gln Lys Pro
1 5 10 15
Ser Phe Glu Leu Ser Gly Lys Leu Ala Glu Glu Thr Asn Arg Val Ala
 20 25 30
Gly Val Asn Leu Leu Tyr Ser Glu Pro Pro Glu Ala Arg Lys Ser Glu
 35 40 45
Ile Arg Trp Arg Leu Tyr Val Phe Lys Asp Gly Glu Pro Leu Asn Glu
50 55 60
Pro Leu Tyr Val His Arg Met Thr Cys Tyr Leu Phe Gly Arg Glu Xaa
65 70 75 80
Lys Val Ala Asp Val Pro Thr Asp His Pro Ser Cys Ser Lys Gln His
 85 90 95
Ala Val Leu Gln Tyr Arg Leu Val Glu Lys Glu Gln Leu Asp Gly Ile
 100 105 110
Leu Thr Lys Arg Ile Arg Pro Xaa Leu Met Asp Leu Asp Ser Thr Asn
115 120 125
```

(2) INFORMATION FOR SEQ ID NO:2287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..461  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502844  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:  
tacgacctgc tcgggatctc agcggatggg agccccgatg atgttcgggc gtcctacagg 60  
cggctggcgc taaagtacca cccagacgtg tccccocgg cgccgcggcc gagaacacgc 120  
gccgcttcat cgaggtgcaq gaggcctacg agacgctctc cgacccaagc cgccgctcca 180  
gctacgaccg tgcaactcgcc cgcggsstct gccgctcgcc ttctccgggc gccgttccca 240  
atcccaccac gcctactacc accaccagga gcaggagag agatctgggt ggagaaggtc 300  
ctgggaggac cagatcgcaq agctgaagag gaggagcgtg gcgaaggatt cagaagagaa 360  
cctgtcgtgg ggcgctcgca tgcggagaag ggccgaggcg tcacagcgna gtagctgcga 420  
caagcgaccc tgccaaatgc agctgtactc gtacgtagca t  
(2) INFORMATION FOR SEQ ID NO:2288:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 137 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..137  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502845  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:  
Tyr Asp Leu Leu Gly Ile Ser Ala Asp Gly Ser Pro Asp Asp Val Arg  
1 5 10 15  
Ala Ser Tyr Arg Arg Leu Ala Leu Lys Tyr His Pro Asp Val Ser Pro  
20 25 30  
Pro Ala Pro Arg Pro Arg Thr Arg Ala Ala Ser Ser Arg Cys Arg Arg  
35 40 45  
Pro Thr Arg Arg Ser Pro Thr Gln Ala Ala Ala Pro Ala Thr Thr Val  
50 55 60  
His Ser Pro Ala Xaa Ser Ala Ala Arg Leu Leu Arg Ala Pro Phe Pro  
65 70 75 80  
Ile Pro Pro Arg Leu Leu Pro Pro Pro Gly Ala Gly Arg Glu Ile Trp  
85 90 95  
Val Glu Lys Val Leu Gly Gly Pro Asp Arg Arg Ala Glu Glu Glu Glu  
100 105 110  
Arg Gly Glu Gly Phe Arg Arg Glu Pro Val Val Gly Arg Ser His Ala  
115 120 125  
Glu Lys Gly Arg Gly Val Thr Ala Xaa  
130 135  
(2) INFORMATION FOR SEQ ID NO:2289:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 503 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..503  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502850  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:  
atgcgtgcat ggcgtgctag ctaggtacct tgcggccaag agcgaggcgg accactacaa 60  
gcgaggagatg agaaggkagc aggaggagat catcgccgtc ccagacaccg aggcckctga 120  
gattggagat atcatgtcac ggtatgggct cgagccgcag agtacggccc tgcgtcgcc 180  
gggctcaggc ggaaccctca agcttkgcta gacttcatgr tgaggttcga gctgggactg 240

gagagaccgg atcccagaag ggctctgcag acgccttcac gatcgcaactg tcctacgtgg 300  
tcggcggggt ggtccctctc ctgccctacg tgctcgtctc cgccgcgcag gatgccatgc 360  
tcacatccgt cggagtcacg ctggccgcgc tgcttttctt cggctacgtc aagggccgct 420  
tcacggggga accgkccgtt cgccagtgc gtccagaccg ctgtcattgg agcgctcgct 480  
tcggcgggcg cgtacssgga tgg

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

Cys Val His Gly Val Leu Ala Arg Tyr Leu Ala Ala Lys Ser Glu Ala  
1 5 10 15  
Asp His Tyr Lys Arg Glu Met Arg Arg Xaa Gln Glu Glu Ile Ile Ala  
20 25 30  
Val Pro Asp Thr Glu Ala Xaa Glu Ile Gly Asp Ile Met Ser Arg Tyr  
35 40 45  
Gly Leu Glu Pro Gln Ser Thr Ala Leu Ser Ser Pro Gly Ser Gly Gly  
50 55 60  
Thr Leu Lys Leu Xaa  
65

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

Met Gly Ser Ser Arg Arg Val Arg Pro Cys Arg Arg Arg Ala Gln Ala  
1 5 10 15  
Glu Pro Ser Ser Xaa Ala Arg Leu His Xaa Glu Val Arg Ala Gly Thr  
20 25 30  
Gly Glu Thr Gly Ser Gln Lys Gly Ser Ala Asp Ala Phe Thr Ile Ala  
35 40 45  
Leu Ser Tyr Val Val Gly Gly Leu Val Pro Leu Leu Pro Tyr Val Leu  
50 55 60  
Val Ser Ala Ala Gln Asp Ala Met Leu Thr Ser Val Gly Val Thr Leu  
65 70 75 80  
Ala Ala Leu Leu Phe Phe Gly Tyr Val Lys Gly Arg Phe Thr Gly Glu  
85 90 95  
Pro Xaa Val Arg Gln Cys Arg Pro Asp Arg Cys His Trp Ser Ala Arg  
100 105 110  
Phe Gly Gly Gly Val Xaa Gly Trp  
115 120

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..95  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502853  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:  
Met Xaa Arg Phe Glu Leu Gly Leu Glu Arg Pro Asp Pro Arg Arg Ala  
1                    5                    10                    15  
Leu Gln Thr Pro Ser Arg Ser His Cys Pro Thr Trp Ser Ala Gly Trp  
                    20                    25                    30  
Ser Leu Ser Cys Pro Thr Cys Ser Pro Pro Arg Arg Met Pro Cys  
                    35                    40                    45  
Ser His Pro Ser Glu Ser Arg Trp Pro Arg Cys Phe Ser Ser Ala Thr  
                    50                    55                    60  
Ser Arg Ala Ala Ser Arg Gly Asn Xaa Pro Phe Ala Ser Ala Val Gln  
65                    70                    75                    80  
Thr Ala Val Ile Gly Ala Leu Ala Ser Ala Ala Ala Tyr Xaa Asp  
                    85                    90                    95

(2) INFORMATION FOR SEQ ID NO:2293:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 475 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
    (B) LOCATION: 1..475  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

|            |            |             |             |            |             |     |
|------------|------------|-------------|-------------|------------|-------------|-----|
| atcccaaagc | acaagagcac | gcactgcagc  | accacttcct  | gcgctgctgc | tcatacacaca | 60  |
| ccgtagtact | aacactccat | cgccacaatg  | gctcccaagg  | ttgcgctctt | ccttgccctc  | 120 |
| agcctcctct | tcgctgccgc | cgcgcatggc  | tgcgaaccct  | actgtcccgc | cccagtcgtc  | 180 |
| ccaacgccgc | ccgtcgtgcc | gtcgcacagc  | cacgggcgct  | gcssatcgac | gcactaaagc  | 240 |
| tcaaggtgtg | cgccaacgtg | ctggacctcg  | tcaaggtcgg  | cctaccccag | cacgagcaat  | 300 |
| gttgcccgtc | gctggagggg | ctgggtggacc | tcgacgccgc  | actgtgcctc | tgcaccgccca | 360 |
| tcaaggctaa | cgtcctcggc | atccacctca  | acgtgccccct | tagcctcaac | ctcatcctca  | 420 |
| acaattgcgg | caagatttgc | ccaaaagact  | ttacttgccc  | caactaattg | agctg       |     |

(2) INFORMATION FOR SEQ ID NO:2294:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 122 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..122  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

|                                                                      |  |
|----------------------------------------------------------------------|--|
| Ser Gln Ser Thr Arg Ala Arg Thr Ala Ala Pro Leu Pro Ala Leu Leu      |  |
| 1                    5                    10                    15   |  |
| Leu Ile Thr His Arg Ser Thr Asn Thr Pro Ser Pro Gln Trp Leu Pro      |  |
| 20                    25                    30                       |  |
| Arg Leu Arg Ser Ser Leu Pro Ser Ala Ser Ser Ser Leu Pro Pro Arg      |  |
| 35                    40                    45                       |  |
| Met Ala Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Pro      |  |
| 50                    55                    60                       |  |
| Ser Cys Arg Arg Thr Ala Thr Gly Ala Xaa Xaa Arg Arg Thr Lys Ala      |  |
| 65                    70                    75                    80 |  |
| Gln Gly Val Arg Gln Arg Ala Gly Pro Arg Gln Gly Arg Pro Thr Pro      |  |

85 90 95  
Ala Arg Ala Met Leu Pro Ala Ala Gly Gly Ala Gly Gly Pro Arg Arg  
100 105 110  
Arg Thr Val Pro Leu His Arg His Gln Gly  
115 120

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

Pro Lys Ala Gln Glu His Ala Leu Gln His His Phe Leu Arg Cys Cys  
1 5 10 15  
Ser Ser His Thr Val Val Leu Thr Leu His Arg His Asn Gly Ser Gln  
20 25 30  
Gly Cys Ala Leu Pro Cys Pro Gln Pro Pro Leu Arg Cys Arg Arg Ala  
35 40 45  
Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro Asn Ala Ala Arg  
50 55 60  
Arg Ala Val Ala Gln Pro Arg Ala Leu Xaa Ile Asp Ala Leu Lys Leu  
65 70 75 80  
Lys Val Cys Ala Asn Val Leu Asp Leu Val Lys Val Gly Leu Pro Gln  
85 90 95  
His Glu Gln Cys Cys Pro Leu Leu Glu Gly Leu Val Asp Leu Asp Ala  
100 105 110  
Ala Leu Cys Leu Cys Thr Ala Ile Lys Ala Asn Val Leu Gly Ile His  
115 120 125  
Leu Asn Val Pro Leu Ser Leu Asn Leu Ile Leu Asn Asn Cys Gly Lys  
130 135 140  
Ile Cys Pro Lys Asp Phe Thr Cys Pro Asn  
145 150

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

cactttctta agacgagttg tggtagcccg aattatgcag cacctgaggt catatctggt 60  
aaactatatg ctggtcctga agttgacgtc tggagctgtg gagttattct ttatgctctt 120  
ctttgtggca ctctccatt tgacgatgag aatattccaa accttttcaa gaaaataaag 180  
ggtggaatat atacccttcc tagtcatttg tcaccttcag cgagggactt gattcccaga 240  
atgctggttg ttgatccaat gaaaaggatt acaatacgtg aaatccgtga acatgtgtg 300  
ttcaagatcc gacttcgcg ctatttggt gtgc

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1502897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:

```
His Phe Leu Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
1 5 10 15
Val Ile Ser Gly Lys Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser
20 25 30
Cys Gly Val Ile Leu Tyr Ala Leu Cys Gly Thr Leu Pro Phe Asp
35 40 45
Asp Glu Asn Ile Pro Asn Leu Phe Lys Lys Ile Lys Gly Gly Ile Tyr
50 55 60
Thr Leu Pro Ser His Leu Ser Pro Ser Ala Arg Asp Leu Ile Pro Arg
65 70 75 80
Met Leu Val Val Asp Pro Met Lys Arg Ile Thr Ile Arg Glu Ile Arg
85 90 95
Glu His Val Trp Phe Lys Ile Arg Leu Pro Arg Tyr Leu Ala Val
100 105 110
```

(2) INFORMATION FOR SEQ ID NO:2298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1502898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:

```
Thr Phe Leu Arg Arg Val Val Val Ala Arg Ile Met Gln His Leu Arg
1 5 10 15
Ser Tyr Leu Val Asn Tyr Met Leu Val Leu Lys Leu Thr Ser Gly Ala
20 25 30
Val Glu Leu Phe Phe Met Leu Phe Val Ala Leu Ser His Leu Thr
35 40 45
Met Arg Ile Phe Gln Thr Phe Ser Arg Lys
50 55
```

(2) INFORMATION FOR SEQ ID NO:2299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1502902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

```
atcagtccctg tccaccagca ccgcnaccac actcgccgac cgnaaatgaa ccacggcgccg 60
ggcgggagga gcagcagccg gtcctgggac cggttgccc ggatgttccg cccgagcgcg 120
ctgctccgct ccacctgcaa caccggccgc gccgcacct cctgctctc ctcgtctccc 180
gcgtccacgg ccaagcctcc gcctccgcct gtggctgcgg cggcctccgc gtgctcctcc 240
agccgcgcgc tgcctggcgc cgctcgtcgc ggggactcgt cgttcctcgc ctccctcgcg 300
cgcgacctcg ccgtc
```

(2) INFORMATION FOR SEQ ID NO:2300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..105  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502903  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:  
Ile Ser Pro Val His Gln His Arg Xaa His Thr Arg Arg Pro Xaa Met  
1 5 10 15  
Asn His Gly Gly Gly Arg Ser Ser Arg Leu Arg Asp Arg Leu  
20 25 30  
Ala Arg Met Phe Arg Pro Ser Ala Leu Leu Arg Ser Thr Cys Asn Thr  
35 40 45  
Ala Ala Ala Ala Ser Ser Cys Ser Ser Ser Ser Pro Ala Ser Thr Ala  
50 55 60  
Lys Pro Pro Pro Pro Pro Val Ala Ala Ala Ala Ser Ala Cys Ser Ser  
65 70 75 80  
Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe Leu  
85 90 95  
Ala Ser Ser Arg Arg Asp Leu Ala Val  
100 105

(2) INFORMATION FOR SEQ ID NO:2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

Gln Ser Cys Pro Pro Ala Pro Xaa Pro His Ser Pro Thr Xaa Asn Glu  
1 5 10 15  
Pro Arg Arg Arg Arg Glu Glu Gln Gln Pro Ala Pro Gly Pro Ala Gly  
20 25 30  
Pro Asp Val Pro Pro Glu Arg Ala Ala Pro Leu His Leu Gln His Gly  
35 40 45  
Arg Arg Arg Ile Leu Leu Leu Leu Leu Val Ser Arg Val His Gly Gln  
50 55 60  
Ala Ser Ala Ser Ala Cys Gly Cys Gly Gly Leu Arg Val Leu Leu Gln  
65 70 75 80  
Pro Arg Ala Ala Arg Arg Arg Arg Arg Gly Leu Val Val Pro Arg  
85 90 95  
Leu Leu Ala Ala Arg Pro Arg Arg  
100

(2) INFORMATION FOR SEQ ID NO:2302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..90  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Met Asn His Gly Gly Gly Arg Ser Ser Ser Arg Leu Arg Asp Arg  
1 5 10 15  
Leu Ala Arg Met Phe Arg Pro Ser Ala Leu Leu Arg Ser Thr Cys Asn  
20 25 30  
Thr Ala Ala Ala Ala Ser Ser Cys Ser Ser Ser Ser Pro Ala Ser Thr  
35 40 45  
Ala Lys Pro Pro Pro Pro Pro Val Ala Ala Ala Ala Ser Ala Cys Ser  
50 55 60  
Ser Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe  
65 70 75 80  
Leu Ala Ser Ser Arg Arg Asp Leu Ala Val  
85 90

(2) INFORMATION FOR SEQ ID NO:2303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aaaacccatt gtgtgcccgc cgtcgacgca gcctccgtcc tcccccgcat ccgaatcacg  | 60  |
| cacgccaacg tcccaccctt gtcattggcca cctccagcga cggcgcgggc accagcggcg | 120 |
| ctcctctcca tcccgaagga aggcgagcgc atcatcgcg ccacgssccg ccccgacggc   | 180 |
| acgtcccgca aggccatccg catccgcgcc ggttacgtgc cccaggagga ggtcgccatc  | 240 |
| taccagtcca agggcgccct aatgaggaag tcaggggccc acgtgccgcc ggggtacgac  | 300 |
| ccggcgcyta gtggccgacg ccaaaccccc cccccc                            |     |

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

Lys Thr His Cys Val Pro Ala Val Asp Ala Ala Ser Val Leu Pro Arg  
1 5 10 15  
Ile Arg Ile Thr His Ala Asn Val Pro Pro Leu Ser Trp Pro Pro Pro  
20 25 30  
Ala Thr Ala Arg Arg Pro Ala Ala Leu Leu Ser Ile Pro Lys Glu Gly  
35 40 45  
Glu Arg Ile Ile Ala Pro Thr Xaa Arg Pro Asp Gly Thr Leu Arg Lys  
50 55 60  
Ala Ile Arg Ile Arg Ala Gly Tyr Val Pro Gln Glu Glu Val Ala Ile  
65 70 75 80  
Tyr Gln Ser Lys Gly Ala Leu Met Arg Lys Ser Gly Pro Asp Val Pro  
85 90 95  
Pro Gly Tyr Asp Pro Ala Xaa Ser Gly Arg Arg Gln Thr Pro Pro Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..86  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502939  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:  
Lys Pro Ile Val Cys Pro Pro Ser Thr Gln Pro Pro Ser Ser Pro Ala  
1 5 10 15  
Ser Glu Ser Arg Thr Pro Thr Ser His Pro Cys His Gly His Leu Gln  
20 25 30  
Arg Arg Arg Gly Asp Gln Arg Arg Ser Ser Pro Ser Pro Arg Lys Ala  
35 40 45  
Ser Ala Ser Ser Arg Pro Xaa Xaa Ala Pro Thr Ala Arg Ser Ala Arg  
50 55 60  
Pro Ser Ala Ser Ala Pro Val Thr Cys Pro Arg Arg Arg Ser Pro Ser  
65 70 75 80  
Thr Ser Pro Arg Ala Pro  
85

(2) INFORMATION FOR SEQ ID NO:2306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:

Asn Pro Leu Cys Ala Arg Arg Arg Arg Ser Leu Arg Pro Pro Pro His  
1 5 10 15  
Pro Asn His Ala Arg Gln Arg Pro Thr Pro Val Met Ala Thr Ser Ser  
20 25 30  
Asp Gly Ala Ala Thr Ser Gly Ala Pro Leu His Pro Gln Gly Arg Arg  
35 40 45  
Ala His His Arg Ala His Xaa Pro Pro Arg Arg His Ala Pro Gln Gly  
50 55 60  
His Pro His Pro Arg Arg Leu Arg Ala Pro Gly Gly Gly Arg His Leu  
65 70 75 80  
Pro Val Gln Gly Arg Pro Asn Glu Glu Val Arg Ala Arg Arg Ala Ala  
85 90 95  
Gly Val Arg Pro Gly Xaa  
100

(2) INFORMATION FOR SEQ ID NO:2307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..443  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:

aatcgggtcaa tcacgtctac ttgcttgacg acgattctcc agggatacgt cccatctgct 60  
gcgaccaggg cgatggggga ggaggagacc cgcgcaggcg acctcccgga gccgtgcctg 120

```
gcgcacgccca tcgcgctcac ctgcgcgcgc gacgcctgcc gctgcgccgc cgtctcccc 180
gccttccgcg cgcgcgccga ctccgactac gtctggggcc gcttcgtccc ggaggatcac 240
cgccgcgccca tcgccctgca tctgcatgcc gccggccggg accgtggggcc gaggaaggac 300
gcgtaccttg cgctctgcga cggcggcggc ggccggcgtcc ccgtcgacgt cgacgtcgas 360
gccttggtgc aggctgtggc tggaccaggc cagcgssgcc aagtgtctac cgctgtcggc 420
gaggaggctc agcctgccgt ggg
```

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

```
Asn Arg Ser Ile Thr Ser Thr Cys Leu Gln Thr Ile Leu Gln Gly Tyr
1 5 10 15
Val Pro Ser Ala Ala Thr Arg Ala Met Gly Glu Glu Glu Thr Arg Ala
20 25 30
Gly Asp Leu Pro Glu Pro Cys Leu Ala His Ala Ile Ala Leu Thr Ser
35 40 45
Pro Arg Asp Ala Cys Arg Cys Ala Ala Val Ser Pro Ala Phe Arg Ala
50 55 60
Ala Ala Asp Ser Asp Tyr Val Trp Gly Arg Phe Val Pro Glu Asp His
65 70 75 80
Arg Arg Ala Ile Ala Leu His Leu His Ala Ala Gly Arg Asp Arg Gly
85 90 95
Pro Arg Lys Asp Ala Tyr Leu Ala Leu Cys Asp Gly Gly Gly Gly Gly
100 105 110
Val Pro Val Asp Val Asp Val Xaa Ala Leu Val Gln Ala Val Ala Gly
115 120 125
Pro Gly Gln Xaa Xaa Gln Val Leu Arg Ala Val Gly Glu Glu Ala Gln
130 135 140
Pro Ala Val
145
```

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

```
Ile Gly Gln Ser Arg Leu Leu Ala Cys Arg Arg Phe Ser Arg Asp Thr
1 5 10 15
Ser His Leu Leu Arg Pro Gly Arg Trp Gly Arg Arg Arg Pro Ala Gln
20 25 30
Ala Thr Ser Arg Ser Arg Ala Trp Arg Thr Pro Ser Arg Ser Pro Arg
35 40 45
Arg Ala Thr Pro Ala Ala Ala Pro Pro Ser Pro Pro Pro Ser Ala Pro
50 55 60
Pro Pro Thr Pro Thr Thr Ser Gly Ala Ala Ser Ser Arg Arg Ile Thr
65 70 75 80
Ala Ala Pro Ser Pro Cys Ile Cys Met Pro Pro Ala Gly Thr Val Gly
```

```

 85 90 95
Arg Gly Arg Thr Arg Thr Leu Arg Ser Ala Thr Ala Ala Ala Ala Ala
 100 105 110
Ser Pro Ser Thr Ser Thr Ser Xaa Pro Trp Cys Arg Leu Trp Leu Asp
 115 120 125
Gln Ala Ser Xaa Ala Lys Cys Tyr Ala Leu Ser Ala Arg Arg Leu Ser
 130 135 140
Leu Pro Trp
145
```

(2) INFORMATION FOR SEQ ID NO:2310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

```

Ser Val Asn His Val Tyr Leu Leu Ala Asp Asp Ser Pro Gly Ile Arg
1 5 10 15
Pro Ile Cys Cys Asp Gln Gly Asp Gly Gly Gly Gly Asp Pro Arg Arg
 20 25 30
Arg Pro Pro Gly Ala Val Pro Gly Ala Arg His Arg Ala His Leu Ala
 35 40 45
Ala Arg Arg Leu Pro Leu Arg Arg Arg Leu Pro Arg Leu Pro Arg Arg
 50 55 60
Arg Arg Leu Arg Leu Arg Leu Gly Pro Leu Arg Pro Gly Gly Ser Pro
 65 70 75 80
Pro Arg His Arg Pro Ala Ser Ala Cys Arg Arg Pro Gly Pro Trp Ala
 85 90 95
Glu Glu Gly Arg Val Pro Cys Ala Leu Arg Arg Arg Arg Arg Arg Arg
 100 105 110
Pro Arg Arg Arg Arg Arg Arg Xaa Leu Gly Ala Gly Cys Gly Trp Thr
 115 120 125
Arg Pro Ala Xaa Pro Ser Ala Thr Arg Cys Arg Arg Gly Gly Ser Ala
 130 135 140
Cys Arg Gly
145
```

(2) INFORMATION FOR SEQ ID NO:2311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1502985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

```

aaacggaaac gggggcagtt ggtgagttgg gacttgggag ccgacgctgt cgggggtgatc 60
cagtcgccgc cgacgcgcgc gaacgcgcgc gcgcccagac ctccctctac gcggacssgg 120
naggaccctt ccactcccag agcggggcgt gtccgacgct gagcccatgg cggaatccat 180
cgtctccggc ccgcgcgcgc cgccgcgggg ckcgcctctg ttctcctacc tggccgtgtt 240
ctccaactgc ccgctcgtcg ccgcggtgct cgccttcgcc atcgcgagct ccatcaaggt 300
cctcaccacc tgggtataagg agaaccggtg ggacg
```

(2) INFORMATION FOR SEQ ID NO:2312:

(i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502986  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:  
Thr Glu Thr Gly Ala Val Gly Glu Leu Gly Leu Gly Ser Arg Arg Cys  
1 5 10 15  
Arg Gly Asp Pro Val Ala Ala Asp Ala Ala Glu Arg Ala Arg Ala Arg  
20 25 30  
Ala Ser Leu Tyr Ala Asp Xaa Xaa Gly Pro Phe His Ser Gln Ser Arg  
35 40 45  
Ala Cys Pro Ile Val Ser Pro Trp Arg Asn Pro Ser Ser Pro Ala Pro  
50 55 60  
Pro Pro Arg Arg Arg Xaa Arg Pro Arg Ser Pro Thr Trp Pro Cys Ser  
65 70 75 80  
Pro Thr Ala Arg Ser Ser Pro Arg Cys Ser Pro Ser Pro Ser Arg Ser  
85 90 95  
Pro Ser Arg Ser Ser Pro Pro Gly Ile Arg Arg Thr Gly Gly Thr  
100 105 110  
(2) INFORMATION FOR SEQ ID NO:2313:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..56  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502987  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:  
Met Ala Glu Ser Ile Val Ser Gly Ala Ala Pro Pro Gly Xaa  
1 5 10 15  
Pro Ser Phe Ser Tyr Leu Ala Val Phe Ser Asn Cys Pro Leu Val Ala  
20 25 30  
Ala Val Leu Ala Phe Ala Ile Ala Gln Ser Ile Lys Val Leu Thr Thr  
35 40 45  
Trp Tyr Lys Glu Asn Arg Trp Asp  
50 55  
(2) INFORMATION FOR SEQ ID NO:2314:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..505  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503000  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:  
gaaggacttc cgcgtcgccg tcaagcaggt gctcgacctg ttccaggaca actaccccgga 60  
gctcgtcgcg agaaacatct tgatcaacgt gccgttctgg tactacgcgt tcagcaccct 120  
gttctacccg ttcctgacgc agaggacgaa gagcaagttc gtcgttgctc gcccggtccaa 180  
ggtcaccgag accctcctca agtacattcc gatcgaggcc atcccgggtga agtacggcgg 240  
cctgaagcgc gacggcgaca ccgagttctc cgcggaacgac ggcgaggtcg cggaggtcac 300

cggtcaagggga agctccacgg agaccatcga gatcgaagcc actgaggctg atgccacgct 360  
gacatggggac ctgacgggtgc tgggggtggga ggtgaactac aaggaggagt tcgtgccggc 420  
ggacgagggc tcctacacca tcatcgctcag gaagggaag aagatggcgt ccggcgagga 480  
kgcggtcgc aactcgttcc gcacc

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

Glu Gly Leu Pro Arg Arg Arg Gln Ala Gly Ala Arg Pro Val Pro Gly  
1 5 10 15  
Gln Leu Pro Arg Ala Arg Arg Glu Lys His Leu Asp Gln Arg Ala Val  
20 25 30  
Leu Val Leu Arg Val Gln His Pro Val Leu Pro Val Pro Asp Ala Glu  
35 40 45  
Asp Glu Glu Gln Val Arg Arg Cys Ser Pro Val Gln Gly His Arg Asp  
50 55 60  
Pro Pro Gln Val His Ser Asp Arg Gly His Pro Gly Glu Val Arg Arg  
65 70 75 80  
Pro Glu Ala Arg Arg Arg His Arg Val Leu Arg Gly Arg Arg Arg Gly  
85 90 95  
Arg Gly Gly His Arg Gln Gly Lys Leu His Gly Asp His Arg Asp Arg  
100 105 110  
Ser His

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Lys Asp Phe Arg Val Ala Val Lys Gln Val Leu Asp Leu Phe Gln Asp  
1 5 10 15  
Asn Tyr Pro Glu Leu Val Ala Arg Asn Ile Leu Ile Asn Val Pro Phe  
20 25 30  
Trp Tyr Tyr Ala Phe Ser Thr Leu Phe Tyr Pro Phe Leu Thr Gln Arg  
35 40 45  
Thr Lys Ser Lys Phe Val Val Ala Arg Pro Ser Lys Val Thr Glu Thr  
50 55 60  
Leu Leu Lys Tyr Ile Pro Ile Glu Ala Ile Pro Val Lys Tyr Gly Gly  
65 70 75 80  
Leu Lys Arg Asp Gly Asp Thr Glu Phe Ser Ala Asp Asp Gly Glu Val  
85 90 95  
Ala Glu Val Thr Val Lys Gly Ser Ser Thr Glu Thr Ile Glu Ile Glu  
100 105 110  
Ala Thr Glu Ala Asp Ala Thr Leu Thr Trp Asp Leu Thr Val Leu Gly  
115 120 125  
Trp Glu Val Asn Tyr Lys Glu Glu Phe Val Pro Ala Asp Glu Gly Ser

130 135 140  
Tyr Thr Ile Ile Val Arg Lys Gly Lys Lys Met Ala Ser Gly Glu Xaa  
145 150 155 160  
Ala Val Arg Asn Ser Phe Arg Thr

165  
(2) INFORMATION FOR SEQ ID NO:2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| gtcgggtccat agcatcgatt cactccgcgc gcgccgctgt ctccctcgctg tcgccgcggtt | 60  |
| cctcgattat ctctccatgg cggccgctca tcccccgctg catccgcgcg ctcccccggt    | 120 |
| agggtgccgg cgaccctccc gcggcassag cggcgcgacg gctgggtgcc cctgccccat    | 180 |
| atgcctcgaa gccttcaaag acgaggccta cctcgacact tgcttccatt ccttttgcta    | 240 |
| caagtgtata tgccagtggg taaggatagt agcgagcaag cacgcagAAC ctttgtcttc    | 300 |
| agttagatgt ccactttgta agactgagaa tctatccgtc atacatgctt ttgatggcga    | 360 |
| atcatttgag cgggtgtaca taaatcagga acytaggaag aggcgttctt tcagatgcac    | 420 |
| acgagttggt gtcacaattc tataacatga aagagaccac aagcaacatt tctaggggtgc   | 480 |
| agcaatactg ggagc                                                     |     |

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ser Val His Ser Ile Asp Ser Leu Arg Ala Arg Arg Cys Leu Leu Val |  |
| 1 5 10 15                                                       |  |
| Val Ala Ala Phe Leu Asp Tyr Leu Ser Met Ala Ala Ala His Pro Pro |  |
| 20 25 30                                                        |  |
| Leu His Pro Pro Pro Pro Pro Val Gly Cys Arg Arg Pro Ser Arg Gly |  |
| 35 40 45                                                        |  |
| Xaa Ser Gly Ala Thr Ala Gly Cys Pro Cys Pro Ile Cys Leu Glu Ala |  |
| 50 55 60                                                        |  |
| Phe Lys Asp Glu Ala Tyr Leu Asp Thr Cys Phe His Ser Phe Cys Tyr |  |
| 65 70 75 80                                                     |  |
| Lys Cys Ile Cys Gln Trp Val Arg Ile Val Ala Ser Lys His Ala Glu |  |
| 85 90 95                                                        |  |
| Pro Leu Ser Ser Val Arg Cys Pro Leu Cys Lys Thr Glu Asn Leu Ser |  |
| 100 105 110                                                     |  |
| Val Ile His Ala Phe Asp Gly Glu Ser Phe Glu Arg Trp Tyr Ile Asn |  |
| 115 120 125                                                     |  |
| Gln Glu Xaa Arg Lys Arg Arg Ser Phe Arg Cys Thr Arg Val Gly Val |  |
| 130 135 140                                                     |  |
| Thr Ile Leu                                                     |  |
| 145                                                             |  |

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..122
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1503012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | His | Pro | Pro | Leu | His | Pro | Pro | Pro | Pro | Pro | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Arg | Arg | Pro | Ser | Arg | Gly | Xaa | Ser | Gly | Ala | Thr | Ala | Gly | Cys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Pro | Ile | Cys | Leu | Glu | Ala | Phe | Lys | Asp | Glu | Ala | Tyr | Leu | Asp | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Phe | His | Ser | Phe | Cys | Tyr | Lys | Cys | Ile | Cys | Gln | Trp | Val | Arg | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Ser | Lys | His | Ala | Glu | Pro | Leu | Ser | Ser | Val | Arg | Cys | Pro | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Lys | Thr | Glu | Asn | Leu | Ser | Val | Ile | His | Ala | Phe | Asp | Gly | Glu | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Glu | Arg | Trp | Tyr | Ile | Asn | Gln | Glu | Xaa | Arg | Lys | Arg | Arg | Ser | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Arg | Cys | Thr | Arg | Val | Gly | Val | Thr | Ile | Leu |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..436

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| cttttttcgg | aggaggcgga | ccaggtaagc | agcagcagga | accctagcac | cgccgcatcc | 60  |
| gcagccatgg | gtatcgacct | cgttgccggt | gggaggaaca | agaagaccaa | gcgcacagcs | 120 |
| cgaagtccga | cgatgtttat | ctcaagctcc | ttgtcaagct | ctaccgtttc | ttggtcagga | 180 |
| ggaccaagag | caacttcaat | gctgtcattc | tcaagaggct | cttcatgagc | aaaaccaatc | 240 |
| gcccaccaat | ctccatgcgc | cgccttgtca | agttcatgga | aggaaaggag | aagaacattg | 300 |
| ctgtgattgt | tggcacagtc | acagatgaca | agaggatcca | agaggttcca | gcaatgaagg | 360 |
| gaagctcgat | gactacatga | agttctttga | tggtcttcct | gcttagatgt | ttatttgtga | 420 |
| ctgctagggg | cgatgt     |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..75

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Ser | Glu | Glu | Ala | Asp | Gln | Val | Ser | Ser | Ser | Arg | Asn | Pro | Ser |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Thr | Ala | Ala | Ser | Ala | Ala | Met | Gly | Ile | Asp | Leu | Val | Ala | Gly | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Asn Lys Lys Thr Lys Arg Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser  
35 40 45  
Ser Ser Leu Ser Ser Ser Thr Val Ser Trp Ser Gly Gly Pro Arg Ala  
50 55 60  
Thr Ser Met Leu Ser Phe Ser Arg Gly Ser Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1503044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg  
1 5 10 15  
Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser Ser Ser Leu Ser Ser Ser  
20 25 30  
Thr Val Ser Trp Ser Gly Gly Pro Arg Ala Thr Ser Met Leu Ser Phe  
35 40 45  
Ser Arg Gly Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1503045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys  
1 5 10 15  
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val  
20 25 30  
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Gly Ser Ser  
35 40 45  
Met Thr Thr  
50

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1503048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

aggacaggtt gcatttgcac ctgagttcct gatcgttgta ttccagtttc ttccgtgagt 60  
tttgtgggat cgcgaggaag aaggatgtcg tgctgcggag gcaactgcgg gtgcggcgcc 120  
ggggcassagg ccggcgggca gtgcctgccg cagctgaacc gcctcctggs stgccgcgcg 180

tacctggtgc cggcgcgccc ggaccccagc gcggactgct gcagcgc

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Cys | Cys | Gly | Gly | Asn | Cys | Gly | Cys | Gly | Ala | Gly | Xaa | Xaa | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gly | Gln | Cys | Leu | Pro | Gln | Leu | Asn | Arg | Leu | Leu | Xaa | Cys | Arg | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Val | Pro | Gly | Ala | Pro | Asp | Pro | Ser | Ala | Asp | Cys | Cys | Ser |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aattctcccc | gcctccccct | ccgacctcc  | gactaccgcc | gcctcctggs | scasstctcc | 60  |
| tccgggggcc | tcttcgagcg | cgtcggcccc | acccccaggg | tacagctcgc | cctgatggcc | 120 |
| gtcctcttct | acggggcgct | ctacctcgtc | ctcgcctgcg | ccassgcctc | ggcssacatg | 180 |
| ctcgtctggg | ggctcatcgg | cttcgtcttg | atccagtcgg | gctggatggg | ccacgactcg | 240 |
| ggccaccacc | gcatacagg  | ccatccgctc | ctggaccgcg | tcgtgcaggt | gctctccgga | 300 |
| aactgcctca | ctggcctcag | catcgctctg | tggaaatgca | accacaacac | gcaccacatc | 360 |
| gcctgcaaca | gcctggacca | tgaccgggac | ctccagcaca | tgccgctctt | cgctgtctcc | 420 |
| cccaagctgt | tcggcaacat | atggtcctac | tkctaccagc | ggaccctggc | cttcgacgcc | 480 |
| gcctcgaaat | tcctcatcag | ctaccagcac | tg         |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Pro | Arg | Leu | Pro | Leu | Arg | Pro | Ser | Asp | Tyr | Arg | Arg | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Xaa | Xaa | Ser | Ser | Ala | Gly | Leu | Phe | Glu | Arg | Val | Gly | Pro | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Gln | Leu | Ala | Leu | Met | Ala | Val | Leu | Phe | Tyr | Ala | Ala | Leu | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Val | Leu | Ala | Cys | Ala | Xaa | Ala | Ser | Xaa | Xaa | Met | Leu | Ala | Gly | Gly |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ile | Gly | Phe | Val | Trp | Ile | Gln | Ser | Gly | Trp | Met | Gly | His | Asp | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | His | His | Arg | Ile | Thr | Gly | His | Pro | Leu | Leu | Asp | Arg | Val | Val | Gln |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |
| Val | Leu | Ser | Gly | Asn | Cys | Leu | Thr | Gly | Leu | Ser | Ile | Ala | Trp | Trp | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Asn | His | Asn | Thr | His | His | Ile | Ala | Cys | Asn | Ser | Leu | Asp | His | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Asp | Leu | Gln | His | Met | Pro | Leu | Phe | Ala | Val | Ser | Pro | Lys | Leu | Phe |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gly | Asn | Ile | Trp | Ser | Tyr | Xaa | Tyr | Gln | Arg | Thr | Leu | Ala | Phe | Asp | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Ser | Lys | Phe | Leu | Ile | Ser | Tyr | Gln | His |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1503066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Pro | Pro | Pro | Pro | Pro | Thr | Leu | Arg | Leu | Pro | Pro | Pro | Pro | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Xaa | Xaa | Leu | Leu | Arg | Gly | Pro | Leu | Arg | Ala | Arg | Arg | Pro | His | Pro | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Thr | Ala | Arg | Pro | Asp | Gly | Arg | Pro | Leu | Leu | Arg | Gly | Ala | Leu | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Pro | Arg | Leu | Arg | Xaa | Xaa | Leu | Gly | Xaa | His | Ala | Arg | Trp | Gly | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| His | Arg | Leu | Arg | Leu | Asp | Pro | Val | Arg | Leu | Asp | Gly | Pro | Arg | Leu | Gly |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Pro | Pro | Pro | His | His | Gly | Pro | Ser | Ala | Pro | Gly | Pro | Arg | Arg | Ala | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Leu | Arg | Lys | Leu | Pro | His | Trp | Pro | Gln | His | Arg | Leu | Val | Glu | Met |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Pro | Gln | His | Ala | Pro | His | Arg | Leu | Gln | Gln | Pro | Gly | Pro |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1503067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Leu | Phe | Tyr | Ala | Ala | Leu | Tyr | Leu | Val | Leu | Ala | Cys | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Xaa | Ala | Ser | Xaa | Xaa | Met | Leu | Ala | Gly | Gly | Leu | Ile | Gly | Phe | Val | Trp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Ser | Gly | Trp | Met | Gly | His | Asp | Ser | Gly | His | His | Arg | Ile | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | His | Pro | Leu | Leu | Asp | Arg | Val | Val | Gln | Val | Leu | Ser | Gly | Asn | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |

Leu Thr Gly Leu Ser Ile Ala Trp Trp Lys Cys Asn His Asn Thr His  
65 70 75 80  
His Ile Ala Cys Asn Ser Leu Asp His Asp Pro Asp Leu Gln His Met  
85 90 95  
Pro Leu Phe Ala Val Ser Pro Lys Leu Phe Gly Asn Ile Trp Ser Tyr  
100 105 110  
Xaa Tyr Gln Arg Thr Leu Ala Phe Asp Ala Ala Ser Lys Phe Leu Ile  
115 120 125  
Ser Tyr Gln His  
130

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| catgaagaaa agaaaggcgg tatccagacc tcaagccctg ctctgaagga ggagctgcgc | 60  |
| aagaggctga gcgttgctga agatgatgag gatttaagct gggatatcga ggatgacgat | 120 |
| gacaatgcct gaataccatt ggtgatatgg aagtgtcagt tgkatttcta cattttgcac | 180 |
| cttccattac tcgtgcaagt tactgtgatt tggccaatwa gattggctat ccttatgcta | 240 |
| tggacacgtt tgtatactgt aaactctcca gtttgatgat atcaagtggc aattggctaa | 300 |
| gcgcc                                                             |     |

(2) INFORMATION FOR SEQ ID NO:2331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| His Glu Glu Lys Lys Gly Gly Ile Gln Thr Ser Ser Pro Ala Leu Lys |  |
| 1 5 10 15                                                       |  |
| Glu Glu Leu Arg Lys Arg Leu Ser Val Ala Glu Asp Asp Glu Asp Leu |  |
| 20 25 30                                                        |  |
| Ser Trp Asp Ile Glu Asp Asp Asp Asn Ala                         |  |
| 35 40                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Glu Val Ser Val Xaa Phe Leu His Phe Ala Pro Ser Ile Thr Arg |  |
| 1 5 10 15                                                       |  |
| Ala Ser Tyr Cys Asp Leu Ala Asn Xaa Ile Gly Tyr Pro Tyr Ala Met |  |



20 25 30  
Asp Thr Phe Val Tyr Cys Lys Leu Ser Ser Leu Met Ile Ser Ser Gly  
35 40 45  
Asn Trp Leu Ser Ala  
50

(2) INFORMATION FOR SEQ ID NO:2333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..414
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| atccccacgaa aacaagcaca gagagagaga gaaccccagc gggcaaacgc ctccctcccc | 60  |
| ctgcctccag gccccagatc cggccatccg ggtagctcca gaccttctcc aatggcggtc  | 120 |
| aaggtctacg tcgtgtttta ctccacctac gggcacgttg ccaagcttgc tgaggagatg  | 180 |
| aagaaaggcg ccgcttcagt tgaaggcgtg gaggtcaaag tatggcaggt cccggagatt  | 240 |
| ctgtccgagg aggtgctcgg caagatgggc gcgccaccca agaccgacgc gccggtcatc  | 300 |
| accccgacga gctggcggag gccgacggcg tcctcttcgg gttccccacg cggttcggca  | 360 |
| tgatggcggc gcagatgaag gccttcttcg acgcgaccgg cgggctgtgg cgcg        |     |

(2) INFORMATION FOR SEQ ID NO:2334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Ile Pro Arg Lys Gln Ala Gln Arg Glu Arg Glu Pro Gln Arg Ala Asn |  |
| 1 5 10 15                                                       |  |
| Ala Ser Leu Pro Leu Pro Pro Gly Pro Arg Ser Gly His Pro Gly Ser |  |
| 20 25 30                                                        |  |
| Ser Arg Pro Ser Pro Met Ala Val Lys Val Tyr Val Val Phe Tyr Ser |  |
| 35 40 45                                                        |  |
| Thr Tyr Gly His Val Ala Lys Leu Ala Glu Glu Met Lys Lys Gly Ala |  |
| 50 55 60                                                        |  |
| Ala Ser Val Glu Gly Val Glu Val Lys Val Trp Gln Val Pro Glu Ile |  |
| 65 70 75 80                                                     |  |
| Leu Ser Glu Glu Val Leu Gly Lys Met Gly Ala Pro Pro Lys Thr Asp |  |
| 85 90 95                                                        |  |
| Ala Pro Val Ile Thr Pro Gln Ser Trp Arg Arg Pro Thr Ala Ser Ser |  |
| 100 105 110                                                     |  |
| Ser Gly Ser Pro Arg Gly Ser Ala                                 |  |
| 115 120                                                         |  |

(2) INFORMATION FOR SEQ ID NO:2335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1503106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

```
Met Ala Val Lys Val Tyr Val Val Phe Tyr Ser Thr Tyr Gly His Val
1 5 10 15
Ala Lys Leu Ala Glu Glu Met Lys Lys Gly Ala Ala Ser Val Glu Gly
20 25 30
Val Glu Val Lys Val Trp Gln Val Pro Glu Ile Leu Ser Glu Glu Val
35 40 45
Leu Gly Lys Met Gly Ala Pro Pro Lys Thr Asp Ala Pro Val Ile Thr
50 55 60
Pro Gln Ser Trp Arg Arg Pro Thr Ala Ser Ser Ser Gly Ser Pro Arg
65 70 75 80
Gly Ser Ala
```

(2) INFORMATION FOR SEQ ID NO:2336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1503107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

```
Met Ala Gly Pro Gly Asp Ser Val Arg Gly Gly Ala Arg Gln Asp Gly
1 5 10 15
Arg Ala Thr Gln Asp Arg Arg Ala Gly His His Pro Ala Glu Leu Ala
20 25 30
Glu Ala Asp Gly Val Leu Phe Gly Phe Pro Thr Arg Phe Gly Met Met
35 40 45
Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu Trp Arg
50 55 60
```

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

```
gtkattgggt tggctgcttg gttcttccct gccggaagat acctttcggt cgggtgcgcc 60
aactcgccat tcttgggagg tcttggtcgg gaccggtgct gatggaggag aggtacgagg 120
cgctgaagga gctggggggc ggcaacttcg gcgtggcgag gctggtcagg gacaagcgga 180
ccaaggagct ggtagccgtc aagtacatcg agaggggcaa gaagattgat gagaacgtgc 240
agagggagat catcaatcac cagtcgctcc ggcaccctaa catcgtagcg ttcaaggagg 300
tttgtctaac acccacacat cttgctattg tcatggaata tgctgctggt ggagagctat 360
ttgagaaaat ctgctcagca gggcgattca gtgaagatgw ktccaggat ttcttccaac 420
agctgatatc aggggttcag ctactgccat tctatggaaa tttgtcaccg tgatctttaa 480
acttkagaac accctccttg atgggagtc
```

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..156  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Trp | Val | Gly | Arg | Leu | Val | Leu | Pro | Cys | Arg | Lys | Ile | Pro | Phe | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Cys | Arg | Gln | Leu | Ala | Ile | Leu | Gly | Arg | Ser | Trp | Ser | Gly | Pro | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Met | Glu | Glu | Arg | Tyr | Glu | Ala | Leu | Lys | Glu | Leu | Gly | Ala | Gly | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Phe | Gly | Val | Ala | Arg | Leu | Val | Arg | Asp | Lys | Arg | Thr | Lys | Glu | Leu | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Ala | Val | Lys | Tyr | Ile | Glu | Arg | Gly | Lys | Lys | Ile | Asp | Glu | Asn | Val | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Glu | Ile | Ile | Asn | His | Gln | Ser | Leu | Arg | His | Pro | Asn | Ile | Val | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Lys | Glu | Val | Cys | Leu | Thr | Pro | Thr | His | Leu | Ala | Ile | Val | Met | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Ala | Ala | Gly | Gly | Glu | Leu | Phe | Glu | Lys | Ile | Cys | Ser | Ala | Gly | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Phe | Ser | Glu | Asp | Xaa | Ser | Arg | Tyr | Phe | Phe | Gln | Gln | Leu | Ile | Ser | Gly |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Gln | Leu | Leu | Pro | Phe | Tyr | Gly | Asn | Leu | Ser | Pro |     |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2339:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Arg | Tyr | Glu | Ala | Leu | Lys | Glu | Leu | Gly | Ala | Gly | Asn | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Ala | Arg | Leu | Val | Arg | Asp | Lys | Arg | Thr | Lys | Glu | Leu | Val | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Tyr | Ile | Glu | Arg | Gly | Lys | Lys | Ile | Asp | Glu | Asn | Val | Gln | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ile | Ile | Asn | His | Gln | Ser | Leu | Arg | His | Pro | Asn | Ile | Val | Arg | Phe |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Lys | Glu | Val | Cys | Leu | Thr | Pro | Thr | His | Leu | Ala | Ile | Val | Met | Glu | Tyr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ala | Gly | Gly | Glu | Leu | Phe | Glu | Lys | Ile | Cys | Ser | Ala | Gly | Arg | Phe |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Glu | Asp | Xaa | Ser | Arg | Tyr | Phe | Phe | Gln | Gln | Leu | Ile | Ser | Gly | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gln | Leu | Leu | Pro | Phe | Tyr | Gly | Asn | Leu | Ser | Pro |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2340:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..263  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503132  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:  
accagccggt gttggtttca gcttgatttc ccactctgtc gcacagcgtc gcccgctcgcc 60  
gctgagatcc taggaagaaa tggagctctc tcgcaagctc ttcacggccg tcctcctcgt 120  
catgctgctg ctgctgtccg cagaggtcgg gccggtggcg gtggcggagg cgcggacgtg 180  
ccagtcgcag agccacaggt tccggggccc ctgcctccgc cggccaact gcgccaacgt 240  
ctgcaggacc gaggggttcc ccg

(2) INFORMATION FOR SEQ ID NO:2341:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503133  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:  
Thr Ser Arg Cys Trp Phe Gln Leu Val Phe Pro Leu Cys Arg Thr Ala  
1 5 10 15  
Ser Pro Val Ala Glu Ile Leu Gly Arg Asn Gly Ala Leu Ser Gln  
20 25 30  
Ala Leu His Gly Arg Pro Pro Arg His Ala Ala Ala Val Arg Arg  
35 40 45  
Gly Arg Ala Gly Gly Gly Gly Gly Gly Ala Asp Val Pro Val Ala Glu  
50 55 60  
Pro Gln Val Pro Gly Pro Leu Pro Pro Pro Val Gln Leu Arg Gln Arg  
65 70 75 80  
Leu Gln Asp Arg Gly Val Pro  
85

(2) INFORMATION FOR SEQ ID NO:2342:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..61  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503134  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:  
Met Glu Leu Ser Arg Lys Leu Phe Thr Ala Val Leu Leu Val Met Leu  
1 5 10 15  
Leu Leu Leu Ser Ala Glu Val Gly Pro Val Ala Val Ala Glu Ala Arg  
20 25 30  
Thr Cys Gln Ser Gln Ser His Arg Phe Arg Gly Pro Cys Leu Arg Arg  
35 40 45  
Ser Asn Cys Ala Asn Val Cys Arg Thr Glu Gly Phe Pro  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2343:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..47  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503135  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:  
Met Leu Leu Leu Leu Ser Ala Glu Val Gly Pro Val Ala Val Ala Glu  
1                  5                  10                  15  
Ala Arg Thr Cys Gln Ser Gln Ser His Arg Phe Arg Gly Pro Cys Leu  
                  20                  25                  30  
Arg Arg Ser Asn Cys Ala Asn Val Cys Arg Thr Glu Gly Phe Pro  
                  35                  40                  45

(2) INFORMATION FOR SEQ ID NO:2344:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 342 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..342  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| tccaccaccg cttcaccatc ccctccaggc ccaccaccac catggcctct ccttcccctt  | 60  |
| cttcccccg cgcgcctcc ggccgccgcg tgccgccgcc gtgctggacg accgacgaga    | 120 |
| ccctcgcgct cgcgssggtc ctacaccgcg cccgcctcgc cgtcggccgg gagcacctga  | 180 |
| cctccaccga ctggggccgc gtagccgcgg cgccccgtcc aagaccgcca gcagtgcgc   | 240 |
| cacaagatcg agaagctccg ccgacgcctc cgttccaacc gccgacgccc atgcccgcctt | 300 |
| ccctcgacgc atggatctcc tcgacggccc tttccccgcc ct                     |     |

(2) INFORMATION FOR SEQ ID NO:2345:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:

Pro Pro Pro Leu His His Pro Leu Gln Ala His His His His Gly Leu  
1                  5                  10                  15  
Ser Phe Pro Phe Phe Pro Arg Pro Arg Leu Arg Pro Pro Arg Ala Ala  
                  20                  25                  30  
Ala Val Leu Asp Asp Arg Arg Asp Pro Arg Ala Arg Xaa Gly Pro Thr  
                  35                  40                  45  
Pro Arg Pro Pro Arg Arg Arg Pro Gly Ala Pro Asp Leu His Arg Leu  
                  50                  55                  60  
Gly Arg Arg Ser Arg Gly Ala Pro Ser Lys Thr Ala Ser Ser Ala Ala  
65                  70                  75                  80  
Thr Arg Ser Arg Ser Ser Ala Asp Ala Ser Gly Pro Thr Ala Asp Ala  
                  85                  90                  95  
His Ala Arg Phe Leu Asp Ala Met Asp Leu Leu Asp Gly Pro Phe Pro  
                  100                  105                  110  
Ala

(2) INFORMATION FOR SEQ ID NO:2346:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..113  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503138  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | His | Arg | Phe | Thr | Ile | Pro | Ser | Arg | Pro | Thr | Thr | Thr | Met | Ala | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Pro | Ser | Ser | Pro | Ala | Arg | Ala | Ser | Gly | Arg | Arg | Val | Pro | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Cys | Trp | Thr | Thr | Asp | Glu | Thr | Leu | Ala | Leu | Ala | Xaa | Val | Leu | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Arg | Leu | Ala | Val | Gly | Arg | Glu | His | Leu | Thr | Ser | Thr | Asp | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ala | Val | Ala | Ala | Ala | Pro | Arg | Pro | Arg | Pro | Pro | Ala | Val | Pro | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Asp | Arg | Glu | Ala | Pro | Pro | Thr | Pro | Pro | Val | Gln | Pro | Pro | Thr | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Pro | Ala | Ser | Ser | Thr | Pro | Trp | Ile | Ser | Ser | Thr | Ala | Leu | Ser | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:2347:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 100 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..100  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503139  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Pro | Ser | Pro | Ser | Ser | Pro | Ala | Arg | Ala | Ser | Gly | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Pro | Pro | Cys | Trp | Thr | Thr | Asp | Glu | Thr | Leu | Ala | Leu | Ala | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | His | Arg | Ala | Arg | Leu | Ala | Val | Gly | Arg | Glu | His | Leu | Thr | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Asp | Trp | Ala | Ala | Val | Ala | Ala | Ala | Pro | Arg | Pro | Arg | Pro | Pro | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Pro | Pro | Gln | Asp | Arg | Glu | Ala | Pro | Pro | Thr | Pro | Pro | Val | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Thr | Pro | Met | Pro | Ala | Ser | Ser | Thr | Pro | Trp | Ile | Ser | Ser | Thr | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Ser | Pro | Pro |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:2348:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 536 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..536  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| attacacacc | agcctcttga | tgcaggtttt | agtgccattg | tggaatcatg  | caaggkcctc | 60  |
| agkcggtttt | ctgtttcagg | tcctttctac | ggacagtgtg | tttaaatacca | tcggggcaca | 120 |
| tgctgaccgt | cttgagatgc | tctcgattgc | cttcgcgggg | aacagtgatt  | tgggcctcca | 180 |
| ttacatccta | tcgggctgca | agagcttgaa | gaagctagag | attagggact  | gcccatttgg | 240 |
| tgacaagccc | ttgctggcaa | acgctgccaa | gctggagaca | atgcgatccc  | tttggatgtc | 300 |
| gacgtgctca | atgaccttgg | gcgcatgcgg | cagcttgccg | gcaagatgcc  | ccgtcttagt | 360 |
| gtggaggtca | tgaatgatcc | tcgacgagga | ttccccttgg | actctctaac  | agatgagagc | 420 |
| cctgttgaga | cgttgatatg | ctaccggaca | atttcaggtc | caakgtccka  | cacaccagct | 480 |
| tgtgtccaga | ttctctaagg | ggcagctgtg | gtctacaaag | gtactatgga  | agcatc     |     |

(2) INFORMATION FOR SEQ ID NO:2349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | His | Thr | Ser | Leu | Leu | Met | Gln | Val | Leu | Val | Pro | Leu | Trp | Asn | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Arg | Xaa | Ser | Xaa | Gly | Phe | Leu | Phe | Gln | Val | Leu | Leu | Thr | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Phe | Lys | Ser | Ile | Gly | Ala | His | Ala | Asp | Arg | Leu | Glu | Met | Leu | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Phe | Ala | Gly | Asn | Ser | Asp | Leu | Gly | Leu | His | Tyr | Ile | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Cys | Lys | Ser | Leu | Lys | Lys | Leu | Glu | Ile | Arg | Asp | Cys | Pro | Phe | Gly |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Lys | Pro | Leu | Leu | Ala | Asn | Ala | Ala | Lys | Leu | Glu | Thr | Met | Arg | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Trp | Met | Ser | Thr | Cys | Ser | Met | Thr | Leu | Gly | Ala | Cys | Gly | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ala | Arg | Cys | Pro | Val | Leu | Val | Trp | Arg | Ser |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Val | Leu | Val | Pro | Leu | Trp | Asn | His | Ala | Arg | Xaa | Ser | Xaa | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Leu | Phe | Gln | Val | Leu | Leu | Thr | Asp | Ser | Val | Phe | Lys | Ser | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | His | Ala | Asp | Arg | Leu | Glu | Met | Leu | Ser | Ile | Ala | Phe | Ala | Gly | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Leu | Gly | Leu | His | Tyr | Ile | Leu | Ser | Gly | Cys | Lys | Ser | Leu | Lys |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |

Lys Leu Glu Ile Arg Asp Cys Pro Phe Gly Asp Lys Pro Leu Leu Ala  
65 70 75 80  
Asn Ala Ala Lys Leu Glu Thr Met Arg Ser Leu Trp Met Ser Thr Cys  
85 90 95  
Ser Met Thr Leu Gly Ala Cys Gly Ser Leu Arg Ala Arg Cys Pro Val  
100 105 110  
Leu Val Trp Arg Ser  
115

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

Met Leu Ser Ile Ala Phe Ala Gly Asn Ser Asp Leu Gly Leu His Tyr  
1 5 10 15  
Ile Leu Ser Gly Cys Lys Ser Leu Lys Lys Leu Glu Ile Arg Asp Cys  
20 25 30  
Pro Phe Gly Asp Lys Pro Leu Leu Ala Asn Ala Ala Lys Leu Glu Thr  
35 40 45  
Met Arg Ser Leu Trp Met Ser Thr Cys Ser Met Thr Leu Gly Ala Cys  
50 55 60  
Gly Ser Leu Arg Ala Arg Cys Pro Val Leu Val Trp Arg Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

atcaatgcgc gggtcaggct ctggaagcca atggtggagg agatgtacgt ggaggagatg 60  
aaggccgagg gcaggacggc gggggccagc agcaggtagg cgtcgcgkcg ccaacaaccc 120  
taaccctagc agcgccggcc acgcctccga ggcggcgtga ggacg

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr  
1 5 10 15  
Val Glu Glu Met Lys Ala Glu Gly Arg Thr Ala Gly Ala Ser Ser Arg  
20 25 30



(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

Gln Cys Ala Gly Gln Ala Leu Glu Ala Asn Gly Gly Gly Asp Val Arg  
1 5 10 15  
Gly Gly Asp Glu Gly Arg Gly Gln Asp Gly Gly Gly Gln Gln Gln Val  
20 25 30  
Gly Val Ala Xaa Pro Thr Thr Leu Thr Leu Ala Ala Pro Ala Thr Pro  
35 40 45  
Pro Arg Arg Arg Glu Asp  
50

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..453
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

ctctccagcg gctccagcca atccggcaat cccgctcccc cagctcgetg ctcgcccgcgt 60  
ctcctccgcc ctccgccatg gsgccttccc ctccgcctcc ccgtcgccgg cgatctccgc 120  
ctcgacctgg agcatggctt cctccgtac gtccctcccc gcactccgcc cctccccgcg 180  
gggcaggctc cgttcgctcg tctcgcccgc ggggcgggtcc acggctgcat cggtcggctg 240  
cctcgggtcc ttctccggcc tcgcgcccggt ctcaaatctc ctctccctcg gcgctgagaa 300  
ctcaagcttt gacatcggt tgtttggatt gatgcccggt gaaggatagt tgcgatgcga 360  
catgggagac gcgttcctaa acttaacagg cctccggatc aaaggaaagc actgctgcgt 420  
gggcttacca cacagctgct gaagcatggg agg

(2) INFORMATION FOR SEQ ID NO:2356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:

Leu Ser Ser Gly Ser Ser Gln Ser Gly Asn Pro Ala Pro Pro Ala Arg  
1 5 10 15  
Cys Ser Pro Ala Leu Leu Arg Pro Pro Pro Trp Xaa Leu Pro Leu Arg  
20 25 30  
Leu Pro Val Ala Gly Asp Leu Arg Leu Asp Leu Glu His Gly Phe Pro  
35 40 45  
Pro Tyr Val Pro Pro Arg Thr Pro Pro Leu Pro Arg Gly Gln Ala Pro

```

 50 55 60
Phe Val Val Leu Ala Arg Gly Ala Val His Gly Cys Ile Gly Arg Leu
65 70 75 80
Pro Arg Val Leu Leu Arg Pro Arg Ala Arg Leu Glu Ser Pro Leu Pro
 85 90 95
Arg Arg
```

(2) INFORMATION FOR SEQ ID NO:2357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1503153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

```

Ser Pro Ala Ala Pro Ala Asn Pro Ala Ile Pro Leu Pro Gln Leu Ala
1 5 10 15
Ala Arg Pro Leu Ser Ser Ala Leu Arg His Xaa Ala Phe Pro Ser Ala
 20 25 30
Ser Pro Ser Pro Ala Ile Ser Ala Ser Thr Trp Ser Met Ala Ser Leu
 35 40 45
Arg Thr Ser Leu Pro Ala Leu Arg Pro Ser Pro Ala Gly Arg Leu Arg
 50 55 60
Ser Ser Phe Ser Pro Ala Gly Arg Ser Thr Ala Ala Ser Val Gly Cys
65 70 75 80
Leu Gly Ser Phe Ser Gly Leu Ala Pro Val Ser Asn Leu Leu Ser Leu
 85 90 95
Gly Ala Glu Asn Ser Ser Phe Xaa His Arg Leu Phe Gly Leu Met Pro
 100 105 110
Val Glu Gly
 115
```

(2) INFORMATION FOR SEQ ID NO:2358:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1503154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

```

Leu Gln Arg Leu Gln Pro Ile Arg Gln Ser Arg Ser Pro Ser Ser Leu
1 5 10 15
Leu Ala Arg Ser Pro Pro Pro Ser Ala Met Xaa Pro Ser Pro Pro Pro
 20 25 30
Pro Arg Arg Arg Arg Ser Pro Pro Arg Pro Gly Ala Trp Leu Pro Ser
 35 40 45
Val Arg Pro Ser Pro His Ser Ala Pro Pro Pro Arg Ala Gly Ser Val
 50 55 60
Arg Arg Ser Arg Pro Arg Gly Gly Pro Arg Leu His Arg Ser Ala Ala
65 70 75 80
Ser Gly Pro Ser Pro Ala Ser Arg Pro Ser Arg Ile Ser Ser Pro Ser
 85 90 95
Ala Leu Arg Thr Gln Ala Leu Xaa Ile Gly Cys Leu Asp
 100 105
```

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| aaaggatgca ctggttccag ttcaacctcc ctgagctgtg atgggaatcg cattccctct | 60  |
| ataattccta taaatagggg ccctcccgtc cccatcaca tcacccatca ctgctatat   | 120 |
| tccattcca agtccccgtc cttggattcc cgacgacgag ctgggagctt cttcttcct   | 180 |
| gctcggtgct cgccgcaaca gctgccgcca tgtctgccgc gaaccagctc gccgctctgg | 240 |
| tcagcaacat gtacgccacg ggtttgcttg acgatcagtt ccagcagctc cagctsstcc | 300 |
| aggacccag cgcccctgac tttcgtctcc gaggtcgtca cgctcttctg tcaggacggc  | 360 |
| gagcgatca tcgaagagct ggccaaactg ctggagaagc ccaacgtgga ttttgacagg  | 420 |
| gttgacgcct ytgtgcatca gctcaaggga agcag                            |     |

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Gly | Cys | Thr | Gly | Ser | Ser | Ser | Thr | Ser | Leu | Ser | Cys | Asp | Gly | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Ile | Pro | Ser | Ile | Ile | Pro | Ile | Asn | Arg | Gly | Pro | Pro | Ala | Pro | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Ile | Thr | His | His | Ser | Leu | Tyr | Ser | His | Ser | Lys | Ser | Pro | Leu | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Ser | Arg | Arg | Arg | Ala | Arg | Ser | Phe | Phe | Phe | Pro | Ala | Arg | Cys | Ser |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Gln | Gln | Leu | Pro | Pro | Cys | Leu | Pro | Arg | Thr | Ser | Ser | Pro | Leu | Trp |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Ala | Thr | Cys | Thr | Pro | Arg | Val | Cys | Leu | Thr | Ile | Ser | Ser | Ser | Ser |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Ser | Ser | Xaa | Ser | Arg | Thr | Pro | Ala | Pro | Leu | Thr | Phe | Val | Ser | Glu | Val |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Val | Thr | Leu | Phe | Cys | Gln | Asp | Gly | Glu | Arg | Ile | Ile | Glu | Glu | Leu | Ala |  |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Lys | Leu | Leu | Glu | Lys | Pro | Asn | Val | Asp | Phe | Asp | Arg | Val | Asp | Ala | Xaa |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | His | Gln | Leu | Lys | Gly | Ser |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1503170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ctatggactt  | cggtgaaggt | ttgcctcgct | cacagcatgc | tgattgcac  | ctgggttattg | 60  |
| tggacaaatt  | ctctaaatat | ggccacttcc | ttccactcag | tcacccctat | actgctcact  | 120 |
| cgggttgctca | cagcttcttg | ttcaatgttt | acaagatcca | tgccctttct | tcagttatta  | 180 |
| tttcggatcg  | tgacctagt  | ttcaccagcc | agttttggca | acaaccgttt | cgctctgcgg  | 240 |
| gcattgagct  | taagccgagt | tcttcttacc | atccccaac  | cgacggacag | accgaacaag  | 300 |
| tcaatcaatg  | cttggaacaa | tatctgcgct | gcttcgcaaa | tgtctgccca | acgaaatgga  | 360 |
| aagagtgggt  | gcctgtgggc | gagtactggt | acaacaccag | cctccactct | gcactggggc  | 420 |
| gtgcaccatt  | tgaggttctt | tatggccgcc | aaccccgta  | c          |             |     |

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Phe | Val | Glu | Gly | Leu | Pro | Arg | Ser | Gln | His | Ala | Asp | Cys | Ile |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Val | Ile | Val | Asp | Lys | Phe | Ser | Lys | Tyr | Gly | His | Phe | Leu | Pro | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | His | Pro | Tyr | Thr | Ala | His | Ser | Val | Ala | His | Ser | Phe | Leu | Phe | Asn |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Tyr | Lys | Ile | His | Gly | Leu | Ser | Ser | Val | Ile | Ile | Ser | Asp | Arg | Asp |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Val | Phe | Thr | Ser | Gln | Phe | Trp | Gln | Gln | Pro | Phe | Arg | Leu | Ala | Gly |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Glu | Leu | Lys | Pro | Ser | Ser | Ser | Tyr | His | Pro | Gln | Thr | Asp | Gly | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Thr | Glu | Gln | Val | Asn | Gln | Cys | Leu | Glu | Thr | Tyr | Leu | Arg | Cys | Phe | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asn | Val | Cys | Pro | Thr | Lys | Trp | Lys | Glu | Trp | Leu | Pro | Val | Gly | Glu | Tyr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Trp | Tyr | Asn | Thr | Ser | Leu | His | Ser | Ala | Leu | Gly | Arg | Ala | Pro | Phe | Glu |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Leu | Tyr | Gly | Arg | Gln | Pro | Arg | Thr |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Phe | Val | Glu | Gly | Leu | Pro | Arg | Ser | Gln | His | Ala | Asp | Cys | Ile |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Val | Ile | Val | Asp | Lys | Phe | Ser | Lys | Tyr | Gly | His | Phe | Leu | Pro | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | His | Pro | Tyr | Thr | Ala | His | Ser | Val | Ala | His | Ser | Phe | Leu | Phe | Asn |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

Val Tyr Lys Ile His Gly Leu Ser Ser Val Ile Ile Ser Asp Arg Asp  
50 55 60  
Leu Val Phe Thr Ser Gln Phe Trp Gln Gln Pro Phe Arg Leu Ala Gly  
65 70 75 80  
Ile Glu Leu Lys Pro Ser Ser Ser Tyr His Pro Gln Thr Asp Gly Gln  
85 90 95  
Thr Glu Gln Val Asn Gln Cys Leu Glu Thr Tyr Leu Arg Cys Phe Ala  
100 105 110  
Asn Val Cys Pro Thr Lys Trp Lys Glu Trp Leu Pro Val Gly Glu Tyr  
115 120 125  
Trp Tyr Asn Thr Ser Leu His Ser Ala Leu Gly Arg Ala Pro Phe Glu  
130 135 140  
Val Leu Tyr Gly Arg Gln Pro Arg Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acacttcgat cagtgtcgcc aacaagtagc tagacgatga gcagaggagc tgagaagaag  | 60  |
| aattggccgc cgtctcggtc ttcttcctcc tcctcttctt caccgacgtc gtcgtngggt  | 120 |
| cgccagcagg tccatggcgg ggtttaccg ctacccgcc tccactcgca cctccggcaw    | 180 |
| kgacagaacc cagccgccgc cagcaccagc tgcaccgaca caacaacaag gcgacaagag  | 240 |
| cagcagcaag aagaagagga ggagtatcag catcgccgg agcatcacgt gcgcgggctc   | 300 |
| catctgcagt accaaggaga gctcgggtcat gagccgggac cgccgcggcg cctccagcag | 360 |
| gtcgtcagg gcaccctacg tcgacgtcga cgtcaacgac gcctctgccg ccgccatctc   | 420 |
| cgccacgtcg tccttcaact cggagaccac cgtggc                            |     |

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met Ser Arg Gly Ala Glu Lys Lys Asn Trp Pro Pro Ser Arg Ser Ser  
1 5 10 15  
Ser Ser Ser Ser Ser Ser Pro Thr Ser Ser Xaa Gly Arg Gln Gln Val  
20 25 30  
His Gly Gly Val Leu Pro Leu Pro Val Leu His Ser His Leu Arg Xaa  
35 40 45  
Xaa Gln Asn Pro Ala Ala Ala Ser Thr Ser Cys Thr Asp Thr Thr Thr  
50 55 60  
Arg Arg Gln Glu Gln Gln Glu Glu Glu Glu Tyr Gln His Arg  
65 70 75 80  
Pro Glu His His Val Arg Gly Leu His Leu Gln Tyr Gln Gly Glu Leu  
85 90 95  
Gly His Glu Pro Gly Pro Pro Arg Arg Leu Gln Gln Val Ala Gln Gly  
100 105 110  
Thr Leu Arg Arg Arg Arg Arg Gln Arg Arg Leu Cys Arg Arg His Leu

115 120 125  
Arg His Val Val Leu Gln Leu Gly Asp His Arg Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

Met Ala Gly Phe Tyr Arg Tyr Pro Ser Ser Thr Arg Thr Ser Gly Xaa  
1 5 10 15  
Asp Arg Thr Gln Pro Pro Pro Ala Pro Ala Ala Pro Thr Gln Gln  
20 25 30  
Gly Asp Lys Ser Ser Ser Lys Lys Arg Arg Ser Ile Ser Ile Gly  
35 40 45  
Arg Ser Ile Thr Cys Ala Gly Ser Ile Cys Ser Thr Lys Glu Ser Ser  
50 55 60  
Val Met Ser Arg Asp Arg Arg Gly Ala Ser Ser Arg Ser Leu Arg Ala  
65 70 75 80  
Pro Tyr Val Asp Val Asp Val Asn Asp Ala Ser Ala Ala Ala Ile Ser  
85 90 95  
Ala Thr Ser Ser Phe Asn Ser Glu Thr Thr Val  
100 105

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

atgcatgctg aaactgtggc aaattggaac cacttattca gttggtgttt tgcaaattca 60  
gatttgggtg aattactgac tctcaactgc cctgctgaca gagcaatggt gctgctgatg 120  
taccaaattg agttgagact gctcaattgg gcctgggcag acgagtgtgt cttcaacctg 180  
tgtctacttc gattacacag tgttgttcat agcagcctag ccaatgctta taaatcctgg 240  
ttgataacag tgattcaccg aacacactca attggccaag atcatttttg gcataacgtg 300  
gataggggtg tgggtgtgtg aattaaggat agatgctgtg caagattggc aaagctagtt 360  
ttatctgcta cactgacaca agattctggc aagctttctc aacttgaatt gcaccatcca 420  
ttgttggtga ataactcagtc aagcggcttg aggacaagcc ggatttcaag cggtggggaa 480  
tatcagcata tcatcttctc ctcaagtcaa ag

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ala | Glu | Thr | Val | Ala | Asn | Trp | Asn | His | Leu | Phe | Ser | Trp | Cys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ala | Asn | Ser | Asp | Leu | Gly | Glu | Leu | Thr | Leu | Asn | Cys | Pro | Ala |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Arg | Ala | Met | Val | Leu | Leu | Met | Tyr | Gln | Ile | Glu | Leu | Arg | Leu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Trp | Ala | Trp | Ala | Asp | Glu | Cys | Val | Phe | Asn | Leu | Cys | Leu | Leu | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | His | Ser | Val | Val | His | Ser | Ser | Leu | Ala | Asn | Ala | Tyr | Lys | Ser | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ile | Thr | Val | Ile | His | Arg | Thr | His | Ser | Ile | Gly | Gln | Asp | His | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | His | Asn | Val | Asp | Arg | Gly | Val | Val | Cys | Gly | Ile | Lys | Asp | Arg | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Ala | Arg | Leu | Ala | Lys | Leu | Val | Leu | Ser | Ala | Thr | Leu | Thr | Gln | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Lys | Leu | Ser | Gln | Leu | Glu | Leu | His | His | Pro | Leu | Leu | Leu | Asn |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Gln | Ser | Ser | Gly | Leu | Arg | Thr | Ser | Arg | Ile | Ser | Ser | Gly | Gly | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Gln | His | Ile | Ile | Phe | Ser | Ser | Ser | Gln |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Ala | Glu | Thr | Val | Ala | Asn | Trp | Asn | His | Leu | Phe | Ser | Trp | Cys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ala | Asn | Ser | Asp | Leu | Gly | Glu | Leu | Thr | Leu | Asn | Cys | Pro | Ala |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asp | Arg | Ala | Met | Val | Leu | Leu | Met | Tyr | Gln | Ile | Glu | Leu | Arg | Leu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Trp | Ala | Trp | Ala | Asp | Glu | Cys | Val | Phe | Asn | Leu | Cys | Leu | Leu | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | His | Ser | Val | Val | His | Ser | Ser | Leu | Ala | Asn | Ala | Tyr | Lys | Ser | Trp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Ile | Thr | Val | Ile | His | Arg | Thr | His | Ser | Ile | Gly | Gln | Asp | His | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Trp | His | Asn | Val | Asp | Arg | Gly | Val | Val | Cys | Gly | Ile | Lys | Asp | Arg | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Ala | Arg | Leu | Ala | Lys | Leu | Val | Leu | Ser | Ala | Thr | Leu | Thr | Gln | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Gly | Lys | Leu | Ser | Gln | Leu | Glu | Leu | His | His | Pro | Leu | Leu | Leu | Asn |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Gln | Ser | Ser | Gly | Leu | Arg | Thr | Ser | Arg | Ile | Ser | Ser | Gly | Gly | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Gln | His | Ile | Ile | Phe | Ser | Ser | Ser | Gln |     |     |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..135
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1503203
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:

```
Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu Asn Trp Ala
1 5 10 15
Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg Leu His Ser
 20 25 30
Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp Leu Ile Thr
 35 40 45
Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe Trp His Asn
 50 55 60
Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys Cys Ala Arg
65 70 75 80
Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp Ser Gly Lys
 85 90 95
Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Leu Asn Thr Gln Ser
 100 105 110
Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu Tyr Gln His
 115 120 125
Ile Ile Phe Ser Ser Ser Gln
 130 135
```

- (2) INFORMATION FOR SEQ ID NO:2371:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 345 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: -
    - (B) LOCATION: 1..345
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1503237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

```
tctccgcgca ctccacccca ctgcgcgccg ccgctgccac cgccgcttgc tgccgcagcc 60
gccatggggg cgtacaagta cgtatcgga ctatggagga ggaagcagtc ggacgtgatg 120
gcggctacgg cggcggcggc ggcggtgga gggactgatg tgtgggcca tctggcttc 180
ggccgagtta tcttatctat ctatagtatc gtgttaccgt tcgcttctgt caccgtgtta 240
gtgtccgttc tacctttgga ttaggtgttg gtacccctgt tgttcccttt ggttgctccc 300
gctatgaaac gagacgagag aagaatgagc aagggttttg ttcgc
```

- (2) INFORMATION FOR SEQ ID NO:2372:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 87 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: peptide
    - (B) LOCATION: 1..87
    - (D) OTHER INFORMATION: / Ceres Seq. ID 1503238
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

```
Ser Pro Arg Thr Pro Pro His Ser Pro Pro Pro Leu Pro Pro Pro Leu
1 5 10 15
Ala Ala Ala Ala Ala Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp
 20 25 30
Arg Arg Lys Gln Ser Asp Val Met Ala Ala Thr Ala Ala Ala Ala
```



35 40 45  
Ala Gly Thr Asp Val Trp Ala His Pro Gly Phe Gly Arg Val Ile  
50 55 60  
Leu Ser Ile Tyr Ser Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu  
65 70 75 80  
Val Ser Val Leu Pro Leu Asp  
85

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Ser Ala His Ser Thr Pro Leu Ala Ala Ala Thr Ala Ala Cys  
1 5 10 15  
Cys Arg Ser Arg His Gly Gly Val Gln Val Arg Ile Gly Thr Met Glu  
20 25 30  
Glu Glu Ala Val Gly Arg Asp Gly Gly Tyr Gly Gly Gly Gly Gly Gly  
35 40 45  
Trp Arg Asp  
50

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp Arg Arg Lys Gln Ser  
1 5 10 15  
Asp Val Met Ala Ala Thr Ala Ala Ala Ala Ala Gly Gly Thr Asp  
20 25 30  
Val Trp Ala His Pro Gly Phe Gly Arg Val Ile Leu Ser Ile Tyr Ser  
35 40 45  
Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu Val Ser Val Leu Pro  
50 55 60  
Leu Asp  
65

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..400
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

cccgttaaaaa tcacgacgcg gtggtgactg gtgagtccac agtccacact cccactcca 60  
ttttctacca tcacactgac acgttcatag ctagctagtc ttcagctagt aacgtacgac 120  
ggactaatct cgatctggga gcgaggagga ggacgacgat aatgaagatg agctccgtgc 180  
ccgcggcass cgggtgatgg tgggtggtgg gctgctctct gcggcgggcg cgactgtgac 240  
ggggcaggcg cttgtgccgg gcgtgatgat cttcggcgac tcggtggttg acgcaggcaa 300  
caacaaccgg ctacgcgacg tgggtgcgcg cgacttcccg ccctacggcc gcgacttccc 360  
ggcgacgcac gcgcccacgg gntnnccctgc aacggcaagc

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

Met Val Val Val Val Leu Leu Ser Ala Ala Ala Thr Val Thr Gly  
1 5 10 15  
Gln Ala Leu Val Pro Gly Val Met Ile Phe Gly Asp Ser Val Val Asp  
20 25 30  
Ala Gly Asn Asn Asn Arg Leu Ala Thr Leu Val Arg Ala Asp Phe Pro  
35 40 45  
Pro Tyr Gly Arg Asp Phe Pro Ala Thr His Ala Pro Thr Xaa Xaa Pro  
50 55 60  
Ala Thr Ala Ser  
65

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

Met Ile Phe Gly Asp Ser Val Val Asp Ala Gly Asn Asn Asn Arg Leu  
1 5 10 15  
Ala Thr Leu Val Arg Ala Asp Phe Pro Pro Tyr Gly Arg Asp Phe Pro  
20 25 30  
Ala Thr His Ala Pro Thr Xaa Xaa Pro Ala Thr Ala Ser  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

ctcttttctcc ccagtagcaa cgaccgcgcg tcctccgcen ccgcactaaa ccctactcca 60  
tgtaccacagg tctgcgtcgg gccccccggc gatgagaacc cgtcagttcc aaagatggct 120

cgctcgtggat tgatggaaca kgacttaagc aaactggatg tgacgaagct tcaccccctg 180  
tcacctgaag ttatctcacg ccaagcaaca atcaatatgg gtaccattgg ccatgtggct 240  
kcatggaaag tccactgttg ttaaagctat atctggtgtt cagactgttc ggttcaagaa 300  
tgagctggaa cgtaacatta ctataaagct gggttacgct aatgcaaaaa tctacaaatg 360  
tgaggatgac agatgtccgc gaccaatgtg ctacaaggcc tatggaagcg gaaaakaaga 420  
tagccctcta tgtgatgtgc ctggatttga aaacactaga atg

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

Leu Phe Leu Pro Ser Ser Asn Asp Arg Ala Ser Ser Ala Xaa Ala Leu  
1 5 10 15  
Asn Pro Thr Pro Cys Thr Gln Val Cys Val Gly Pro Pro Gly Asp Glu  
20 25 30  
Asn Pro Ser Val Pro Lys Met Ala Arg Arg Gly Leu Met Glu Xaa Asp  
35 40 45  
Leu Ser Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu Val  
50 55 60  
Ile Ser Arg Gln Ala Thr Ile Asn Met Gly Thr Ile Gly His Val Ala  
65 70 75 80  
Xaa Trp Lys Val His Cys Cys  
85

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

Met Ala Arg Arg Gly Leu Met Glu Xaa Asp Leu Ser Lys Leu Asp Val  
1 5 10 15  
Thr Lys Leu His Pro Leu Ser Pro Glu Val Ile Ser Arg Gln Ala Thr  
20 25 30  
Ile Asn Met Gly Thr Ile Gly His Val Ala Xaa Trp Lys Val His Cys  
35 40 45  
Cys

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:

Met Trp Xaa His Gly Lys Ser Thr Val Val Lys Ala Ile Ser Gly Val  
1 5 10 15  
Gln Thr Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys  
20 25 30  
Leu Gly Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Arg Cys  
35 40 45  
Pro Arg Pro Met Cys Tyr Lys Ala Tyr Gly Ser Gly Lys Xaa Asp Ser  
50 55 60  
Pro Leu Cys Asp Val Pro Gly Phe Glu Asn Thr Arg Met  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

ttgttgatga tttagtgtcaa tctgggggaa ctcttagaga atgccagaad agttctagct 60  
ttgcatggcg ctgcaaaagt cagtgttat gtgactcatg ctgtgtttcc taagcagtca 120  
tatgaacgtt tcatggcgtc tagttctgct gggccagggtg acagatttgc ttacttctgg 180  
atcacggact catgcccaca cacagtaaaa gctattgggc aaagacctcc atttgagggtt 240  
ctgagcctcg ctggctcaat tgcagatgct cttcagatat gagcgtacac tggtagatgg 300  
gcatgggctt ggattgttga tgcccaccag attgaaactt gtactatgag gtggaatgct 360  
cccgcttttc ctaaaatgtaa gagttggttt ccagttcctg gaaaagcaaa taatgtgtag 420  
taagtttaag tacctgaagg ttccataaac agccctgtgg ctt

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

Val Asp Asp Leu Val Gln Ser Gly Gly Thr Leu Arg Glu Cys Gln Xaa  
1 5 10 15  
Ser Ser Ser Phe Ala Trp Arg Cys Lys Ser Gln Cys Leu Cys Asp Ser  
20 25 30  
Cys Cys Val Ser  
35

(2) INFORMATION FOR SEQ ID NO:2384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:

Met Leu Cys Phe Leu Ser Ser His Met Asn Val Ser Trp Arg Leu Val  
1 5 10 15  
Leu Leu Gly Gln Val Thr Asp Leu Leu Thr Ser Gly Ser Arg Thr His  
20 25 30  
Ala His Thr Gln  
35

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

Met Ala Ser Ser Ser Ala Gly Pro Gly Asp Arg Phe Ala Tyr Phe Trp  
1 5 10 15  
Ile Thr Asp Ser Cys Pro His Thr Val Lys Ala Ile Gly Gln Arg Pro  
20 25 30  
Pro Phe Glu Val Leu Ser Leu Ala Gly Ser Ile Ala Asp Ala Leu Gln  
35 40 45  
Ile

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

|              |             |            |            |            |             |     |
|--------------|-------------|------------|------------|------------|-------------|-----|
| cacagggtgc   | tgatgtgata  | gagaaagctc | cagatggcac | tccagctggt | ggtggcttgc  | 60  |
| tttatgttgt   | tgttcatgaa  | gcccaagatc | ttgaggggaa | gcaccataca | aacccatatg  | 120 |
| caaaaataat   | tttcaaaggc  | gaggagaaga | aaactaaggt | catcaagaag | aatagggatc  | 180 |
| caagatggga   | ggatgagttt  | gagttcgtgt | gtgaggagcc | tcctgtgaat | gataaaactgc | 240 |
| atgttgaagt   | cataagtaaa  | gccccgaagc | agggctgata | catggcaagg | aaactttggg  | 300 |
| ctatatattgat | attagccttg  | cagacgtgat | cagcaacaag | cggattaatg | aaaagtacca  | 360 |
| tctcatagac   | tcgaaaaaatg | gtcagatcca | gatcgagttg | cagtggagaa | cttcctagac  | 420 |
| aggaagwgc    | cagaatgcct  | tgatgttcct | ctattcagtt | tgcgtatatc | tgtgattgag  | 480 |
| gattgaggtc   | atgtagataa  | tttcttttt  |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

Gln Gly Ala Asp Val Ile Glu Lys Ala Pro Asp Gly Thr Pro Ala Gly  
1 5 10 15

Gly Gly Leu Leu Tyr Val Val Val His Glu Ala Gln Asp Leu Glu Gly  
20 25 30  
Lys His His Thr Asn Pro Tyr Ala Lys Ile Ile Phe Lys Gly Glu Glu  
35 40 45  
Lys Lys Thr Lys Val Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Asp  
50 55 60  
Glu Phe Glu Phe Val Cys Glu Glu Pro Pro Val Asn Asp Lys Leu His  
65 70 75 80  
Val Glu Val Ile Ser Lys Ala Pro Lys Gln Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1503299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tacatcgtga | tattaagtct | agcaacatct | tgcttgatgg | cagtttcgag | gcccggtgat | 60  |
| cagactttgg | acttgcaaag | cttttagagg | atgaagaatc | acatattact | acaatagttg | 120 |
| caggaacatt | tggtacatt  | gcaccagagt | atatgcaatt | tggcagagca | ccgagaagac | 180 |
| tgatgtctac | agttttgggg | ttttggtact | cgaaatactc | agtggaaagc | ggcctactga | 240 |
| tgcacccctc | attgagaagg | gactaaacat | tgttggatgg | ttaaattttc | ttgctagtga | 300 |
| gaaccgggag | agggaaattg | tcgacctgaa | ctgtgaagga | gtgcagactg | agaccttaga | 360 |
| tgccctgctc | tctcttgcca | agcaatgtgt | tagctcctcg | ccagagagag | gccgacaatg | 420 |
| cacaggggtg | tacatatgct | gggagtcgga | tgtaattaca | ccgtgcccta | gcgacttcta | 480 |
| tg         |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1503300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| His Arg Asp Ile Lys Ser Ser Asn Ile Leu Leu Asp Gly Ser Phe Glu |  |
| 1 5 10 15                                                       |  |
| Ala Arg Val Ser Asp Phe Gly Leu Ala Lys Leu Leu Glu Asp Glu Glu |  |
| 20 25 30                                                        |  |
| Ser His Ile Thr Thr Ile Val Ala Gly Thr Phe Gly Tyr Leu Ala Pro |  |
| 35 40 45                                                        |  |
| Glu Tyr Met Gln Phe Gly Arg Ala Pro Arg Arg Leu Met Ser Thr Val |  |
| 50 55 60                                                        |  |
| Leu Gly Phe Trp Tyr Ser Lys Tyr Ser Val Glu Ser Gly Leu Leu Met |  |
| 65 70 75 80                                                     |  |
| His Pro Ser Leu Arg Arg Asp                                     |  |
| 85                                                              |  |

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..448

(D) OTHER INFORMATION: / Ceres Seq. ID 1503305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| aagcagcaac  | atatcaagct | cagagcctca | gagcgccass | caagtcttgc | ggtcgcgaag | 60  |
| agcaacgcaa  | caagatggtg | aagctcgcat | tcggaagcgt | cggcgactcc | ttcagcgta  | 120 |
| cctccatcaa  | ggcctacgtn | gcggagtca  | tcgccaccct | cctcttcgtc | ttcgccggcg | 180 |
| tgggttccgc  | catcgcttc  | gggcaactga | cgaatggcgg | cgcgctggac | cctgcgggac | 240 |
| tggtggcgat  | cgcggtggcg | cacgcgctgg | ccctcttcgt | gggcgctctc | gtggccgcga | 300 |
| acacctccgg  | cggccacctg | aaccccgccg | tgacgttcgg | cctggccgtg | ggcggcacat | 360 |
| tcaccgtcct  | caccggcctc | ttctactggg | tgggcccagc | tgctgggcgc | gtccgtggcg | 420 |
| tgccctggctc | ctcaggttcg | tgaccac    |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Asn | Ile | Ser | Ser | Ser | Glu | Pro | Gln | Ser | Ala | Xaa | Gln | Val | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ser | Arg | Arg | Ala | Thr | Gln | Gln | Asp | Gly | Glu | Ala | Arg | Ile | Arg | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Arg | Leu | Leu | Gln | Arg | His | Leu | His | Gln | Gly | Leu | Arg | Xaa | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | His | Arg | His | Pro | Pro | Leu | Arg | Leu | Arg | Arg | Arg | Gly | Phe | Arg | His |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Leu | Arg | Ala | Thr | Asp | Glu | Trp | Arg | Arg | Ala | Gly | Pro | Cys | Gly | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Gly | Asp | Arg | Gly | Gly | Ala | Arg | Ala | Gly | Pro | Leu | Arg | Gly | Arg | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Arg | Gly | Arg | Glu | His | Leu | Arg | Arg | Pro | Pro | Glu | Pro | Arg | Arg | Asp | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Arg | Pro | Gly | Arg | Gly | Arg | His | Ile | His | Arg | Pro | His | Arg | Pro | Leu | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Leu | Gly | Gly | Pro | Ser | Cys | Trp | Ala | Arg | Pro | Trp | Arg | Ala | Trp | Leu | Leu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Arg | Phe | Val | Thr | His |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1503307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Thr | Tyr | Gln | Ala | Gln | Ser | Leu | Arg | Ala | Pro | Xaa | Lys | Ser | Cys |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     | 15  |     |
| Gly | Arg | Glu | Glu | Gln | Arg | Asn | Lys | Met | Val | Lys | Leu | Ala | Phe | Gly | Ser |

```

 20 25 30
Val Gly Asp Ser Phe Ser Val Thr Ser Ile Lys Ala Tyr Xaa Ala Glu
 35 40 45
Phe Ile Ala Thr Leu Leu Phe Val Phe Ala Gly Val Gly Ser Ala Ile
 50 55 60
Ala Phe Gly Gln Leu Thr Asn Gly Gly Ala Leu Asp Pro Ala Gly Leu
65 70 75 80
Val Ala Ile Ala Val Ala His Ala Leu Ala Leu Phe Val Gly Val Ser
 85 90 95
Val Ala Ala Asn Thr Ser Gly Gly His Leu Asn Pro Ala Val Thr Phe
 100 105 110
Gly Leu Ala Val Gly Gly Thr Phe Thr Val Leu Thr Gly Leu Phe Tyr
 115 120 125
Trp Val Gly Pro Ala Ala Gly Arg Val Arg Gly Val Pro Gly Ser Ser
130 135 140
Gly Ser
145
```

(2) INFORMATION FOR SEQ ID NO:2393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1503308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

```

Met Val Lys Leu Ala Phe Gly Ser Val Gly Asp Ser Phe Ser Val Thr
1 5 10 15
Ser Ile Lys Ala Tyr Xaa Ala Glu Phe Ile Ala Thr Leu Leu Phe Val
 20 25 30
Phe Ala Gly Val Gly Ser Ala Ile Ala Phe Gly Gln Leu Thr Asn Gly
 35 40 45
Gly Ala Leu Asp Pro Ala Gly Leu Val Ala Ile Ala Val Ala His Ala
50 55 60
Leu Ala Leu Phe Val Gly Val Ser Val Ala Ala Asn Thr Ser Gly Gly
65 70 75 80
His Leu Asn Pro Ala Val Thr Phe Gly Leu Ala Val Gly Gly Thr Phe
 85 90 95
Thr Val Leu Thr Gly Leu Phe Tyr Trp Val Gly Pro Ala Ala Gly Arg
 100 105 110
Val Arg Gly Val Pro Gly Ser Ser Gly Ser
115 120
```

(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1503322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

```

gtggcctcgt ctccttcccc acttcggcct cggcagttcc gacttccgcg tgccgggccgg 60
agcctcgtcc cgcttcgcat ctcgcacttc ggccttcgc cgctgcgatt ccttagcagc 120
tcctcgcccg ctccaccac cctgcgccg gcgagatgga gctcaagccc ggcattgcgg 180
cgctcgtcac cggcggcgcc tccggcatcg ggaaagcact ttgtattgct tttgcaagga 240
```



gggggtttatt tgtgactgtc gttgatttct cagaggaaaa tggaagagaa gttgctacat 300  
tagttcaaaa agaaaatagc aaatttcacg gagatcttag aattccatct tcaatatttg 360  
ttaagtgtga tgtagtaaat gcagataatc ttgctgcttg ttttgagaag catgtacaga 420  
catacaatgg actagatatc tgcataact gtgctggaat tgct

(2) INFORMATION FOR SEQ ID NO:2395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

Trp Pro Arg Leu Leu Pro His Phe Gly Leu Gly Ser Ser Asp Phe Arg  
1 5 10 15  
Val Pro Ala Gly Ala Ser Ser Arg Phe Ala Ser Arg Thr Ser Arg Leu  
20 25 30  
Arg Arg Cys Asp Ser Leu Ala Ala Pro Arg Pro Leu His Pro Pro Leu  
35 40 45  
Arg Arg Arg Asp Gly Ala Gln Ala Arg His Val Gly Ala Arg His Arg  
50 55 60  
Arg Arg Leu Arg His Arg Glu Ser Thr Leu Tyr Cys Phe Cys Lys Glu  
65 70 75 80  
Gly Phe Ile Cys Asp Cys Arg  
85

(2) INFORMATION FOR SEQ ID NO:2396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

Met Glu Leu Lys Pro Gly Met Ser Ala Leu Val Thr Gly Gly Ala Ser  
1 5 10 15  
Gly Ile Gly Lys Ala Leu Cys Ile Ala Phe Ala Arg Arg Gly Leu Phe  
20 25 30  
Val Thr Val Val Asp Phe Ser Glu Asn Gly Arg Glu Val Ala Thr  
35 40 45  
Leu Val Gln Lys Glu Asn Ser Lys Phe His Gly Asp Leu Arg Ile Pro  
50 55 60  
Ser Ser Ile Phe Val Lys Cys Asp Val Ser Asn Ala Asp Asn Leu Ala  
65 70 75 80  
Ala Cys Phe Glu Lys His Val Gln Thr Tyr Asn Gly Leu Asp Ile Cys  
85 90 95  
Ile Asn Cys Ala Gly Ile Ala  
100

(2) INFORMATION FOR SEQ ID NO:2397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1503325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:

```
Met Ser Ala Leu Val Thr Gly Gly Ala Ser Gly Ile Gly Lys Ala Leu
1 5 10 15
Cys Ile Ala Phe Ala Arg Arg Gly Leu Phe Val Thr Val Val Asp Phe
 20 25 30
Ser Glu Glu Asn Gly Arg Glu Val Ala Thr Leu Val Gln Lys Glu Asn
 35 40 45
Ser Lys Phe His Gly Asp Leu Arg Ile Pro Ser Ser Ile Phe Val Lys
 50 55 60
Cys Asp Val Ser Asn Ala Asp Asn Leu Ala Ala Cys Phe Glu Lys His
 65 70 75 80
Val Gln Thr Tyr Asn Gly Leu Asp Ile Cys Ile Asn Cys Ala Gly Ile
 85 90 95
Ala
```

(2) INFORMATION FOR SEQ ID NO:2398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1503330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

```
tgtagagagt ttcaggtgct cagcaacaag gataggatct gatggtggag tcgcatttgt 60
ctgaggcatt ggggacatgc actcgtctga agaaacttga tcttagggac aacttgtttg 120
gtgttgatgc agggtagct ctcagcgaaa cccttccaaa actacctgat cttgttgagc 180
tttatctcag tgatctcaat cttgagaaca aggttactat agcaattgca aaagccctca 240
aacagtcagc actgcagttg gaggtccttg aaattgctgg aaatgaaata aatgccaaag 300
cagccccaga tttggctgaa tgtctagcag taatgcagtc actcaagaag ctgaccttgg 360
ctgaaaatga actgaaggac aatggtgctg tgataattgc aaaatcattg gaagatggcc 420
actcagatct caaggaactt gatgtgagca cgaacatgct gcagaggggt ggagctcggt 480
gctttacgc
```

(2) INFORMATION FOR SEQ ID NO:2399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

```
Met Val Glu Ser His Leu Ser Glu Ala Leu Gly Thr Cys Thr Arg Leu
1 5 10 15
Lys Lys Leu Asp Leu Arg Asp Asn Leu Phe Gly Val Asp Ala Gly Leu
 20 25 30
Ala Leu Ser Glu Thr Leu Pro Lys Leu Pro Asp Leu Val Glu Leu Tyr
 35 40 45
Leu Ser Asp Leu Asn Leu Glu Asn Lys Gly Thr Ile Ala Ile Ala Lys
 50 55 60
Ala Leu Lys Gln Ser Ala Leu Gln Leu Glu Val Leu Glu Ile Ala Gly
```

(2) INFORMATION FOR SEQ ID NO:2400:

(A) LENGTH: 449 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..449  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503332

| (X1) SEQUENCE DESCRIPTION SEE FIG. 1 |            |             |             |            |            |  |     |
|--------------------------------------|------------|-------------|-------------|------------|------------|--|-----|
| tctctttcttc                          | caatcattgg | tggttgtgct  | ctagctgctg  | tcacagagct | gaactttaat |  | 60  |
| atggttggat                           | ttatgggtgc | catgatatcc  | aaccttgcat  | ttgttttccg | caacatcttc |  | 120 |
| tcgaagaggg                           | catgaagggg | aagtcggtca  | gtggcatgaa  | ttactacgct | tgctgtcaa  |  | 180 |
| ttatgtccct                           | ggtcatactg | actccatttg  | ctatagctat  | ggaaggccct | caaagtggg  |  | 240 |
| ctgctggttg                           | gcaaaaggct | cttgacagaag | ttggacccaa  | tgttgtctgg | tggattgctg |  | 300 |
| cacagagcgt                           | gttctaccac | ttatataaac  | aggtgtcccta | catgtctctc | gacagagatt |  | 360 |
| ctccattgac                           | attcagcatt | ggcaatacaa  | tgaagcgat   | atcagtgatt | gtttcatcaa |  | 420 |
| tcattatctt                           | ccacactcct | gtccgcgct   |             |            |            |  |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- ```
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..106
      (D) OTHER INFORMATION: / Ceres Seq. ID 1503333
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

(X1) SEQUENCE DESCRIPTION																
Met	Lys	Gly	Lys	Ser	Val	Ser	Gly	Met	Asn	Tyr	Tyr	Ala	Cys	Leu	Ser	
1				5					10					15		
Ile	Met	Ser	Leu	Val	Ile	Leu	Thr	Pro	Phe	Ala	Ile	Ala	Met	Glu	Gly	
			20					25					30			
Pro	Gln	Met	Trp	Ala	Ala	Gly	Trp	Gln	Lys	Ala	Leu	Ala	Glu	Val	Gly	
			35				40					45				
Pro	Asn	Val	Val	Trp	Trp	Ile	Ala	Ala	Gln	Ser	Val	Phe	Tyr	His	Leu	
	50					55					60					
Tyr	Asn	Gln	Val	Ser	Tyr	Met	Ser	Leu	Asp	Gln	Ile	Ser	Pro	Leu	Thr	
65				70					75					80		
Phe	Ser	Ile	Gly	Asn	Thr	Met	Lys	Arg	Ile	Ser	Val	Ile	Val	Ser	Ser	
				85					90					95		
Ile	Ile	Ile	Phe	His	Thr	Pro	Val	Arg	Ala							
			100					105								

(2) INFORMATION FOR SEQ ID NO:2402:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503334
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:

Met Asn Tyr Tyr Ala Cys Leu Ser Ile Met Ser Leu Val Ile Leu Thr
1 5 10 15
Pro Phe Ala Ile Ala Met Glu Gly Pro Gln Met Trp Ala Ala Gly Trp
 20 25 30
Gln Lys Ala Leu Ala Glu Val Gly Pro Asn Val Val Trp Trp Ile Ala
 35 40 45
Ala Gln Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser
 50 55 60
Leu Asp Gln Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys
65 70 75 80
Arg Ile Ser Val Ile Val Ser Ser Ile Ile Phe His Thr Pro Val
 85 90 95
Arg Ala

- (2) INFORMATION FOR SEQ ID NO:2403:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503335
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

Met Ser Leu Val Ile Leu Thr Pro Phe Ala Ile Ala Met Glu Gly Pro
1 5 10 15
Gln Met Trp Ala Ala Gly Trp Gln Lys Ala Leu Ala Glu Val Gly Pro
 20 25 30
Asn Val Val Trp Trp Ile Ala Ala Gln Ser Val Phe Tyr His Leu Tyr
 35 40 45
Asn Gln Val Ser Tyr Met Ser Leu Asp Gln Ile Ser Pro Leu Thr Phe
 50 55 60
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ser Ser Ile
65 70 75 80
Ile Ile Phe His Thr Pro Val Arg Ala
 85

- (2) INFORMATION FOR SEQ ID NO:2404:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..233
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503336
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

aacacataga gcgctgagga cgcttggtcat cagtcatcac ctatctaact agctagctag 60
cttgaacaag agcgtacgta gcaagaaacg agctccgctg cgagagaaag ctaagggacc 120
tagctagcta tcatgtcttg gacctaccgt gagaacgcgc tgttcgagcg sctctggcca 180

cctacgaccg ggacacgccc aggcgggtggg agctcgtggc cgccgcggtg ggc

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

Met	Ser	Trp	Thr	Tyr	Arg	Glu	Asn	Ala	Leu	Phe	Glu	Xaa	Leu	Trp	Pro
1				5					10				15		
Pro	Thr	Thr	Gly	Thr	Arg	Pro	Gly	Gly	Gly	Ser	Ser	Trp	Pro	Pro	Arg
			20				25					30			
Trp															

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

actttccatt	gaggatggta	cagtattgaa	gtccttcagc	caccttctcc	atcgtaacaa	60
gaaggtagat	ttcattgaac	agttcaatga	aaagcttctg	gtcaagcagg	aaggggagaa	120
tcttcaaatt	cttgatgtaa	ggaacttcca	attgacagaa	gtgagcagaa	ctgagtttat	180
gactccatct	gcctttatct	ttctgtatga	gctgcaactg	ttcctgacgt	tccggaatcg	240
atcagtagca	gtttggaact	ttcgagggtga	actggtcaca	tcatttgaag	atcacctggt	300
gtggcaccct	gactgcaaca	caaacaacat	atacattaca	agtgatcaag	atcttattat	360
ttcatactgc	aaggctgact	caactgattc	ctcttcagaa	gaaaatgctg	gctctataaa	420
cataagcagc	atactgaccg	gcaaatgctt	ggcaaaaata	aaccctggaa	attcgcgcg	

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

Leu	Ser	Ile	Glu	Asp	Gly	Thr	Val	Leu	Lys	Ser	Phe	Ser	His	Leu	Leu
1				5					10					15	
His	Arg	Asn	Lys	Lys	Val	Asp	Phe	Ile	Glu	Gln	Phe	Asn	Glu	Lys	Leu
			20				25					30			
Leu	Val	Lys	Gln	Glu	Gly	Glu	Asn	Leu	Gln	Ile	Leu	Asp	Val	Arg	Asn
		35				40					45				
Phe	Gln	Leu	Thr	Glu	Val	Ser	Arg	Thr	Glu	Phe	Met	Thr	Pro	Ser	Ala
		50				55				60					
Phe	Ile	Phe	Leu	Tyr	Glu	Leu	Gln	Leu	Phe	Leu	Thr	Phe	Arg	Asn	Arg
65					70				75					80	

Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu Val Thr Ser Phe Glu
85 90 95
Asp His Leu Leu Trp His Pro Asp Cys Asn Thr Asn Asn Ile Tyr Ile
100 105 110
Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys Lys Ala Asp Ser Thr
115 120 125
Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile Asn Ile Ser Ser Ile
130 135 140
Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro Gly Asn Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

Met Thr Pro Ser Ala Phe Ile Phe Leu Tyr Glu Leu Gln Leu Phe Leu
1 5 10 15
Thr Phe Arg Asn Arg Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu
20 25 30
Val Thr Ser Phe Glu Asp His Leu Trp His Pro Asp Cys Asn Thr
35 40 45
Asn Asn Ile Tyr Ile Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys
50 55 60
Lys Ala Asp Ser Thr Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile
65 70 75 80
Asn Ile Ser Ser Ile Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro
85 90 95
Gly Asn Ser Arg
100

(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

agagttgttg attgcaggga aaccgccaat tggcaaggat gaagcttggt accgccttcg 60
ttgtgctgct cttttctctc ctcccgact cgtccaccgc ggaggacttc gatttcttct 120
accttgatcca acagtggccg ggctcgttct ggcacacgcg gcagggttgc tgcttcccg 180
acggcgcggg caagccggab sncttttcgg catccacggg ctgtggccaa ctacgccaak 240
tgccgcggcc gccaccaccg

(2) INFORMATION FOR SEQ ID NO:2410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

```
Glu Leu Leu Ile Ala Gly Lys Pro Pro Ile Gly Lys Asp Glu Ala Cys
1           5           10           15
Asp Arg Leu Arg Cys Ala Ala Leu Phe Ser Pro Pro Arg Leu Val His
          20           25           30
Arg Gly Gly Leu Arg Phe Leu Leu Pro Cys Pro Thr Val Ala Gly Leu
          35           40           45
Val Leu Arg His Ala Ala Gly Leu Leu Leu Pro Gly Arg Arg Gly Gln
          50           55           60
Ala Gly Xaa Arg Phe Gly Ile His Gly Leu Trp Pro Thr Thr Pro Xaa
65           70           75           80
Ala Ala Ala Ala Thr Thr
          85
```

(2) INFORMATION FOR SEQ ID NO:2411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

```
Met Lys Leu Val Thr Ala Phe Val Val Leu Phe Ser Leu Leu Pro
1           5           10           15
Asp Ser Ser Thr Ala Glu Asp Phe Asp Phe Phe Tyr Leu Val Gln Gln
          20           25           30
Trp Pro Gly Ser Phe Cys Asp Thr Arg Gln Gly Cys Cys Phe Pro Asp
          35           40           45
Gly Ala Gly Lys Pro Xaa Xaa Val Ser Ala Ser Thr Gly Cys Gly Gln
          50           55           60
Leu Arg Gln Xaa Pro Arg Pro Pro Pro Pro
65           70
```

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

```
aatctactaa aaaaactctc caactgcggc aattgccaac cgccagcacc agcgccgccc 60
ccccgntccc cccgcggcg cctcggagaa ttggattggc tgggcgcgtg acccgccgcc 120
gccgtccgcg agcagcagcg acccccctcg ccggccatga cctctgctca ttccaagc
```

(2) INFORMATION FOR SEQ ID NO:2413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1503352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:

```

Asn Leu Leu Lys Lys Leu Ser Asn Cys Gly Asn Cys Gln Pro Pro Ala
1           5           10           15
Pro Ala Pro Pro Pro Xaa Leu Pro Arg Arg Leu Gly Glu Leu Asp
          20           25           30
Trp Leu Gly Ala
          35

```

(2) INFORMATION FOR SEQ ID NO:2414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1503353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

```

Ser Thr Lys Lys Thr Leu Gln Leu Arg Gln Leu Pro Thr Ala Ser Thr
1           5           10           15
Ser Ala Ala Ala Pro Xaa Pro Pro Pro Ala Pro Arg Arg Ile Gly Leu
          20           25           30
Ala Gly Arg Val Thr Arg Arg Arg Pro Arg Ala Ala Ala Thr Pro
          35           40           45
Leu Ala Gly His Asp Leu Cys Ser Phe Gln
          50           55

```

(2) INFORMATION FOR SEQ ID NO:2415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..492

(D) OTHER INFORMATION: / Ceres Seq. ID 1503354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

```

atacagaaat ggtagggttc ttccggcgct ctgctgcac tgatcactgt cgtttgctga      60
caacaaatgg atcagttcac catgaactga ttagacgaca ccatggcaga ccaagaagtg      120
cgatcaggtg ctgcagcagc acggcaaggg gaaggaccag ggactattac ataccaggtg      180
ctgggcatcg caattcaatc cacacctcag cagatcaagg aggcttacag gaaactccag      240
aagcaacacc atccagacat cgccggctac aagggccacg actacacgct gctgctgaac      300
gaggcgtaca aggttctgat gcgggatgtt tccagttcca ggcacgccga tggaaggggc      360
aggagtaggg tggggtcagg agccggttac accgtggacg gatacagttc ttgggaaggg      420
cccgtgagaa gccaaactct cttcgtggac gagaacaagt gcataggatg ccgggagtgc      480
gtgcaccatg cc

```

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

Thr	Glu	Met	Val	Gly	Phe	Phe	Gly	Ala	Ser	Ala	Ala	Ser	Asp	His	Cys	
1				5				10						15		
Arg	Leu	Leu	Thr	Thr	Asn	Gly	Ser	Val	His	His	Glu	Leu	Ile	Arg	Arg	
			20					25					30			
His	His	Gly	Arg	Pro	Arg	Ser	Ala	Ile	Arg	Cys	Cys	Ser	Ser	Thr	Ala	
		35					40					45				
Arg	Gly	Arg	Thr	Arg	Asp	Tyr	Tyr	Ile	Pro	Gly	Ala	Gly	His	Arg	Asn	
	50					55					60					
Ser	Ile	His	Thr	Ser	Ala	Asp	Gln	Gly	Gly	Leu	Gln	Glu	Thr	Pro	Glu	
65					70					75					80	
Ala	Thr	Pro	Ser	Arg	His	Arg	Arg	Leu	Gln	Gly	Pro	Arg	Leu	His	Ala	
				85					90					95		
Ala	Ala	Glu	Arg	Gly	Val	Gln	Gly	Ser	Asp	Ala	Gly	Cys	Phe	Gln	Phe	
				100				105						110		
Gln	Ala	Arg	Arg	Trp	Lys	Gly	Gln	Glu								
				115				120								

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1503356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

Met	Val	Gly	Phe	Phe	Gly	Ala	Ser	Ala	Ala	Ser	Asp	His	Cys	Arg	Leu	
1				5				10						15		
Leu	Thr	Thr	Asn	Gly	Ser	Val	His	His	Glu	Leu	Ile	Arg	Arg	His	His	
			20					25					30			
Gly	Arg	Pro	Arg	Ser	Ala	Ile	Arg	Cys	Cys	Ser	Ser	Thr	Ala	Arg	Gly	
		35					40					45				
Arg	Thr	Arg	Asp	Tyr	Tyr	Ile	Pro	Gly	Ala	Gly	His	Arg	Asn	Ser	Ile	
	50					55					60					
His	Thr	Ser	Ala	Asp	Gln	Gly	Gly	Leu	Gln	Glu	Thr	Pro	Glu	Ala	Thr	
65					70					75					80	
Pro	Ser	Arg	His	Arg	Arg	Leu	Gln	Gly	Pro	Arg	Leu	His	Ala	Ala	Ala	
				85					90					95		
Glu	Arg	Gly	Val	Gln	Gly	Ser	Asp	Ala	Gly	Cys	Phe	Gln	Phe	Gln	Ala	
			100					105						110		
Arg	Arg	Trp	Lys	Gly	Gln	Glu										
				115												

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

Met	Ala	Asp	Gln	Glu	Val	Arg	Ser	Gly	Ala	Ala	Ala	Ala	Arg	Gln	Gly	
1				5				10						15		
Glu	Gly	Pro	Gly	Thr	Ile	Thr	Tyr	Gln	Val	Leu	Gly	Ile	Ala	Ile	Gln	

	20		25		30
Ser Thr Pro Gln Gln Ile Lys Glu Ala Tyr Arg Lys Leu Gln Lys Gln					
	35		40		45
His His Pro Asp Ile Ala Gly Tyr Lys Gly His Asp Tyr Thr Leu Leu					
	50		55		60
Leu Asn Glu Ala Tyr Lys Val Leu Met Arg Asp Val Ser Ser Ser Arg					
65		70		75	80
His Ala Asp Gly Arg Gly Arg Ser Arg Val Gly Ser Gly Ala Gly Tyr					
	85		90		95
Thr Val Asp Gly Tyr Ser Ser Trp Glu Gly Pro Val Arg Ser Gln Ala					
	100		105		110
Leu Phe Val Asp Glu Asn Lys Cys Ile Gly Cys Arg Glu Cys Val His					
	115		120		125
His Ala					
130					

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

acatgcaaag tataacacag accagatcaa acccaagttc aggcctcccg aatcattcag	60
caagccacta ttgagtgccg atccatctat catctccgc gatcttgaac caaatgactg	120
tttcatcata ttcgcacag atggattgtg ggagcacctc agcaatcaag aagccgttga	180
gattgttcac agccatcaac gtgctggaag cgcaagaaga ctcatataag cgcctctaca	240
agaagcagcg cgnaasstga gatgcgttac tcggatctta caaagatcga taagaaagtt	300
cgcaggcatt tccatgatga cattactgtc atcgtcttat ttataaacta tgacctatta	360
ttgaaaggtg ctccgcagga caaccctct ccatcagatg tgccctagat tattgacagt	420
gagctagttc acccactggt attcaagctc ctgcgtgcag cc	

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

His Ala Lys Tyr Asn Thr Asp Gln Ile Lys Pro Lys Phe Arg Leu Pro	
1	15
Glu Ser Phe Ser Lys Pro Leu Leu Ser Ala Asp Pro Ser Ile Ile Ser	
	30
Arg Asp Leu Glu Pro Asn Asp Cys Phe Ile Ile Phe Ala Ser Asp Gly	
	45
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Glu Ile Val His Ser	
	60
His Gln Arg Ala Gly Ser Ala Arg Arg Leu Ile Lys Ala Ala Leu Gln	
65	80
Glu Ala Ala Xaa Xaa Xaa Arg Cys Val Thr Arg Ile Leu Gln Arg Ser	
	95
Ile Arg Lys Phe Ala Gly Ile Ser Met Thr Leu Leu Ser Ser Ser	
	110

Tyr Leu

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

tttccgtgcc gccacccagc cccttaacnc tcgttcctct agccgtctcg cgcagcacag	60
cctccatttc tctccgacg gcggtgcggc tagtcaacc atggcggact ccaagggcac	120
ctcggcggtc accctccgca ctckcaagtt catgaccaac cggggcccn tgctggcccg	180
cwaacaattt gtgcttgagg ttatccaccc cggccgcgcc aacgtctcca aggcggagtt	240
gaagggaaga ggcttgccaa gatgtacgag gtgaaggacc ccaacacccat cttcgtcttc	300
aagttccgca cccacttcgg tggaggcaag tccactggct tcggcc	

(2) INFORMATION FOR SEQ ID NO:2422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

Phe Arg Ala Ala Thr Gln Pro Leu Asn Xaa Arg Ser Ser Ser Arg Leu	
1 5 10 15	
Ala Gln His Ser Leu His Phe Ser Ser Asp Gly Gly Ala Ala Ser Ser	
20 25 30	
Thr Met Ala Asp Ser Lys Ala Thr Ser Ala Val Thr Leu Arg Thr Xaa	
35 40 45	
Lys Phe Met Thr Asn Arg Gly Pro Xaa Leu Ala Arg Xaa Gln Phe Val	
50 55 60	
Leu Glu Val Ile His Pro Gly Arg Ala Asn Val Ser Lys Ala Glu Leu	
65 70 75 80	
Lys Gly Arg Gly Leu Pro Arg Cys Thr Arg	
85 90	

(2) INFORMATION FOR SEQ ID NO:2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

Ser Val Pro Pro Pro Ser Pro Leu Xaa Leu Val Pro Leu Ala Val Ser	
1 5 10 15	
Arg Ser Thr Ala Ser Ile Ser Pro Pro Thr Ala Val Arg Leu Ala Gln	
20 25 30	
Pro Trp Arg Thr Pro Arg Pro Pro Arg Arg Ser Pro Ser Ala Leu Xaa	

35 40 45

Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

Met Ala Asp Ser Lys Ala Thr Ser Ala Val Thr Leu Arg Thr Xaa Lys
1 5 10 15
Phe Met Thr Asn Arg Gly Pro Xaa Leu Ala Arg Xaa Gln Phe Val Leu
20 25 30
Glu Val Ile His Pro Gly Arg Ala Asn Val Ser Lys Ala Glu Leu Lys
35 40 45
Gly Arg Gly Leu Pro Arg Cys Thr Arg
50 55

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1503422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

tatgaaaaat caagatctcc tgggaggttc tttgacctag tttatcatga aaatgcccg 60
gtttactactcc atgatgagag catataccga tttgaatggt gtcgagtc gacaagggtg 120
tctattcagc tgatggaata tggtcacgaa aagccagaag tgactgcagt atcaattgaa 180
ccaaattttt cttcgtatct ttttagcgag tacttgtgta gtacgccaga caagaaatta 240
tctgaaggcg tctaccttgg aaggaataag cggaaatatt caaataatga tgaaccttca 300
gattctttga aggcaatgga tggatcaat gttgtgaatg gtcttgaatg caagatatcc 360
tgcaagacct cgaaagtttc atatgtcctt gatactgaag atttcttgtt ccggcttcgg 420
aagagaagga aaattttgcg gggcggaat gtgccgacc gtttgcagat ttcacataa 480
tctgctg

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1503423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

Tyr Glu Lys Ser Arg Ser Pro Gly Arg Phe Phe Asp Leu Val Tyr His
1 5 10 15
Glu Asn Ala Arg Val Leu Leu His Asp Glu Ser Ile Tyr Arg Phe Glu
20 25 30
Cys Cys Ser Ser Pro Thr Arg Leu Ser Ile Gln Leu Met Glu Tyr Gly

acacctactt	cataagcttg	gccttctccc	cgacggccct	catcggcctc	aactccgacc	60
tgaaagtgcc	caagtttgag	ttcctgtcga	acgcgamscg	tcgctgttcg	attaccccaa	120
gccagtgacc	cagcagacca	cagccacgtc	agtcaaggtg	ccggcggsca	tcctgtcgac	180
ctatgccaag	tccaaatcca	gggcaaggaa	ggacgcagag	agcaaggcca	aggcgaaagc	240

agaggactct tccagtgcctt ctacttcgat gcagggtggac ggcgcttctg ctgctgggtgc 300
tgctgcagag aagaaggccc cggagccaga gcctacgttc cagatcctga cgaacccggc 360
ccgggtcggt ccagcccagg agaagttcat aaagttcctg gaagacagca ggtacaagcc 420
ggtgaaggct gccccctcg

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Thr Tyr Phe Ile Ser Leu Ala Phe Ser Pro Thr Ala Leu Ile Gly Leu
1 5 10 15
Asn Ser Asp Leu Lys Val Pro Lys Phe Glu Phe Leu Ser Asn Ala Xaa
20 25 30
Arg Arg Cys Ser Ile Thr Pro Ser Gln
35 40

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

Met Pro Ser Pro Asn Pro Gly Gln Gly Arg Thr Gln Arg Ala Arg Pro
1 5 10 15
Arg Arg Lys Gln Arg Thr Leu Pro Val Leu Leu Leu Arg Cys Arg Trp
20 25 30
Thr Ala Leu Leu Leu Leu Val Leu Leu Gln Arg Arg Arg Pro Arg Ser
35 40 45
Gln Ser Leu Arg Ser Arg Ser
50 55

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

Met Gln Val Asp Gly Ala Ser Ala Ala Gly Ala Ala Glu Lys Lys
1 5 10 15
Ala Pro Glu Pro Glu Pro Thr Phe Gln Ile Leu Thr Asn Pro Ala Arg
20 25 30
Val Val Pro Ala Gln Glu Lys Phe Ile Lys Phe Leu Glu Asp Ser Arg
35 40 45
Tyr Lys Pro Val Lys Ala Ala Pro Ser

50 55

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

actggcggtg aacagcgaga acctaaacag gacagcgaac acgactcgcc taacctccgg	60
acagccacgt ctttccccac tctccggacg aaccttcccg atggcgacgc gacctcccct	120
ccagctgccc ccgcgtccac cgccaccacc tccgtctcgc gtctccggcc actgcgccct	180
ttccttccgc gccttcgctt ctggccagca ccagtggcgg ccgcgcggst gtgcctttct	240
cgattgctct gggcccaggc tgtcgtccct tgcccggcat acgctgtcga gccgcgcgcg	300
ggccctcgcc gccctcctca gagccccctc ctccatcccc gcacggttgg caagagaggc	360
tgtcaagttt gcaggataga gcaaggatct tctttgccgt tctgttctgg atgtcattgt	420
ttttctgggg aagtgccttg gatggaagta acaactcggg aggcaagaag c	

(2) INFORMATION FOR SEQ ID NO:2433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Thr Gly Gly Glu Gln Arg Glu Pro Lys Gln Asp Ser Glu His Asp Ser	
1 5 10 15	
Pro Asn Leu Arg Thr Ala Thr Ser Phe Pro Thr Leu Arg Thr Asn Leu	
20 25 30	
Pro Asp Gly Asp Ala Thr Ser Pro Ala Ala Pro Ala Ser Thr Ala	
35 40 45	
Thr Thr Ser Val Ser Arg Leu Arg Pro Leu Arg Pro Phe Leu Pro Arg	
50 55 60	
Leu Arg Phe Trp Pro Ala Pro Val Ala Ala Ala Pro Xaa Cys Leu Ser	
65 70 75 80	
Arg Leu Leu Trp Ala Gln Ala Val Val Pro Cys Pro Ala Tyr Ala Val	
85 90 95	
Glu Pro Pro Pro Gly Pro Arg Arg Pro Pro Gln Ser Pro Leu Leu His	
100 105 110	
Pro Arg Thr Val Gly Lys Arg Gly Cys Gln Val Cys Arg Ile Glu Gln	
115 120 125	
Gly Ser Ser Leu Pro Phe Cys Ser Gly Cys His Cys Phe Ser Gly Glu	
130 135 140	
Val Leu Gly Met Glu Val Thr Thr Arg Glu Ala Arg Ser	
145 150 155	

(2) INFORMATION FOR SEQ ID NO:2434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1503445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

Leu Ala Val Asn Ser Glu Asn Leu Asn Arg Thr Ala Asn Thr Thr Arg
1 5 10 15
Leu Thr Ser Gly Gln Pro Arg Leu Ser Pro Leu Ser Gly Arg Thr Phe
20 25 30
Pro Met Ala Thr Arg Pro Pro Leu Gln Leu Pro Pro Arg Pro Pro Pro
35 40 45
Pro Pro Pro Ser Arg Val Ser Gly His Cys Ala Leu Ser Phe Arg Ala
50 55 60
Phe Ala Ser Gly Gln His Gln Trp Arg Pro Arg Xaa Cys Ala Phe Leu
65 70 75 80
Asp Cys Ser Gly Pro Arg Leu Ser Ser Leu Ala Arg His Thr Leu Ser
85 90 95
Ser Arg Arg Arg Ala Leu Ala Ala Leu Leu Arg Ala Pro Ser Ser Ile
100 105 110
Pro Ala Arg Leu Ala Arg Glu Ala Val Lys Phe Ala Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1503446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

Met Ala Thr Arg Pro Pro Leu Gln Leu Pro Pro Arg Pro Pro Pro Pro
1 5 10 15
Pro Pro Ser Arg Val Ser Gly His Cys Ala Leu Ser Phe Arg Ala Phe
20 25 30
Ala Ser Gly Gln His Gln Trp Arg Pro Arg Xaa Cys Ala Phe Leu Asp
35 40 45
Cys Ser Gly Pro Arg Leu Ser Ser Leu Ala Arg His Thr Leu Ser Ser
50 55 60
Arg Arg Arg Ala Leu Ala Ala Leu Leu Arg Ala Pro Ser Ser Ile Pro
65 70 75 80
Ala Arg Leu Ala Arg Glu Ala Val Lys Phe Ala Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..445
(D) OTHER INFORMATION: / Ceres Seq. ID 1503476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

gaaactcact cgccatcgcc gggcatcgcg ggcacgcac acaaacgcaa cctgcagcca 60
tggcacagaa gctcgcgcca ccgacggcgg sggctcgtcgt cgtcctgctg gcgctcgcct 120
tgtcggccgc cgcgcagaac tgcgggtgcg cgtcgggcct gtgctgcagc cggttcgggt 180
actgcgggac gggcgaggac tactgcggcg ccgggtgccca gtcgggcccc tgcgacgtgc 240
cggagaccaa caacgcgtcc gtggccagca tcgtgacgcc ggccttcttc gacgcgctcc 300

tgcgcagcgc cgcgcctcg tgcgaggcca acggcttcta caccgcgcac gccttcctcg 360
ccgcgcgcgg ctactaccgc gcgttcggcc gcaccggcac cgtcgacgac tccaagcgcg 420
agatcgccgc cttcttcggc aacgc

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

Lys	Leu	Thr	Arg	His	Arg	Arg	Ala	Ser	Arg	Ala	Ser	His	Thr	Asn	Ala
1				5				10						15	
Thr	Cys	Ser	His	Gly	Thr	Glu	Ala	Arg	Ala	Thr	Asp	Gly	Xaa	Gly	Arg
			20					25					30		
Arg	Arg	Pro	Ala	Gly	Ala	Arg	Leu	Val	Gly	Arg	Arg	Ala	Glu	Leu	Arg
			35				40					45			
Val	Arg	Val	Gly	Pro	Val	Leu	Gln	Pro	Val	Arg	Val	Leu	Arg	Asp	Gly
			50				55				60				
Arg	Gly	Leu	Leu	Arg	Arg	Arg	Val	Pro	Val	Gly	Pro	Leu	Arg	Arg	Ala
65						70				75				80	
Gly	Asp	Gln	Gln	Arg	Val	Arg	Gly	Gln	His	Arg	Asp	Ala	Gly	Leu	Leu
			85					90						95	
Arg	Arg	Ala	Pro	Arg	Ala	Gly	Arg	Arg	Leu	Val	Arg	Gly	Gln	Arg	Leu
			100					105					110		
Leu	His	Pro	Arg	Arg	Leu	Pro	Arg	Arg	Arg	Arg	Leu	Leu	Pro	Gly	Val
			115				120					125			
Arg	Pro	His	Arg	His	Arg	Arg	Arg	Leu	Gln	Ala	Arg	Asp	Arg	Arg	Leu
			130				135					140			
Leu	Arg	Gln	Arg												
145															

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

Asn	Ser	Leu	Ala	Ile	Ala	Gly	His	Arg	Gly	His	Arg	Thr	Gln	Thr	Gln
1				5					10					15	
Pro	Ala	Ala	Met	Ala	Gln	Lys	Leu	Ala	Pro	Pro	Thr	Ala	Xaa	Val	Val
			20					25					30		
Val	Val	Leu	Leu	Ala	Leu	Ala	Leu	Ser	Ala	Ala	Ala	Gln	Asn	Cys	Gly
			35				40					45			
Cys	Ala	Ser	Gly	Leu	Cys	Cys	Ser	Arg	Phe	Gly	Tyr	Cys	Gly	Thr	Gly
			50				55				60				
Glu	Asp	Tyr	Cys	Gly	Ala	Gly	Cys	Gln	Ser	Gly	Pro	Cys	Asp	Val	Pro
65						70				75				80	
Glu	Thr	Asn	Asn	Ala	Ser	Val	Ala	Ser	Ile	Val	Thr	Pro	Ala	Phe	Phe
			85					90						95	
Asp	Ala	Leu	Leu	Ala	Gln	Ala	Ala	Ala	Ser	Cys	Glu	Ala	Asn	Gly	Phe
			100					105					110		

Tyr Thr Arg Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe
115 120 125
Gly Arg Thr Gly Thr Val Asp Asp Ser Lys Arg Glu Ile Ala Ala Phe
130 135 140
Phe Gly Asn
145

(2) INFORMATION FOR SEQ ID NO:2439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1503479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Xaa Val Val Val Val Leu
1 5 10 15
Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys Gly Cys Ala Ser
20 25 30
Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr Gly Glu Asp Tyr
35 40 45
Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val Pro Glu Thr Asn
50 55 60
Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe Phe Asp Ala Leu
65 70 75 80
Leu Ala Gln Ala Ala Ser Cys Glu Ala Asn Gly Phe Tyr Thr Arg
85 90 95
Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe Gly Arg Thr
100 105 110
Gly Thr Val Asp Asp Ser Lys Arg Glu Ile Ala Ala Phe Phe Gly Asn
115 120 125

(2) INFORMATION FOR SEQ ID NO:2440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1503480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

caaagtcaag agcagcaact gtttaagtgat gaaaaacagt gtgccgagca cataatgctt	60
gtggacttgg gaaggaatga tggtggcaag gtatccaaac caggatcagt gaaggtggag	120
aagttgatga acattgagag atactcccat gttatgcaca tcagctcaac ggtagtgga	180
cagttggatg atcatctcca gagttgggat gccttgagag ctgccttgcc cgttgaaca	240
gtcagtggtg caccaaaggt gaaggccatg gagttgattg ataagttgga agttacgagg	300
cgaggaccat atagtgggtg tctaggagga atatcgtttg atggtgacat gcaaattgca	360
ctttctctcc gcaccatcgt attctcaaca ggcgcgagcc acaacacgat gtactcatat	420
aaagacgcag ataggcgctcg gggagtgggt cgctcatctt caggctggtg caggcattgt	480
tgccgacagt agcccagatg acgaacaacg t	

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..163
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

Gln	Met	Gln	Glu	Gln	Gln	Leu	Leu	Ser	Asp	Glu	Lys	Gln	Cys	Ala	Glu
1			5						10					15	
His	Ile	Met	Leu	Val	Asp	Leu	Gly	Arg	Asn	Asp	Val	Gly	Lys	Val	Ser
			20					25					30		
Lys	Pro	Gly	Ser	Val	Lys	Val	Glu	Lys	Leu	Met	Asn	Ile	Glu	Arg	Tyr
		35					40					45			
Ser	His	Val	Met	His	Ile	Ser	Ser	Thr	Val	Ser	Gly	Gln	Leu	Asp	Asp
		50				55				60					
His	Leu	Gln	Ser	Trp	Asp	Ala	Leu	Arg	Ala	Ala	Leu	Pro	Val	Gly	Thr
65					70				75					80	
Val	Ser	Gly	Ala	Pro	Lys	Val	Lys	Ala	Met	Glu	Leu	Ile	Asp	Lys	Leu
			85					90					95		
Glu	Val	Thr	Arg	Arg	Gly	Pro	Tyr	Ser	Gly	Gly	Leu	Gly	Gly	Ile	Ser
			100					105					110		
Phe	Asp	Gly	Asp	Met	Gln	Ile	Ala	Leu	Ser	Leu	Arg	Thr	Ile	Val	Phe
		115					120					125			
Ser	Thr	Ala	Pro	Ser	His	Asn	Thr	Met	Tyr	Ser	Tyr	Lys	Asp	Ala	Asp
		130				135				140					
Arg	Arg	Arg	Gly	Val	Gly	Arg	Ser	Ser	Ser	Gly	Trp	Cys	Arg	His	Cys
145					150					155				160	
Cys	Arg	Gln													

- (2) INFORMATION FOR SEQ ID NO:2442:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..162
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503482
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

Met	Gln	Glu	Gln	Gln	Leu	Leu	Ser	Asp	Glu	Lys	Gln	Cys	Ala	Glu	His
1				5					10					15	
Ile	Met	Leu	Val	Asp	Leu	Gly	Arg	Asn	Asp	Val	Gly	Lys	Val	Ser	Lys
			20					25					30		
Pro	Gly	Ser	Val	Lys	Val	Glu	Lys	Leu	Met	Asn	Ile	Glu	Arg	Tyr	Ser
		35					40					45			
His	Val	Met	His	Ile	Ser	Ser	Thr	Val	Ser	Gly	Gln	Leu	Asp	Asp	His
		50				55				60					
Leu	Gln	Ser	Trp	Asp	Ala	Leu	Arg	Ala	Ala	Leu	Pro	Val	Gly	Thr	Val
65				70					75					80	
Ser	Gly	Ala	Pro	Lys	Val	Lys	Ala	Met	Glu	Leu	Ile	Asp	Lys	Leu	Glu
			85					90					95		
Val	Thr	Arg	Arg	Gly	Pro	Tyr	Ser	Gly	Gly	Leu	Gly	Gly	Ile	Ser	Phe
		100						105					110		
Asp	Gly	Asp	Met	Gln	Ile	Ala	Leu	Ser	Leu	Arg	Thr	Ile	Val	Phe	Ser
		115				120						125			
Thr	Ala	Pro	Ser	His	Asn	Thr	Met	Tyr	Ser	Tyr	Lys	Asp	Ala	Asp	Arg
		130				135				140					
Arg	Arg	Gly	Val	Gly	Arg	Ser	Ser	Ser	Gly	Trp	Cys	Arg	His	Cys	Cys

145 150 155 160
Arg Gln

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

```
Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser Lys Pro
1           5           10           15
Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr Ser His
20           25           30
Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp His Leu
35           40           45
Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr Val Ser
50           55           60
Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu Glu Val
65           70           75           80
Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser Phe Asp
85           90           95
Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe Ser Thr
100          105          110
Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp Arg Arg
115          120          125
Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys Cys Arg
130          135          140
Gln
145
```

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

```
aatcaacacc agaagctctc gatcccaccg aggaagaaga gaggaatggc gtccgaggag      60
gagggagtcg tgatcgcccg ccacaccaag gccgacttcg acgcccacat ggccaaggcc      120
aaggaggccg gcaagctggg gatcattgac ttcacggcct cctggtgcgg cccctgccgt      180
ttcatcgcg cactgttcgt cgagcacgcc aagaagttca cccaggctgt gttcctgaag      240
gtggacgtgg acgagctgaa ggaagttgcc gcggcctacg atgtcgaggc gatgccgacc      300
ttccacttcg tcaagaacgg ggtgacgggt gagaccgtcg tcggtgccag gaaggagaac      360
ctcctggccc agatcgagaa gcactgcgcc gcggccgtgt ctgctgcgtc tgcgtagaga      420
ggatggacca gcacgtacgt ggcgggtggg gtggtcttgt cgtttcagtt tgggcttgtc      480
agcgctgtgg ctgggtgggc gattgtgaac tggag
```

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..138
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

Asn	Gln	His	Gln	Lys	Leu	Ser	Ile	Pro	Pro	Arg	Lys	Lys	Arg	Gly	Met
1				5					10					15	
Ala	Ser	Glu	Glu	Glu	Gly	Val	Val	Ile	Ala	Cys	His	Thr	Lys	Ala	Asp
		20						25					30		
Phe	Asp	Ala	His	Met	Ala	Lys	Ala	Lys	Glu	Ala	Gly	Lys	Leu	Val	Ile
		35				40						45			
Ile	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala	Pro
	50					55					60				
Leu	Phe	Val	Glu	His	Ala	Lys	Lys	Phe	Thr	Gln	Ala	Val	Phe	Leu	Lys
65					70					75					80
Val	Asp	Val	Asp	Glu	Leu	Lys	Glu	Val	Ala	Ala	Ala	Tyr	Asp	Val	Glu
				85					90				95		
Ala	Met	Pro	Thr	Phe	His	Phe	Val	Lys	Asn	Gly	Val	Thr	Val	Glu	Thr
		100						105					110		
Val	Val	Gly	Ala	Arg	Lys	Glu	Asn	Leu	Leu	Ala	Gln	Ile	Glu	Lys	His
		115				120							125		
Cys	Ala	Ala	Ala	Val	Ser	Ala	Ala	Ser	Ala						
130						135									

(2) INFORMATION FOR SEQ ID NO:2446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

Met	Ala	Ser	Glu	Glu	Gly	Val	Val	Ile	Ala	Cys	His	Thr	Lys	Ala
1				5					10				15	
Asp	Phe	Asp	Ala	His	Met	Ala	Lys	Ala	Lys	Glu	Ala	Gly	Lys	Leu
		20						25					30	
Ile	Ile	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile
		35				40						45		
Pro	Leu	Phe	Val	Glu	His	Ala	Lys	Lys	Phe	Thr	Gln	Ala	Val	Phe
	50					55				60				
Lys	Val	Asp	Val	Asp	Glu	Leu	Lys	Glu	Val	Ala	Ala	Tyr	Asp	Val
65					70				75					80
Glu	Ala	Met	Pro	Thr	Phe	His	Phe	Val	Lys	Asn	Gly	Val	Thr	Val
				85					90				95	
Thr	Val	Val	Gly	Ala	Arg	Lys	Glu	Asn	Leu	Leu	Ala	Gln	Ile	Glu
		100						105					110	
His	Cys	Ala	Ala	Ala	Val	Ser	Ala	Ala	Ser	Ala				
		115				120								

(2) INFORMATION FOR SEQ ID NO:2447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1503487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

```
Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr
1           5           10           15
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu
20           25           30
His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp
35           40           45
Glu Leu Lys Glu Val Ala Ala Tyr Asp Val Glu Ala Met Pro Thr
50           55           60
Phe His Phe Val Lys Asn Gly Val Thr Val Glu Thr Val Val Gly Ala
65           70           75           80
Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala
85           90           95
Val Ser Ala Ala Ser Ala
100
```

(2) INFORMATION FOR SEQ ID NO:2448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..522
(D) OTHER INFORMATION: / Ceres Seq. ID 1503492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

```
aacctctagc tgattgatct ctgggtttacc actctttcct tccctccttc aattctaaat      60
accacaaatc aaagtgtgctt tgcgatgggtg agcagcagca tggacacgac gagtgcacaa      120
cgtgcgtcat ccatgctggc tcctaaccct ggcaaggcca cgatcctcgc cttggccac      180
gccttcccgc agcagntgtc atgcaggact acgtcgtcga cggcttcatg aagaacacca      240
tcgtgtacgt gctggagaac atggtggagg acaccggcg gaggaggctg ctggctgccg      300
acgacggtgg agaggactgc gagtgggggc tcatcctcdc gttcggggccg gggatcacgt      360
tcgagggcat cctcgccagg aacttgcagg caaccgcgcg cgcctcagcc cagccctgat      420
cacctcttgt tgggttgctt ttctgcttgc tctgcacctc tgcttccgtg tgattgctgc      480
tttgagggag aatgctgagc atcaacattg ctcatgagca tc
```

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1503493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

```
Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Ile Val Tyr
1           5           10           15
Val Leu Glu Asn Met Val Glu Asp Thr Arg Arg Arg Arg Leu Leu Ala
20           25           30
Ala Asp Asp Gly Gly Glu Asp Cys Glu Trp Gly Leu Ile Leu Xaa Phe
35           40           45
Gly Pro Gly Ile Thr Phe Glu Gly Ile Leu Ala Arg Asn Leu Gln Ala
50           55           60
Thr Ala Arg Ala Ser Ala Gln Pro
65           70
```

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

Met	Lys	Asn	Thr	Ile	Val	Tyr	Val	Leu	Glu	Asn	Met	Val	Glu	Asp	Thr
1				5				10					15		
Arg	Arg	Arg	Arg	Leu	Leu	Ala	Ala	Asp	Asp	Gly	Gly	Glu	Asp	Cys	Glu
				20				25					30		
Trp	Gly	Leu	Ile	Leu	Xaa	Phe	Gly	Pro	Gly	Ile	Thr	Phe	Glu	Gly	Ile
				35				40					45		
Leu	Ala	Arg	Asn	Leu	Gln	Ala	Thr	Ala	Arg	Ala	Ser	Ala	Gln	Pro	
				50				55					60		

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

Met	Val	Glu	Asp	Thr	Arg	Arg	Arg	Arg	Leu	Leu	Ala	Ala	Asp	Asp	Gly
1				5					10				15		
Gly	Glu	Asp	Cys	Glu	Trp	Gly	Leu	Ile	Leu	Xaa	Phe	Gly	Pro	Gly	Ile
				20				25					30		
Thr	Phe	Glu	Gly	Ile	Leu	Ala	Arg	Asn	Leu	Gln	Ala	Thr	Ala	Arg	Ala
				35				40					45		
Ser	Ala	Gln	Pro												
				50											

(2) INFORMATION FOR SEQ ID NO:2452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

atgtcgacac	tctacacca	ccctcctgtc	gagccacggg	tctccccact	agtgaaccg	60
ctttctcctc	cacgggtgac	ccctcccccc	cagcgacggg	cctgcgaggc	tgcgacactg	120
cagcatgccc	gacgccatct	atctcttcct	cgcgccagc	tagacctccc	ccgtgcctac	180
gcccattccct	ggcgcgccg	cgctgcccc	tcatgcggcc	aacatcgaca	tccctccctt	240
ctcccagtac	cggttgcaac	tgcaggcatc	aacccttcc	tcacgcccag	ttcatctgct	300
tgtggcgggc	gcgcgcctcc	tccccgcacg	ctggccttgc	gtcggacagc	tcctccgacg	360
ccagcgtccc	ctcctccaaa	gatgacgagt	gaggcgctcyc	ctccccagc	tccagcgagc	420
gcaasscagg	gaccataccc	acgcctccct	ccctcctggg	cgcg		

(2) INFORMATION FOR SEQ ID NO:2453:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503497
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:
Met Ser Thr Leu Tyr Thr His Pro Pro Val Glu Pro Arg Val Ser Pro
1 5 10 15
Leu Val Gln Pro Leu Ser Pro Pro Arg Val Thr Pro Pro Pro Gln Arg
 20 25 30
Thr Ala Cys Glu Ala Ala Thr Leu Gln His Ala Arg Arg His Leu Ser
 35 40 45
Leu Pro Arg Val Gln Leu Asp Leu Pro Arg Ala Tyr Ala His Pro Trp
50 55 60
Cys Gly Arg Ala Ala Pro Ser Cys Gly Gln His Arg His Pro Ser Pro
65 70 75 80
Leu Pro Val Pro Ala Ala Thr Ala Gly Ile Asn Pro Phe Leu Thr Pro
 85 90 95
Ser Ser Ser Ala Cys Gly Gly Gly Ala Pro Pro Pro Arg Thr Leu Ala
 100 105 110
Leu Arg Arg Thr Ala Pro Pro Thr Pro Ala Ser Pro Pro Pro Lys Met
 115 120 125
Thr Ser Glu Ala Xaa Pro Pro Pro Ala Pro Ala Ser Ala Xaa Gln Gly
130 135 140
Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2454:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:
Met Ser Thr Leu Tyr Thr His Pro Pro Val Glu Pro Arg Val Ser Pro
1 5 10 15
Leu Val Gln Pro Leu Ser Pro Pro Arg Val Thr Pro Pro Pro Gln Arg
 20 25 30
Thr Ala Cys Glu Ala Ala Thr Leu Gln His Ala Arg Arg His Leu Ser
 35 40 45
Leu Pro Arg Val Gln Leu Asp Leu Pro Arg Ala Tyr Ala His Pro Trp
50 55 60
Cys Gly Arg Ala Ala Pro Ser Cys Gly Gln His Arg His Pro Ser Pro
65 70 75 80
Leu Pro Val Pro Ala Ala Thr Ala Gly Ile Asn Pro Phe Leu Thr Pro
 85 90 95
Ser Ser Ser Ala Cys Gly Gly Gly Ala Pro Pro Pro Arg Thr Leu Ala
 100 105 110
Leu Arg Arg Thr Ala Pro Pro Thr Pro Ala Ser Pro Pro Pro Lys Met
 115 120 125
Thr Ser Glu Ala Xaa Pro Pro Pro Ala Pro Ala Ser Ala Xaa Gln Gly
130 135 140

Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

```
Val Asp Thr Leu His Pro Pro Ser Cys Arg Ala Thr Gly Leu Pro Thr
1      5      10      15
Ser Ala Thr Ala Phe Ser Ser Thr Gly Asp Pro Ser Pro Pro Ala His
      20      25      30
Gly Leu Arg Gly Cys Asp Thr Ala Ala Cys Pro Thr Pro Ser Ile Ser
      35      40      45
Ser Ser Arg Pro Ala Arg Pro Pro Cys Leu Arg Pro Ser Leu Val
      50      55      60
Arg Pro Arg Cys Pro Leu Met Arg Pro Thr Ser Thr Ser Leu Pro Ser
65      70      75      80
Pro Ser Thr Gly Cys Asn Cys Arg His Gln Pro Leu Pro His Ala Gln
      85      90      95
Phe Ile Cys Leu Trp Arg Arg Arg Ala Ser Ser Pro His Ala Gly Leu
      100     105     110
Ala Ser Asp Ser Ser Ser Asp Ala Ser Val Pro Ser Ser Lys Asp Asp
      115     120     125
Glu
```

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

```
ttctcattga aaagcttatt gtaaagkttg ttctacctga aggggtcaaag gatatacgaag      60
tttcagctcc ctttccaaca cagcagcagc aagagggttaa gtattcacac cttgacattg      120
tcggaagacc agttgtttgtc ttggagaaac ctgatgttat tccagagcat aatttgtatt      180
tccagggttta ctacagattc aacaacatat ccttgctcag agagccgttg atgctgatta      240
ctggtttctt cctcctgttt gtggcctgta ttgtttacat gcgtactgat atgtcaatat      300
ccaagagctc tccttcctac ttggccaagc tgcaatggga tgaggtgcaa gcaactgttc      360
agaaaatcca gggatatctt gagcaatgct tagcagttca tgataaactg gaggcctcat      420
tgcgggattt gtctaggaca ggagacattc agtcttgcaa ggcagctcgt
```

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1503508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

```
Leu Ile Glu Lys Leu Ile Val Lys Xaa Val Leu Pro Glu Gly Ser Lys
1           5           10           15
Asp Ile Glu Val Ser Ala Pro Leu Pro Thr Gln Gln Gln Gln Glu Val
20           25           30
Lys Tyr Ser His Leu Asp Ile Val Gly Arg Pro Val Val Val Leu Glu
35           40           45
Lys Pro Asp Val Ile Pro Glu His Asn Leu Tyr Phe Gln Val Tyr Tyr
50           55           60
Arg Phe Asn Asn Ile Ser Leu Leu Arg Glu Pro Leu Met Leu Ile Thr
65           70           75           80
Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr Met Arg Thr Asp
85           90           95
Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala Lys Leu Gln Trp
100          105          110
Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly Ile Phe Glu Gln
115          120          125
Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu Arg Asp Leu Ser
130          135          140
Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg
145          150          155
```

(2) INFORMATION FOR SEQ ID NO:2458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1503509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

```
Met Leu Ile Thr Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr
1           5           10           15
Met Arg Thr Asp Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala
20           25           30
Lys Leu Gln Trp Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly
35           40           45
Ile Phe Glu Gln Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu
50           55           60
Arg Asp Leu Ser Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg
65           70           75           80
```

(2) INFORMATION FOR SEQ ID NO:2459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1503510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

```
ttggatttga caaagatgcc aggagaaggc tcttcacccat gattaacaac ctgcccactg      60
tttatgaagt tgtgacgggg gttgctaaga agcaatcgaa agccccaac ggcagcagca      120
```

aaagcagcaa gcctaactct aaaccatcaa aactgaccaa ttctaacagt aagccccgca 180
mscagcccac cc

(2) INFORMATION FOR SEQ ID NO:2460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1503511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

Gly	Phe	Asp	Lys	Asp	Ala	Arg	Arg	Arg	Leu	Phe	Thr	Met	Ile	Asn	Asn
1			5						10					15	
Leu	Pro	Thr	Val	Tyr	Glu	Val	Val	Thr	Gly	Val	Ala	Lys	Lys	Gln	Ser
			20					25					30		
Lys	Ala	Pro	Asn	Gly	Ser	Ser	Lys	Ser	Ser	Lys	Pro	Asn	Ser	Lys	Pro
		35				40						45			
Ser	Lys	Leu	Thr	Asn	Ser	Asn	Ser	Lys	Pro	Ala	Xaa	Gln	Pro	Thr	
		50				55						60			

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1503512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

Met	Ile	Asn	Asn	Leu	Pro	Thr	Val	Tyr	Glu	Val	Val	Thr	Gly	Val	Ala
1			5						10					15	
Lys	Lys	Gln	Ser	Lys	Ala	Pro	Asn	Gly	Ser	Ser	Lys	Ser	Ser	Lys	Pro
			20					25					30		
Asn	Ser	Lys	Pro	Ser	Lys	Leu	Thr	Asn	Ser	Asn	Ser	Lys	Pro	Ala	Xaa
		35				40						45			
Gln	Pro	Thr													
		50													

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1503522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

ctcgagcctg	acccttacgc	cttcgctcgc	gccgcccgcg	ccgcccgcgc	tacgccccgc	60
acctcgcttc	atttcgtgtc	gccaaagatga	cgaagcgcac	taagaaggca	ggaattgttg	120
gcaaatatgg	aaccaggtat	ggtgctagct	tgcgtaassa	atcaagaaga	tggaggtatc	180
tcagcattcc	aattactttt	gcgagttctg	tgggaagttt	gctgtgaaga	ggaaagaatg	240
agcaaggttt	ttgttcgcag	ctatttttgt	ccaatgat	tgatatt		

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..46
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503523
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:
Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr
1 5 10 15
Arg Tyr Gly Ala Ser Leu Arg Xaa Xaa Ser Arg Arg Trp Arg Tyr Leu
 20 25 30
Ser Ile Pro Ile Thr Phe Ala Ser Ser Val Gly Ser Leu Leu
 35 40 45
(2) INFORMATION FOR SEQ ID NO:2464:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503524
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:
Met Glu Pro Gly Met Val Leu Ala Cys Val Xaa Asn Gln Glu Asp Gly
1 5 10 15
Gly Ile Ser Ala Phe Gln Leu Leu Leu Arg Val Leu Trp Glu Val Cys
 20 25 30
Cys Glu Glu Glu Arg Met Ser Lys Val Phe Val Arg Ser Tyr Phe Cys
 35 40 45
Pro Met Ile Leu Ile
 50
(2) INFORMATION FOR SEQ ID NO:2465:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..49
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503525
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:
Met Val Leu Ala Cys Val Xaa Asn Gln Glu Asp Gly Gly Ile Ser Ala
1 5 10 15
Phe Gln Leu Leu Leu Arg Val Leu Trp Glu Val Cys Cys Glu Glu Glu
 20 25 30
Arg Met Ser Lys Val Phe Val Arg Ser Tyr Phe Cys Pro Met Ile Leu
 35 40 45
Ile
(2) INFORMATION FOR SEQ ID NO:2466:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..498
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

```
ctagtagaga gaaaggaaga gaagggggcg gagaagcacg tacgtcgtac atcgcccacc      60
gccctttgcc tcgcctcgcc tcgcctcgcc tgcatatcta acagccggag ccggagccgg      120
agccggagcc gacgccggcg ccgacaatcg ttccaactga tatggctacg acgccaccag      180
gattcacggg caacctgaag aaagcacttg caggtctgag aagaatcagt ttagatgggt      240
tgcgatggcg cgtatttgat gctaagggtc aggtgctcgg gcgattggct tccaaatag      300
ctgttggtgt tcaaggcaag gataaaccga cctatgcacc acatgtagaa aatggagaca      360
tgtgcattgt acttaatgca aaggatatca gtgtttacag gaaggaaaat gacagataag      420
atttactatt ggcatacagg gtatgttggc catttgaagg aaaggaggct caaggaccag      480
atggagaaa gacccaact
```

(2) INFORMATION FOR SEQ ID NO:2467:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..65
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

```
Leu Val Glu Arg Lys Glu Glu Lys Gly Ala Glu Lys His Val Arg Arg
1           5           10           15
Thr Ser Pro Thr Ala Leu Cys Leu Ala Ser Pro Arg Leu Ala Cys Ile
          20          25          30
Ser Asn Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Arg Arg Arg Arg
          35          40          45
Gln Ser Phe Gln Leu Ile Trp Leu Arg Arg His Gln Asp Ser Arg Ala
          50          55          60
Thr
65
```

(2) INFORMATION FOR SEQ ID NO:2468:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

```
Met Ala Thr Thr Pro Pro Gly Phe Thr Gly Asn Leu Lys Lys Ala Leu
1           5           10           15
Ala Gly Leu Arg Arg Ile Ser Leu Asp Gly Leu Arg Trp Arg Val Phe
          20          25          30
Asp Ala Lys Gly Gln Val Leu Gly Arg Leu Ala Ser Gln Ile Ala Val
          35          40          45
Val Leu Gln Gly Lys Asp Lys Pro Thr Tyr Ala Pro His Val Glu Asn
          50          55          60
Gly Asp Met Cys Ile Val Leu Asn Ala Lys Asp Ile Ser Val Tyr Arg
          65          70          75          80
Lys Glu Asn Asp Arg
```

85

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

```
Met Glu Thr Cys Ala Leu Tyr Leu Met Gln Arg Ile Ser Val Phe Thr
1           5           10           15
Gly Arg Lys Met Thr Asp Lys Ile Tyr Tyr Trp His Thr Gly Tyr Val
          20          25          30
Gly His Leu Lys Glu Arg Arg Leu Lys Asp Gln Met Glu Lys Asp Pro
          35          40          45
Thr
```

(2) INFORMATION FOR SEQ ID NO:2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

```
ataaccaagg ataaccagag tgtgctgggt tattgcttct catggggtgt aattttcggt      60
gttttactcg ttatgaagac cgtatcagtg gggaggagga ggttcagtgc agagttccag      120
ctagtgttcc ggctgatcaa gggctctcata tttataactt ttacagccat cgtggtaatc      180
ctaatagcaa tccctggcat gacggttctg gacatctttg tttgcatcct tgccttcatg      240
cccactggat ggggtttgct cctgattgcc caagctatca ggctgtgat tcaaaagatc      300
gggctgtggg ggtcgatcaa ggctcttgcc cggggctacg agatcctaata ggggcttctc      360
ctgttcacgc ccattgcttt ccttgccctg tccccgttcg tgtccgagtt ccagaccagg      420
atgctgttca accaggcctt cagcagaggt tctgcagatc tccccgtatcc tgggagg
```

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

```
Ile Thr Lys Asp Asn Gln Ser Val Leu Val Tyr Cys Phe Ser Trp Val
1           5           10           15
Val Ile Phe Val Val Leu Leu Val Met Lys Thr Val Ser Val Gly Arg
          20          25          30
Arg Arg Phe Ser Ala Glu Phe Gln Leu Val Phe Arg Leu Ile Lys Gly
          35          40          45
Leu Ile Phe Ile Thr Phe Thr Ala Ile Val Val Ile Leu Ile Ala Ile
          50          55          60
```

Pro Gly Met Thr Val Leu Asp Ile Phe Val Cys Ile Leu Ala Phe Met
65 70 75 80
Pro Thr Gly Trp Gly Leu Leu Leu Ile Ala Gln Ala Ile Arg Pro Val
85 90 95
Ile Gln Lys Ile Gly Leu Trp Gly Ser Ile Lys Ala Leu Ala Arg Gly
100 105 110
Tyr Glu Ile Leu Met Gly Leu Leu Leu Phe Thr Pro Ile Ala Phe Leu
115 120 125
Ala Trp Phe Pro Phe Val Ser Glu Phe Gln Thr Arg Met Leu Phe Asn
130 135 140
Gln Ala Phe Ser Arg Gly Ser Ala Asp Leu Pro Tyr Pro Gly Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Gly Cys Asn Phe Arg Cys Phe Thr Arg Tyr Glu Asp Arg Ile Ser
1 5 10 15
Gly Glu Glu Glu Val Gln Cys Arg Val Pro Ala Ser Val Pro Ala Asp
20 25 30
Gln Gly Ser His Ile Tyr Asn Phe Thr Ser His Arg Gly Asn Pro Asn
35 40 45
Ser Asn Pro Trp His Asp Gly Ser Gly His Leu Cys Leu His Pro Cys
50 55 60
Leu His Ala His Trp Met Gly Phe Ala Pro Asp Cys Pro Ser Tyr Gln
65 70 75 80
Ala Cys Asp Ser Lys Asp Arg Ala Val Gly Val Asp Gln Gly Ser Cys
85 90 95
Pro Gly Leu Arg Asp Pro Asn Gly Ala Ser Pro Val His Ala His Cys
100 105 110
Phe Pro Cys Leu Val Pro Val Arg Val Arg Val Pro Asp Gln Asp Ala
115 120 125
Val Gln Pro Gly Leu Gln Gln Arg Phe Cys Arg Ser Pro Val Ser Trp
130 135 140
Glu
145

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Lys Thr Val Ser Val Gly Arg Arg Arg Phe Ser Ala Glu Phe Gln
1 5 10 15
Leu Val Phe Arg Leu Ile Lys Gly Leu Ile Phe Ile Thr Phe Thr Ala
20 25 30
Ile Val Val Ile Leu Ile Ala Ile Pro Gly Met Thr Val Leu Asp Ile

```

      35              40              45
Phe Val Cys Ile Leu Ala Phe Met Pro Thr Gly Trp Gly Leu Leu Leu
  50              55              60
Ile Ala Gln Ala Ile Arg Pro Val Ile Gln Lys Ile Gly Leu Trp Gly
  65              70              75              80
Ser Ile Lys Ala Leu Ala Arg Gly Tyr Glu Ile Leu Met Gly Leu Leu
      85              90              95
Leu Phe Thr Pro Ile Ala Phe Leu Ala Trp Phe Pro Phe Val Ser Glu
      100             105             110
Phe Gln Thr Arg Met Leu Phe Asn Gln Ala Phe Ser Arg Gly Ser Ala
      115             120             125
Asp Leu Pro Tyr Pro Gly Arg
  130             135
```

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

```

caggctcctag ctccggcctc cgccgccgtc tctcacctcc gctcccccttc cctgcccccca      60
tggcgaaggc gacgcccgtg gccgaggccg ggccgcctct cacgtcccca ctcccacatg      120
ggcgcacnca cggaggccct gaccacagtc ctgacccacc cgtcccacgc gccgtcactc      180
cactcgcagc tcttcctcgc ctcccgctgc cgtgcccgc cgcggggcct cggctccacc      240
acgtcgtacc cgccgctcct ctgccccgny gcctcgctcc tccgctgggc tctcgctcc      300
gtgttcctcc cgcgcgcgcg agcctctgcc tcccgccttc gtcttgccgg tcccggtgcc      360
ccttcaggc tccccgccgc cggctcgtgcc ctccgcggcc atcgagccgg gcgcccagac      420
```

(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

```

Gly Pro Ser Ser Gly Leu Arg Arg Arg Leu Ser Pro Pro Leu Pro Phe
  1              5              10              15
Pro Ala Pro Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro
      20              25              30
Leu Thr Ser Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro
      35              40              45
Arg Pro Asp Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu
      50              55              60
Pro Arg Leu Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His
      65              70              75              80
Val Val Pro Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly
      85              90              95
Ser Arg Leu Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro
      100             105             110
Ser Ser Trp Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Arg Ser
      115             120             125
```


Cys Pro Pro Arg Pro Ser Ser Arg Ala Pro Glu
130 135

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

```
Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro Leu Thr Ser
1          5          10          15
Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro Arg Pro Asp
          20          25          30
Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu Pro Arg Leu
          35          40          45
Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His Val Val Pro
          50          55          60
Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly Ser Arg Leu
65          70          75          80
Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro Ser Ser Trp
          85          90          95
Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Arg Ser Cys Pro Pro
          100          105          110
Arg Pro Ser Ser Arg Ala Pro Glu
          115          120
```

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

```
Met Gly Ala Xaa Thr Glu Ala Leu Thr His Val Leu Thr His Pro Ser
1          5          10          15
His Ala Pro Ser Leu His Ser Gln Leu Phe Leu Ala Ser Arg Val Pro
          20          25          30
Cys Pro Pro Arg Gly Leu Gly Ser Thr Thr Ser Tyr Pro Pro Leu Leu
          35          40          45
Cys Pro Xaa Ala Ser Leu Leu Arg Trp Ala Leu Ala Ser Val Phe Leu
          50          55          60
Pro Arg Ala Arg Ala Ser Ala Ser Arg Pro Arg Pro Gly Gly Pro Gly
65          70          75          80
Ala Pro Ser Arg Leu Pro Ala Ala Gly Arg Ala Leu Arg Gly His Arg
          85          90          95
Ala Gly Arg Pro Ser
          100
```

(2) INFORMATION FOR SEQ ID NO:2478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..418
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503569
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:
ttctggctcc tcctgcttcc tcatgatcaa gcgtgtgtcc tctgctccgt ccttgtccag 60
gcaccacaag gcaaaagaag ctcaggtgag aatgttgtga tggttgatcc actggaagct 120
aagcgcctag ctgctaaaca aatgcaagaa attagggcca aagaaaagct gaagaggcgc 180
cgtcaagcag aagcgatcaa cggggcattg gcagtgatag gactcacggc tggattgcta 240
gtggaggctc agacaggaaa ggacatctta gggcagctag ctggatatct gacggctatt 300
tctagtttat ttgggcaata acactggacc atggttggag atttattttt cacgttccac 360
ggccaggaga ggtcttatct gaatcttatt tgatggatcc acccaatttt tttgggag

(2) INFORMATION FOR SEQ ID NO:2479:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..106
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503570
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:
Phe Trp Leu Leu Leu Pro His Asp Gln Ala Cys Val Leu Cys Ser
1 5 10 15
Val Leu Val Gln Ala Pro Gln Gly Lys Arg Ser Ser Gly Glu Asn Val
20 25 30
Val Met Val Asp Pro Leu Glu Ala Lys Arg Leu Ala Ala Lys Gln Met
35 40 45
Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala Glu
50 55 60
Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu Leu
65 70 75 80
Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly Tyr
85 90 95
Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln
100 105

(2) INFORMATION FOR SEQ ID NO:2480:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..73
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503571
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:
Met Val Asp Pro Leu Glu Ala Lys Arg Leu Ala Ala Lys Gln Met Gln
1 5 10 15
Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala Glu Ala
20 25 30
Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu Leu Val
35 40 45
Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly Tyr Leu
50 55 60
Thr Ala Ile Ser Ser Leu Phe Gly Gln

65

70

(2) INFORMATION FOR SEQ ID NO:2481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

```
Met Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala
1           5           10           15
Glu Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu
20           25           30
Leu Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly
35           40           45
Tyr Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln
50           55
```

(2) INFORMATION FOR SEQ ID NO:2482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..438
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

```
cagaggatat caatatttgg tggatgaattc ccatcagggc atacagctga tgttcaaagt      60
gtgtccatca actcatcaat acaaatatgt ttgtctctgg ctcatgtgat acaactgtga      120
ggctgtggga tatcagaatt gcaagtcgag ctgttcgaac ctacatgga catgaggatg      180
atgttaacag tgtgaagttt ttccctgatg gccataggtt tggtagtgga tcagattatg      240
gcacatgtag attatttgat atgagaacag ggcatacaact tcaggtgtac agtagggagc      300
ctgatagaaa tagtaatgaa ctacctactg ttacatctat tgcattttca atatcaggaa      360
ggctactttt tgctgggttac tccaatgggt actgttatgt gtgggacacm ttctcgccga      420
ggtggtactt aatttggg
```

(2) INFORMATION FOR SEQ ID NO:2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

```
Met Phe Val Ser Gly Ser Cys Asp Thr Val Arg Leu Trp Asp Ile
1           5           10           15
Arg Ile Ala Ser Arg Ala Val Arg Thr Tyr His Gly His Glu Asp Asp
20           25           30
Val Asn Ser Val Lys Phe Phe Pro Asp Gly His Arg Phe Gly Thr Gly
35           40           45
Ser Asp Tyr Gly Thr Cys Arg Leu Phe Asp Met Arg Thr Gly His Gln
50           55           60
```

Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg Asn Ser Asn Glu Leu Pro
65 70 75 80
Thr Val Thr Ser Ile Ala Phe Ser Ile Ser Gly Arg Leu Leu Phe Ala
85 90 95
Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp Asp Xaa Phe Ser Pro Arg
100 105 110
Trp Tyr Leu Ile Trp
115

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

Met Arg Thr Gly His Gln Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg
1 5 10 15
Asn Ser Asn Glu Leu Pro Thr Val Thr Ser Ile Ala Phe Ser Ile Ser
20 25 30
Gly Arg Leu Leu Phe Ala Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp
35 40 45
Asp Xaa Phe Ser Pro Arg Trp Tyr Leu Ile Trp
50 55

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..506
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

ttcgccgccc cgcgcctcgg agaagagata gagcgggccg ctgcatcgac cccgcgccac 60
ccccgcctgc ctcccccggc accgatcggg tttgatcgat ggcgtcgaag aggatcctga 120
aggagttgaa ggacctgcag aaggacccgc ccacctcctg cagcgertcc tgttggtgag 180
gacatgttcc attggcaagc gaccatcatg gggccttcgg acagccatt tgcaggtggg 240
gtattcttgg tgaacattca cttcccaccg gattaccctt tcaagccacc aaaggtgtct 300
ttccgcacca aggttttcca cccgaacatc aacagcaacg gcagcatttg ccttgacatt 360
cttaaggaac agtggagtcc tgctttaact atctcaaagg ttctcctgtc aatctgctca 420
ctgctcacgg acccaaacc tcatgatcct cttgtccctg agattgctca catgtacaat 480
tcattcgttg gaaaacctgg aacgtg

(2) INFORMATION FOR SEQ ID NO:2486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Phe
1 5 10 15
Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro
20 25 30
Phe Lys Pro Pro Lys Val Ser Phe Arg Thr Lys Val Phe His Pro Asn
35 40 45
Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp
50 55 60
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu
65 70 75 80
Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His
85 90 95
Met Tyr Asn Ser Phe Val Gly Lys Pro Gly Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1503590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

Met Gly Pro Ser Asp Ser Pro Phe Ala Gly Gly Val Phe Leu Val Asn
1 5 10 15
Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe
20 25 30
Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys
35 40 45
Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys
50 55 60
Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp
65 70 75 80
Pro Leu Val Pro Glu Ile Ala His Met Tyr Asn Ser Phe Val Gly Lys
85 90 95
Pro Gly Thr

(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1503591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

gtacgagcgg acgcacgacg agcttgactt cgagttcctc gggaacgtgc gcggaaggga	60
gtggcgcggtg cagaccaacg tgtacggcaa cggcagcacg gcggccggcc gggaggagcg	120
ctacggcctc tggttcgacc ccacggagga cttccaccgc tacgccatcc actggaccgc	180
cgacaggatc atattctaca tcgacgacac gccaatcatg gagatggtgc ggacggagtc	240
aatgggcgcg cagttcccgt ccaagcccat gtcgctgtac gccaccatct gggacggctc	300
cagctggggc acctcggggg gccgctacaa ggtggactac aagtacgcgc cctacgtcgc	360
cgagttcgcc gacctcgcg tcc	

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

Tyr	Glu	Arg	Thr	His	Asp	Glu	Leu	Asp	Phe	Glu	Phe	Leu	Gly	Asn	Val
1				5				10						15	
Arg	Gly	Lys	Glu	Trp	Arg	Val	Gln	Thr	Asn	Val	Tyr	Gly	Asn	Gly	Ser
			20				25						30		
Thr	Ala	Ala	Gly	Arg	Glu	Glu	Arg	Tyr	Gly	Leu	Trp	Phe	Asp	Pro	Thr
			35				40					45			
Glu	Asp	Phe	His	Arg	Tyr	Ala	Ile	His	Trp	Thr	Arg	Asp	Arg	Ile	Ile
	50					55					60				
Phe	Tyr	Ile	Asp	Asp	Thr	Pro	Ile	Met	Glu	Met	Val	Arg	Thr	Glu	Ser
65					70					75				80	
Met	Gly	Ala	Gln	Phe	Pro	Ser	Lys	Pro	Met	Ser	Leu	Tyr	Ala	Thr	Ile
				85					90					95	
Trp	Asp	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Gly	Gly	Arg	Tyr	Lys	Val	Asp
			100					105					110		
Tyr	Lys	Tyr	Ala	Pro	Tyr	Val	Ala	Glu	Phe	Ala	Asp	Leu	Ala	Leu	
			115					120					125		

- (2) INFORMATION FOR SEQ ID NO:2490:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503593
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:

Thr	Ser	Gly	Arg	Thr	Thr	Ser	Leu	Thr	Ser	Ser	Ser	Ser	Gly	Thr	Cys
1				5				10						15	
Ala	Ala	Arg	Ser	Gly	Ala	Cys	Arg	Pro	Thr	Cys	Thr	Ala	Thr	Ala	Ala
			20					25					30		
Arg	Arg	Pro	Ala	Gly	Arg	Ser	Ala	Thr	Ala	Ser	Gly	Ser	Thr	Pro	Arg
			35				40					45			
Arg	Thr	Ser	Thr	Ala	Thr	Pro	Ser	Thr	Gly	Pro	Ala	Thr	Gly	Ser	Tyr
	50					55					60				
Ser	Thr	Ser	Thr	Thr	Arg	Gln	Ser	Trp	Arg	Trp	Cys	Gly	Arg	Ser	Gln
65					70					75				80	
Trp	Ala	Arg	Ser	Ser	Arg	Pro	Ser	Pro	Cys	Arg	Cys	Thr	Pro	Pro	Ser
				85					90					95	
Gly	Thr	Ala	Pro	Ala	Gly	Pro	Pro	Arg	Gly	Ala	Ala	Thr	Arg	Trp	Thr
			100					105					110		
Thr	Ser	Thr	Arg	Pro	Thr	Ser	Pro	Ser	Pro	Thr	Ser	Arg	Ser		
			115					120					125		

- (2) INFORMATION FOR SEQ ID NO:2491:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..365
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

```
actgaacatt ctgcgtgaag attggaagcc tgttctcaac atcaacaccg ttatttatgg      60
cctgaatcctt cttttttacgc aaccaaacga cgaggatcct ttgaaccacg aagctgcagc      120
tgtcctccgt ggcaacccaa agatgtttga ggcaaagtgtg aaaagagcca tgaccggagc      180
tacgtaggcc aacactatatt ccaaagatgc ttggcttgat gtgatggctt caagccagcg      240
ggcccatgta tcagcaccag cgcgccagg tttggaggat ttttgtggat ttagggcgct      300
tctggaagca aaggtcaaatt cggtcgttgt tgataatgtg atgtactccc tcagttcttt      360
ttatt
```

(2) INFORMATION FOR SEQ ID NO:2492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

```
Leu Asn Ile Leu Arg Glu Asp Trp Lys Pro Val Leu Asn Ile Asn Thr
1          5          10          15
Val Ile Tyr Gly Leu Asn Leu Leu Phe Thr Gln Pro Asn Asp Glu Asp
20          25          30
Pro Leu Asn His Glu Ala Ala Ala Val Leu Arg Gly Asn Pro Lys Met
35          40          45
Phe Glu Ala Asn Val Lys Arg Ala Met Thr Gly Ala Thr
50          55          60
```

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

```
Met Ala Ser Ser Gln Arg Ala His Val Ser Ala Pro Ala Arg Pro Gly
1          5          10          15
Leu Glu Asp Phe Cys Gly Phe Arg Ala Leu Leu Glu Ala Lys Val Lys
20          25          30
Ser Val Val Val Asp Asn Val Met Tyr Ser Leu Ser Ser Phe Tyr
35          40          45
```

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:
Met Tyr Gln His Gln Arg Ala Gln Val Trp Arg Ile Phe Val Asp Leu
1 5 10 15
Gly Arg Phe Trp Lys Gln Arg Ser Asn Arg Ser Leu Leu Ile Met
20 25 30

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..413
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

```
atatccgcct ccaaacccta gctcttccat tcttccccct ccggcgccgc ctccccccaga      60
cacttcgccg ccggcaagat gggccgcgtg attcgcgctc agssaagggt gcgggggtccg      120
tgttcaagtc ccatacccat caccgcaagg ccctgccggt tccgggtccct cgacttcggc      180
gagcgcaacg ggtacctgaa gggcgtggtc accgacgtca tccacgaccc gggccgcggc      240
gcgcccgtgg ccaaggtcac cttccgccat ccattccggt acaagcacca gaaggagctg      300
ttcgtggctg ctgagggcat gtacactggc cagttcggtt actgcggacg ccgtgctaca      360
ctctccattg gcaacgtcct gccgctcagg gggatccctg agggtgccgt tgt
```

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:

```
Ile Arg Leu Gln Thr Leu Ala Leu Pro Phe Phe Pro Leu Arg Arg Arg
1 5 10 15
Leu Pro Gln Thr Leu Arg Arg Arg Gln Asp Gly Pro Arg Asp Ser Arg
20 25 30
Ser Xaa Lys Gly Ala Gly Ser Val Phe Lys Ser His Thr His His Arg
35 40 45
Lys Ala Leu Pro Val Pro Val Pro Arg Leu Arg Arg Ala Gln Arg Val
50 55 60
Pro Glu Gly Arg Gly His Arg Arg His Pro Arg Pro Gly Pro Arg Arg
65 70 75 80
Ala Ala Gly Gln Gly His Leu Pro Pro Ser Ile Pro Val Gln Ala Pro
85 90 95
Glu Gly Ala Val Arg Gly Cys
100
```

(2) INFORMATION FOR SEQ ID NO:2497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:

Met	Gly	Arg	Val	Ile	Arg	Ala	Gln	Xaa	Arg	Val	Arg	Gly	Pro	Cys	Ser
1				5					10					15	
Ser	Pro	Ile	Pro	Ile	Thr	Ala	Arg	Pro	Cys	Arg	Phe	Arg	Ser	Leu	Asp
			20					25					30		
Phe	Gly	Glu	Arg	Asn	Gly	Tyr	Leu	Lys	Gly	Val	Val	Thr	Asp	Val	Ile
			35				40					45			
His	Asp	Pro	Gly	Arg	Gly	Ala	Pro	Leu	Ala	Lys	Val	Thr	Phe	Arg	His
	50					55					60				
Pro	Phe	Arg	Tyr	Lys	His	Gln	Lys	Glu	Leu	Phe	Val	Ala	Ala	Glu	Gly
65				70						75				80	
Met	Tyr	Thr	Gly	Gln	Phe	Val	Tyr	Cys	Gly	Arg	Arg	Ala	Thr	Leu	Ser
				85					90					95	
Ile	Gly	Asn	Val	Leu	Pro	Leu	Arg	Gly	Ile	Pro	Glu	Gly	Ala	Val	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:2498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:

attccattcc	atcgattgg	attgcattcc	catccattc	cccgctctac	tcattcagat	60
ctcgtaactc	gctctccaca	agcagagcac	cgcagcagaa	cgaggatgct	ggccatcttc	120
cagaagcagg	tggcgcacgc	gtcsgcagga	gcntcaacag	cccccgccgc	ggcgcgctgc	180
ccagcaagcc	ccggaacccc	gacgagatcc	tgcgcgactt	ccacgccgcg	caccgcggccg	240
ccgccttctc	cgctctcttc	ggcggcgctgc	gntgctcgcc	ttgcgttcgg	cccctcctcc	300
gccaccgcca	cctaccagcg	ggatgtttct	gcggccttgg	accacatcta	ctgcgtcttc	360
ctcgcccgcc	tcgacaacct	cagcggcctc	atccgccagt	wacggcctgt	gcggccgctc	420
ccaccaacga	ggcgatgctg	gtcatcgagg	cctaccgcac	gctgcg		

(2) INFORMATION FOR SEQ ID NO:2499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:

Ile	Pro	Phe	His	Arg	Ile	Gly	Leu	His	Ser	His	Pro	Ile	Pro	Arg	Ser
1				5					10					15	
Thr	His	Ser	Asp	Leu	Val	Thr	Arg	Ser	Pro	Gln	Ala	Glu	His	Arg	Ser
			20					25					30		
Arg	Thr	Arg	Met	Leu	Ala	Ile	Phe	Gln	Lys	Gln	Val	Ala	His	Ala	Xaa
			35				40					45			
Ala	Gly	Xaa	Ser	Thr	Ala	Pro	Ala	Pro	Ala	Arg	Arg	Pro	Ala	Ser	Pro
	50					55					60				
Gly	Thr	Pro	Thr	Arg	Ser	Cys	Ala	Thr	Ser	Thr	Pro	Arg	Thr	Arg	Pro
65				70						75				80	
Pro	Pro	Ser	Pro	Pro	Pro	Ser	Ala	Ala	Cys	Xaa	Ala	Arg	Leu	Ala	Phe
				85					90					95	
Gly	Pro	Ser	Ser	Ala	Thr	Ala	Thr	Tyr	Gln	Arg	Asp	Val	Ser	Ala	Ala
			100					105					110		

Leu Asp His Ile Tyr Cys Val Phe Leu Gly Arg Leu Asp Asn Leu Ser
115 120 125
Gly Leu Ile Arg Gln Xaa Arg Pro Val Arg Pro Leu Pro Pro Thr Arg
130 135 140
Arg Cys Trp Ser Ser Arg Pro Thr Ala Arg Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1503617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Phe His Ser Ile Ala Leu Asp Cys Ile Pro Ile Pro Phe Pro Ala Leu
1 5 10 15
Leu Ile Gln Ile Ser Ser Leu Ala Leu His Lys Gln Ser Thr Ala Ala
20 25 30
Glu Arg Gly Cys Trp Pro Ser Ser Arg Ser Arg Trp Arg Thr Arg Xaa
35 40 45
Gln Glu Xaa Gln Gln Pro Pro Arg Arg Arg Val Ala Gln Gln Ala Pro
50 55 60
Glu Pro Arg Arg Asp Pro Ala Arg Leu Pro Arg Ala Pro Gly Arg
65 70 75 80
Arg Leu Leu Arg Leu Leu Arg Arg Arg Ala Xaa Leu Ala Leu Arg Ser
85 90 95
Ala Pro Pro Pro Pro Pro Pro Pro Thr Ser Gly Met Phe Leu Arg Pro
100 105 110
Trp Thr Thr Ser Thr Ala Ser Ser Ser Ala Ala Ser Thr Thr Ser Ala
115 120 125
Ala Ser Ser Ala Ser Xaa Gly Leu Cys Gly Arg Ser His Gln Arg Gly
130 135 140
Asp Ala Gly His Arg Gly Leu Pro His Ala Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1503618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

Ser Ile Pro Ser His Trp Ile Ala Phe Pro Ser His Ser Pro Leu Tyr
1 5 10 15
Ser Phe Arg Ser Arg His Ser Leu Ser Thr Ser Arg Ala Pro Gln Gln
20 25 30
Asn Glu Asp Ala Gly His Leu Pro Glu Ala Gly Gly Ala Arg Val Xaa
35 40 45
Arg Ser Xaa Asn Ser Pro Arg Ala Gly Ala Ser Pro Ser Lys Pro Arg
50 55 60
Asn Pro Asp Glu Ile Leu Arg Asp Phe His Ala Ala His Pro Ala Ala
65 70 75 80
Ala Phe Ser Ala Ser Phe Gly Gly Val Xaa Cys Ser Pro Cys Val Arg

```

      85                      90                      95
Pro Leu Leu Arg His Arg His Leu Pro Ala Gly Cys Phe Cys Gly Leu
      100                      105                      110
Gly Pro His Leu Leu Arg Leu Pro Arg Pro Pro Arg Gln Pro Gln Arg
      115                      120                      125
Pro His Pro Pro Xaa Thr Ala Cys Ala Ala Ala Pro Thr Asn Glu Ala
      130                      135                      140
Met Leu Val Ile Glu Ala Tyr Arg Thr Leu
145                      150
```

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..403
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

```

agtgtcgggtg tcggcggttg cgagtggcga ctggcgactt ctctgcctcg tccctccccg      60
ttttcccctc cgcgtccagc cckgcgcgac gccaccacgc acctagccgc ggantccgag      120
gcgcagatcc aatccagcga tggcgctccac ggcgcgcgag cggttgccgg asstgcaggc      180
ccagacgggg aacaagacct gcgtggactg cgcgcrssta acccgagtg ggcgagcgtc      240
tcctacggcg tgttcattgt cctcgagtgc tcyggcaagc accggggcct cggcggtgcac      300
atcagtttcg tgcgctcggg caccatggac tcctggaccg aggcgcasst ccgcaagatg      360
gaggccggcg gcaacgaccg cctcaacgcc ttcctcacag cgc
```

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

```

Ser Val Gly Val Gly Val Gly Glu Trp Arg Leu Ala Thr Ser Leu Pro
1      5      10      15
Arg Pro Ser Pro Phe Ser Pro Pro Arg Pro Ala Xaa Arg Asp Ala Thr
      20      25      30
Thr His Leu Ala Ala Xaa Ser Glu Ala Gln Ile Gln Ser Ser Asp Gly
      35      40      45
Val His Gly Gly Glu Ala Val Ala Gly Xaa Ala Gly Pro Asp Gly Glu
      50      55      60
Gln Asp Leu Arg Gly Leu Arg Xaa Xaa Asn Pro Gln Trp Ala Ser Val
      65      70      75      80
Ser Tyr Gly Val Phe Met Cys Leu Glu Cys Xaa Gly Lys His Arg Gly
      85      90      95
Leu Gly Val His Ile Ser Phe Val Arg Ser Val Thr Met Asp Ser Trp
      100     105     110
Thr Glu Ala Xaa Xaa Arg Lys Met Glu Ala Gly Gly Asn Asp Arg Leu
      115     120     125
Asn Ala Phe Leu Thr Ala
130
```

(2) INFORMATION FOR SEQ ID NO:2504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1503623
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:
Cys Arg Cys Arg Arg Trp Arg Val Ala Thr Gly Asp Phe Ser Ala Ser
1 5 10 15
Ser Leu Pro Val Phe Pro Ser Ala Ser Ser Xaa Ala Arg Arg His His
20 25 30
Ala Pro Ser Arg Gly Xaa Arg Gly Ala Asp Pro Ile Gln Arg Trp Arg
35 40 45
Pro Arg Arg Arg Gly Gly Cys Gly Xaa Cys Arg Pro Arg Arg Gly Thr
50 55 60
Arg Pro Ala Trp Thr Ala Arg Xaa
65 70

(2) INFORMATION FOR SEQ ID NO:2505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..88
(D) OTHER INFORMATION: / Ceres Seq. ID 1503624
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505:
Met Ala Ser Thr Ala Ala Arg Arg Leu Arg Xaa Xaa Gln Ala Gln Thr
1 5 10 15
Gly Asn Lys Thr Cys Val Asp Cys Ala Xaa Xaa Thr Arg Ser Gly Arg
20 25 30
Ala Ser Pro Thr Ala Cys Ser Cys Ala Ser Ser Ala Xaa Ala Ser Thr
35 40 45
Gly Ala Ser Ala Cys Thr Ser Val Ser Cys Ala Arg Ser Pro Trp Thr
50 55 60
Pro Gly Pro Arg Arg Xaa Ser Ala Arg Trp Arg Pro Ala Ala Thr Thr
65 70 75 80
Ala Ser Thr Pro Ser Ser Gln Arg
85

(2) INFORMATION FOR SEQ ID NO:2506:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..389
(D) OTHER INFORMATION: / Ceres Seq. ID 1503662
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:
actcgcgac agsstccaat ttctctccacc tcccgaaccc taccggcggc gcmagcattc 60
acaaccacca cccgaagatg gtgaagtttc tgaagcccgg caaggccgta atcctcctcc 120
agggcagatt cgccggccgg aagssggtga tcgtgcgcgt gttcgaggag ggcacccgag 180
accgtcccta tgggcaactgc ctgcgtgccg gcctggccaa gtacccaag aaggatgatcc 240
gcaagactcc gccagaaga cggccaagaa gtcccgcgtc aagtgttca tcaagctcat 300
caatttcact cacctcatgc ccaccgcga caccctcgac gtcgacttca aggacgtcgc 360

(2) INFORMATION FOR SEO ID NO:2507:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503663

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503664

[illegible]

(2) INFORMATION FOR SEQ ID NO:2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

```
Met Val Lys Phe Leu Lys Pro Gly Lys Ala Val Ile Leu Leu Gln Gly
1           5           10           15
Arg Phe Ala Gly Arg Lys Xaa Val Ile Val Arg Val Phe Glu Glu Gly
20           25           30
Thr Arg Asp Arg Pro Tyr Gly His Cys Leu Val Ala Gly Leu Ala Lys
35           40           45
Tyr Pro Lys Lys Val Ile Arg Lys Thr Pro Pro Arg Arg Pro Arg
50           55           60
Ser Pro Ala Ser Ser Ala Ser Ser Ser Ser Ile Ser Leu Thr Ser
65           70           75           80
Cys Pro Pro Ala Thr Pro Ser Thr Ser Thr Ser Arg Thr Ser Pro Arg
85           90           95
Gly Gly Pro Thr Arg Ser Pro Pro
100
```

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

```
atgtgtgcgt gcacacccac tcctgagaat gctaattgtac gtgaccttga actcncatt      60
gcangtgccc ttctgaatac catatgatta agtacctttc ggcatgttaa tttcatctcc      120
aaaagtctct atacgaggcc gcagcaactt ggattatata tccctagtcg tgcgtccacgg      180
cgggtgcggt cgccgacgcc gacgccgacg ccgccacctc ctccggcgcg gccgcggttg      240
tgtccttggc cggggcgcta ccgctccctt cggagcttcc cttgtttttc cggcggttg      300
acttcttggg aacggcgggg aggtcctggc atgtgcccga ggcgtcgtcg cggnccgact      360
tgtcctgctt cttgcggttc tttcggggtt gcaacaagag gaggatgaag atcgaagacc      420
```

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

```
Met Leu Ile Ser Ser Pro Lys Val Leu Ile Arg Gly Arg Ser Asn Leu
1           5           10           15
Asp Tyr Ile Ser Leu Val Val Val His Gly Gly Cys Gly Arg Arg Arg
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

aaagcagagt	ctgcccctcc	ccgcgcggtt	cttttttggtt	ccccagtccc	cgccgcccgc	60
gaaacccgca	gatggaggtc	gtcgtcgccg	cgamssagaa	ggcgaagaaa	cacatacacc	120
tcttctactg	ctcagaatgc	gaggagctcg	ccctcaagat	cgccgccagc	tccgacgcca	180
tcgagctcca	atccatcaac	tggcggasst	tgcagcagcg	gttcccgaac	ctattcatcg	240
cctcattcac	gctcgtgctg	ccattcttcc	ccacgggctc	attcgagcgc	gttgaggagg	300
agggcgatgt	cgccaccgcg	ttcacccctg	cgcgcattct	ctcgatgata	cccaagtcgc	360
gcggcgggcc	taccagcgct	gtcatctacg	acatccacgc	gctccaggag	aggttttact	420
tcggggacga	tgtctgccat	gcttcgagac	agggatcccg	ctcctgctgc	agcgcctccg	480
ccagctcccg	gacgc					

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

Lys	Ala	Glu	Ser	Ala	Pro	Pro	Arg	Ala	Val	Leu	Phe	Gly	Ser	Pro	Val
1				5					10					15	
Pro	Ala	Ala	Ala	Glu	Thr	Arg	Arg	Trp	Arg	Ser	Ser	Ser	Pro	Arg	Xaa
				20				25					30		
Arg	Arg	Arg	Arg	Asn	Thr	Tyr	Thr	Ser	Ser	Thr	Ala	Gln	Asn	Ala	Arg
				35				40					45		
Ser	Ser	Pro	Ser	Arg	Ser	Pro	Pro	Ala	Pro	Thr	Pro	Ser	Ser	Ser	Asn
				50				55				60			
Pro	Ser	Thr	Gly	Gly	Xaa	Ser	Thr	Thr	Gly	Ser	Arg	Thr	Tyr	Ser	Ser
65					70				75					80	
Pro	His	Ser	Arg	Ser	Cys	Cys	His	Ser	Ser	Pro	Arg	Ala	His	Ser	Ser
				85				90						95	
Ala	Leu	Arg	Arg	Arg	Ala	Met	Ser	Pro	Pro	Arg	Ser	Pro	Ser	Arg	Ala
				100				105						110	
Phe	Ser	Arg													

(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:


```

Ser Arg Val Cys Pro Ser Pro Arg Arg Ser Phe Trp Phe Pro Ser Pro
1          5          10          15
Arg Arg Arg Arg Asn Pro Gln Met Glu Val Val Val Ala Ala Xaa Xaa
20          25          30
Lys Ala Lys Lys His Ile His Leu Phe Tyr Cys Ser Glu Cys Glu Glu
35          40          45
Leu Ala Leu Lys Ile Ala Ala Ser Ser Asp Ala Ile Glu Leu Gln Ser
50          55          60
Ile Asn Trp Arg Xaa Phe Asp Asp Gly Phe Pro Asn Leu Phe Ile Ala
65          70          75          80
Ser Phe Thr Leu Val Leu Pro Phe Phe Pro Thr Gly Ser Phe Glu Arg
85          90          95
Val Glu Glu Glu Gly Asp Val Ala Thr Ala Phe Thr Leu Ala Arg Ile
100         105         110
Leu Ser Met Ile Pro Lys Ser Arg Gly Gly Pro Thr Ser Val Val Ile
115         120         125
Tyr Asp Ile His Ala Leu Gln Glu Arg Phe Tyr Phe Gly Asp Asp Val
130         135         140
Cys His Ala Ser Arg Gln Gly Ser Arg Ser Cys Cys Ser Ala Ser Ala
145         150         155         160
Ser Ser Arg Thr

```

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

```

Met Glu Val Val Val Ala Ala Xaa Xaa Lys Ala Lys Lys His Ile His
1          5          10          15
Leu Phe Tyr Cys Ser Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala
20          25          30
Ser Ser Asp Ala Ile Glu Leu Gln Ser Ile Asn Trp Arg Xaa Phe Asp
35          40          45
Asp Gly Phe Pro Asn Leu Phe Ile Ala Ser Phe Thr Leu Val Leu Pro
50          55          60
Phe Phe Pro Thr Gly Ser Phe Glu Arg Val Glu Glu Gly Asp Val
65          70          75          80
Ala Thr Ala Phe Thr Leu Ala Arg Ile Leu Ser Met Ile Pro Lys Ser
85          90          95
Arg Gly Gly Pro Thr Ser Val Val Ile Tyr Asp Ile His Ala Leu Gln
100         105         110
Glu Arg Phe Tyr Phe Gly Asp Asp Val Cys His Ala Ser Arg Gln Gly
115         120         125
Ser Arg Ser Cys Cys Ser Ala Ser Ala Ser Ser Arg Thr
130         135         140

```

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1503714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

aacttcaccg	gcctcctcct	ccttcccgtc	catcgccgtc	gccggggcgc	cctacaactt	60
caaaatggcg	gctaccgcac	tcgccaatggc	tatagcaact	atytcccccg	ccgctccgat	120
cccatccgcg	cccttcccat	ccctccccct	cggcctccgc	ctccgccctc	aaccctcctt	180
tttcgtgct	tcccgccgcc	gccttcctcc	atgttcccaa	agccgcctcc	tgggacgaat	240
ccgtcccccg	aggatggtgg	agatgcggag	gaatccgttg	ccgctgggga	cgacgaggac	300
gaggacgaga	agccgcggcc	cgagccgggtg	tcttcctccg	agttccagtt	cgcggcgcca	360
cccagagggt	acgtcgagcc	cgcggckktt	tgacgagcta	ccgccggagt	ccccasaaga	420
cgtggcggcg	gcgtacgaat	ctctctacgg	gccggccttc	agcggcgaga	catt	

(2) INFORMATION FOR SEQ ID NO:2519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

Asn	Phe	Thr	Gly	Leu	Leu	Leu	Leu	Pro	Val	His	Arg	Arg	Arg	Arg	Gly	
1				5				10						15		
Ala	Leu	Gln	Leu	Gln	Asn	Gly	Gly	Tyr	Arg	Thr	Arg	His	Gly	Tyr	Ser	
		20						25					30			
Asn	Tyr	Xaa	Pro	Arg	Arg	Ser	Asp	Pro	Ile	Arg	Ala	Leu	Pro	Ile	Pro	
		35					40					45				
Pro	Pro	Arg	Pro	Pro	Pro	Pro	Pro	Ser	Thr	Pro	Pro	Phe	Arg	Cys	Phe	
		50					55					60				
Pro	Pro	Pro	Pro	Ser	Ser	Met	Phe	Pro	Lys	Pro	Pro	Pro	Gly	Thr	Asn	
				70						75				80		
Pro	Ser	Pro	Glu	Asp	Gly	Gly	Asp	Ala	Glu	Glu	Ser	Val	Ala	Ala	Gly	
				85						90				95		
Asp	Asp	Glu	Asp	Glu	Asp	Glu	Lys	Pro	Arg	Pro	Glu	Pro	Val	Ser	Ser	
		100						105					110			
Ser	Glu	Phe	Gln	Phe	Ala	Ala	Pro	Pro	Glu	Gly	Tyr	Val	Glu	Pro	Ala	
		115					120						125			
Xaa	Xaa															
		130														

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Thr	Ser	Pro	Ala	Ser	Ser	Ser	Phe	Pro	Ser	Ile	Ala	Val	Ala	Gly	Ala	
1				5				10						15		
Pro	Tyr	Asn	Phe	Lys	Met	Ala	Ala	Thr	Ala	Leu	Ala	Met	Ala	Ile	Ala	
		20						25					30			
Thr	Xaa	Ser	Pro	Ala	Ala	Pro	Ile	Pro	Ser	Ala	Pro	Phe	Pro	Ser	Leu	
		35					40					45				
Pro	Leu	Gly	Leu	Arg	Leu	Arg	Pro	Gln	Pro	Leu	Leu	Phe	Ala	Ala	Ser	
		50					55					60				

Arg Arg Arg Leu Pro Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile
65 70 75 80
Arg Pro Pro Arg Met Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly
85 90 95
Thr Thr Arg Thr Arg Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro
100 105 110
Pro Ser Ser Ser Ser Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg
115 120 125
Xaa Phe Asp Glu Leu Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Ala
130 135 140
Tyr Glu Ser Leu Tyr Gly Pro Ala Phe Ser Gly Glu Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:2521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

Met Ala Ala Thr Ala Leu Ala Met Ala Ile Ala Thr Xaa Ser Pro Ala
1 5 10 15
Ala Pro Ile Pro Ser Ala Pro Phe Pro Ser Leu Pro Leu Gly Leu Arg
20 25 30
Leu Arg Pro Gln Pro Leu Leu Phe Ala Ala Ser Arg Arg Arg Leu Pro
35 40 45
Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile Arg Pro Pro Arg Met
50 55 60
Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly Thr Thr Arg Thr Arg
65 70 75 80
Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro Pro Ser Ser Ser Ser
85 90 95
Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg Xaa Phe Asp Glu Leu
100 105 110
Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Ala Tyr Glu Ser Leu Tyr
115 120 125
Gly Pro Ala Phe Ser Gly Glu Thr
130 135

(2) INFORMATION FOR SEQ ID NO:2522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..412
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

agagcagcca agcgccacac acacgcccgc gcgaaccaac caaccagctg gtagtaggtt 60
cgccgcggcg ccgcgctgac gatgatgcct cgccgcgccc ttctcttcgc cgcggtgctc 120
ctcgcgccct ccgcgcgcgc gtctccgggt ttacactcgc cggggacgag agcggtctcg 180
tgaggggtgt gctgcgcgcg ctccgcagcg kgtccgaggc cgtggacgcc gctcgcttcg 240
ccgtcgccca ctacaacaag aaccagggcg ccgctttgga gtttactagg gtgctcaaat 300
ccaagcggca ggtggtgacc gggaccctgc atgacctgat actggaggca gctgatgctg 360
gaaaaaagag tgtgtacaga gcaaaggttt ggggtgaagcg tgggaagatt tc

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

Ser	Ser	Gln	Ala	Pro	His	Thr	Arg	Arg	Arg	Glu	Pro	Thr	Asn	Gln	Leu	
1				5					10					15		
Val	Val	Gly	Ser	Pro	Arg	Arg	Arg	Ala	Asp	Asp	Asp	Ala	Ser	Pro	Arg	
			20					25					30			
Pro	Ser	Leu	Arg	Arg	Gly	Ala	Pro	Arg	Gly	Leu	Arg	Arg	Ala	Val	Ser	
		35					40					45				
Gly	Phe	His	Leu	Gly	Gly	Asp	Glu	Ser	Gly	Leu	Val	Arg	Gly	Val	Leu	
		50				55					60					
Ala	Ala	Leu	Arg	Ser	Xaa	Ser	Glu	Ala	Val	Asp	Ala	Ala	Arg	Phe	Ala	
65				70						75					80	
Val	Ala	His	Tyr	Asn	Lys	Asn	Gln	Gly	Ala	Ala	Leu	Glu	Phe	Thr	Arg	
				85				90						95		
Val	Leu	Lys	Ser	Lys	Arg	Gln	Val	Val	Thr	Gly	Thr	Leu	His	Asp	Leu	
			100				105						110			
Ile	Leu	Glu	Ala	Ala	Asp	Ala	Gly	Lys	Lys	Ser	Val	Tyr	Arg	Ala	Lys	
		115				120						125				
Val	Trp	Val	Lys	Arg	Gly	Lys	Ile									
		130				135										

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

ccccacacac	tgcacgcnc	cgccgggtcc	tcctagggtt	tcgccgcgat	gtcgcgccgg	60
cgcgagcgagc	gggagcagat	gcggaagggc	aactacaagc	agacggtgga	cgcgaggagg	120
agccgcccgc	gccgcgaggg	ccagatgatg	gacatgcgca	aggccaagcg	cgaggaaagt	180
ctccagaaga	agcgtgcca	tgggtttccc	gcctccgccg	ccggtgtgcc	gccgatgggc	240
cactccaccg	cgctccagca	gaagtcccc	aatcgaagag	gtgatcagca	caggagtgtg	300
gtcgcgattc	attgagtttc	ttacacgtga	ggaccatccc	caactccagt	ttgaggctgc	360
atgggcactc	accaacattg	catcaggcac	atcagagaac	actaagggtg	tcgttgagag	420
tgggtgctgtg	cgcctgtgcc	catctttgtc	aagctactca	actccctcaa	gcgaggatgt	480
tc						

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1503721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Pro His Thr Ala Arg Xaa Arg Arg Val Leu Leu Gly Phe Arg Arg Asp
1 5 10 15
Val Ala Pro Ala Glu Arg Ala Gly Ala Asp Ala Glu Gly Gln Leu Gln
20 25 30
Ala Asp Gly Gly Arg Gly Gly Glu Pro Pro Pro Arg Gly Pro Asp
35 40 45
Asp Gly His Ala Gln Gly Gln Ala Arg Gly Lys Ser Pro Glu Glu Ala
50 55 60
Leu Arg Trp Val Ser Arg Leu Arg Arg Arg Cys Ala Ala Asp Gly Pro
65 70 75 80
Leu His Arg Ala Pro Ala Glu Val Pro Gln Ser Lys Arg
85 90

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1503722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

Met Ser Leu Arg Pro Ser Glu Arg Glu Gln Met Arg Lys Gly Asn Tyr
1 5 10 15
Lys Gln Thr Val Asp Ala Glu Glu Ser Arg Arg Arg Glu Gly Gln
20 25 30
Met Met Asp Met Arg Lys Ala Lys Arg Glu Glu Ser Leu Gln Lys Lys
35 40 45
Arg Cys Asp Gly Phe Pro Ala Ser Ala Ala Gly Val Pro Pro Met Gly
50 55 60
His Ser Thr Ala Leu Gln Gln Lys Ser Pro Asn Arg Arg Gly Asp Gln
65 70 75 80
His Arg Ser Gly Val Ala Ile His
85

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1503723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

Met Gly Phe Pro Pro Pro Pro Val Cys Arg Arg Trp Ala Thr Pro
1 5 10 15
Pro Arg Ser Ser Arg Ser Pro Pro Ile Glu Glu Val Ile Ser Thr Gly
20 25 30
Val Val Ser Arg Phe Ile Glu Phe Leu Thr Arg Glu Asp His Pro Gln
35 40 45
Leu Gln Phe Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser Gly Thr
50 55 60
Ser Glu Asn Thr Lys Val Val Val Glu Ser Gly Ala Val Arg Leu Cys
65 70 75 80
Pro Ser Leu Ser Ser Tyr Ser Thr Pro Ser Ser Glu Asp Val

85

90

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

agataacagc	aaaggctctg	caacacggct	tgagttcaaa	caaaggctct	caatagctat	60
tggggcagct	aaagggttga	atcatctgca	cagtcttgat	cctcctttga	tacacaagga	120
cttcaagaca	aacaatgtgc	tggttgatga	aaatttcatt	gcaaagggtg	ctgatgctgg	180
acttgtagg	ttaattagag	gatctgacga	tgccggccca	tcgctgggt	tcagtaacag	240
tgtttaccaa	gatccagagg	tacagtcgat	gactcagttc	tctgaaagca	gtgatgttta	300
cagcttgag	tttttctttt	ggagctaatt	actggcaggg	aagcagcttc	cttgatacct	360
acagagtcca	gagaatattt	ggcacactgg	atggaagcgc	atttcagttc	aatgaactg	420
attgacccaa	gattagccgg	caacttcact	gcagaaggtg	tgaaggagct	t	

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

Asp	Asn	Arg	Lys	Gly	Ser	Ala	Thr	Arg	Leu	Glu	Phe	Lys	Gln	Arg	Leu
1				5					10					15	
Ser	Ile	Ala	Ile	Gly	Ala	Ala	Lys	Gly	Leu	Asn	His	Leu	His	Ser	Leu
			20					25					30		
Asp	Pro	Pro	Leu	Ile	His	Lys	Asp	Phe	Lys	Thr	Asn	Asn	Val	Leu	Val
			35				40					45			
Asp	Glu	Asn	Phe	Ile	Ala	Lys	Val	Ala	Asp	Ala	Gly	Leu	Val	Arg	Leu
			50			55					60				
Ile	Arg	Gly	Ser	Asp	Asp	Ala	Gly	Pro	Ser	Arg	Gly	Phe	Ser	Asn	Ser
65					70					75				80	
Val	Tyr	Gln	Asp	Pro	Glu	Val	Gln	Ser	Met	Thr	Gln	Phe	Ser	Glu	Ser
				85					90					95	
Ser	Asp	Val	Tyr	Ser	Leu	Glu	Phe	Phe	Trp	Ser					
			100					105							

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..469
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

atcctttggc	aaccgaactg	gtttggtgtg	cccacctctc	tctcttccat	gggatatggc	60
aggggacggaa	tccagatgag	gatgaactcg	tggcaggacg	gcgtcacggg	caccaactgc	120

```
cccatccctc ccgatggaa ctggacctac gagttccagc tcaaggacca gatcggcagc 180
ttcttctact tccgctcgt cggcctccag cgagctgccg gcgggttcgg ccccatcacc 240
gtcaacaacc gcgccaccgt gccnntccc ttcgaccagc ctcattggcga catcacctg 300
ttcatcgggg actggtacac caagggccac gttgtaagag ctttgttttt ctgtttctgt 360
caatgcaaatt ctagctagat ggttcgctcct tttgtttcag atcgagatat atagccaggg 420
aaaaatatcg cgcttttccc ttgatctcag tgaactggat ttcactgag
```

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1503735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

```
Ile Leu Trp Gln Pro Asn Trp Phe Gly Val Pro Thr Ser Leu Ser Ser
1      5      10      15
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln
20     25     30
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp
35     40     45
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe
50     55     60
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr
65     70     75     80
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly
85     90     95
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val
100    105    110
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser
115    120    125
```

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

```
Pro Leu Ala Thr Glu Leu Val Trp Cys Ala His Leu Ser Leu Phe His
1      5      10      15
Gly Ile Trp Gln Gly Arg Asn Pro Asp Glu Asp Glu Leu Val Ala Gly
20     25     30
Arg Arg His Gly His Gln Leu Pro His Pro Ser Arg Met Glu Leu Asp
35     40     45
Leu Arg Val Pro Ala Gln Gly Pro Asp Arg Gln Leu Leu Leu Pro
50     55     60
Val Ala Arg Pro Pro Ala Ser Cys Arg Arg Val Arg Pro His His Arg
65     70     75     80
Gln Gln Pro Arg His Arg Ala Xaa Pro Leu Arg Pro Ala Ser Trp Arg
85     90     95
His His Pro Val His Arg Gly Leu Val His Gln Gly Pro Arg Cys Lys
100    105    110
Ser Phe Val Phe Leu Phe Leu Ser Met Gln Ile
```

115 120
(2) INFORMATION FOR SEQ ID NO:2533:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1503737
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln
1 5 10 15
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp
20 25 30
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe
35 40 45
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr
50 55 60
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly
65 70 75 80
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val
85 90 95
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser
100 105

(2) INFORMATION FOR SEQ ID NO:2534:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1503743
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:
aattcttttca ctcactctcc agatccggtg cttgtgggag cctaacacgc cccccgcctc 60
cctctccgcc gtcgccgagt cctcgccgg cttaccccggt cgctggcgaa ggcactccgg 120
cgtggacgc

(2) INFORMATION FOR SEQ ID NO:2535:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..42
(D) OTHER INFORMATION: / Ceres Seq. ID 1503744
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:
Ile Leu Ser Leu Thr Leu Gln Ile Arg Cys Leu Trp Glu Pro Asn Thr
1 5 10 15
Pro Pro Ala Ser Leu Ser Ala Val Ala Glu Ser Leu Ala Gly Leu Pro
20 25 30
Arg Arg Trp Arg Arg His Ser Gly Val Asp
35 40

(2) INFORMATION FOR SEQ ID NO:2536:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503745
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:
Phe Phe His Ser Leu Ser Arg Ser Gly Ala Cys Gly Ser Leu Thr Arg
1 5 10 15
Pro Pro Pro Pro Ser Pro Pro Ser Pro Ser Pro Ser Pro Ala Tyr Pro
 20 25 30
Val Ala Gly Glu Gly Thr Pro Ala Trp Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:2537:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..409
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503746
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:
ctagccgccg ccagaccatt cgtttctcgc gagccatcct tctgtaattc tcaggcatcc 60
ggaagaaatg gccaagtcca agaaccacac ggcgcacaa cagtcgttca aggcgcacaa 120
gaacggcatt aagaaaccca agcgccaccg ccagacctcc accaagggga tggaccccaa 180
gttcctgagg aacctgaggt attctaggaa gggcaacaaa aagagtgggt aggcgtgaagc 240
tgaggagtag gaaggaaagc atggctttgt ggtaatgtgc tgctgtgggg gttcattagt 300
atgaagagga agacgtgct ggcgcgaggat ctttttctct ttattagtat tttgttttaa 360
actatgtatg accgaatggg ggtatttatt tgtgtcatcc ttgactctc

(2) INFORMATION FOR SEQ ID NO:2538:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503747
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:
Leu Ala Ala Ala Arg Pro Phe Val Ser Arg Glu Pro Ser Phe Cys Asn
1 5 10 15
Ser Gln Ala Ser Gly Arg Asn Gly Gln Val Glu Glu Pro His Gly Ala
 20 25 30
Gln Pro Val Val Gln Gly Ala Gln Glu Arg His
 35 40

(2) INFORMATION FOR SEQ ID NO:2539:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1503748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

```
Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala
1          5          10          15
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr
          20          25          30
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys
          35          40          45
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu
50          55          60
```

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1503749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

```
Met Lys Arg Lys Thr Leu Leu Ala Arg Ser Leu Phe Leu Phe Ile Ser
1          5          10          15
Ile Leu Phe Lys Thr Met Tyr Asp Arg Met Val Val Phe Ile Cys Val
          20          25          30
Ile Leu Asp Ser
          35
```

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1503769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

```
aaaatgatcg agtgggctcc catgtgattt tgtcatccta gtgacagaaa ttttctccct      60
ttttttttct caagtcaca acactcctct gctgtgattc cagatggagc gcactttcat      120
tgccatcaag cccgacggcg tccaaagagg cctgatttct gagattgtga accgattcga      180
gagaaaaggc tacaagcttg ttgccatcaa gctgattgtc ccatccaaag gattcgtga      240
gaagcactac catgatctca aggaaaggcc tttcttcaac gggttgtgtg acttcctcag      300
ctctggccct gtacttgcaa tggtttggga aggagagggt gtcatcaagt atgggagaaa      360
actaattggt gccacagacc cacagaaatc tgaaccagga accatcaggg gcgatcttgg      420
cgttgttggt ggaagaaaca tcattcatgg
```

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1503770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

```
Met Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly
1           5           10           15
Leu Ile Ser Glu Ile Val Asn Arg Phe Glu Arg Lys Gly Tyr Lys Leu
          20          25          30
Val Ala Ile Lys Leu Ile Val Pro Ser Lys Gly Phe Ala Glu Lys His
          35          40          45
Tyr His Asp Leu Lys Glu Arg Pro Phe Phe Asn Gly Leu Cys Asp Phe
          50          55          60
Leu Ser Ser Gly Pro Val Leu Ala Met Val Trp Glu Gly Glu Gly Val
65          70          75          80
Ile Lys Tyr Gly Arg Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser
          85          90          95
Glu Pro Gly Thr Ile Arg Gly Asp Leu Gly Val Val Val Gly Arg Asn
          100         105         110
Ile Ile His
          115
```

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1503775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

```
tgattatttg cacaaaaagc aatctggcgg tcaagggtcag tatggacgag tttgtgggta      60
cattgagcct ctaccttcag gttctgatgg taaattcgaa ttgataaca tgattattgg      120
acaagcaatt ccttcaaact ttataccagc aatagagaag ggttttaagg aagcttgcaa      180
ttcaggctcg ttgattggtc atoctgttga aaatttaaga attgtattga ctgatggggc      240
ttcacatcag gtggattcca gtgaacttgc ttttaagcta gctgctatct atgcttttcg      300
acagtgtac acttctgcca aacctgtaat attagaacct gtgatgaagg tggaactcaa      360
atttccaact gagtttcagg gcacagtaac tgggtgatatg aacaagagaa aagggatcat      420
tgttggaaat gagcaggaag gtgacgacac cattgtagtt tgccatgtcc gctaaacaat      480
atgtttggat atgcacagc
```

(2) INFORMATION FOR SEQ ID NO:2544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

```
Asp Tyr Leu His Lys Lys Gln Ser Gly Gly Gln Gly Gln Tyr Gly Arg
1           5           10           15
Val Cys Gly Tyr Ile Glu Pro Leu Pro Ser Gly Ser Asp Gly Lys Phe
          20          25          30
Glu Phe Asp Asn Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile
          35          40          45
Pro Ala Ile Glu Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu
          50          55          60
Ile Gly His Pro Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala
65          70          75          80
```

Ser His Gln Val Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile
85 90 95
Tyr Ala Phe Arg Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu
100 105 110
Pro Val Met Lys Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr
115 120 125
Val Thr Gly Asp Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu
130 135 140
Gln Glu Gly Asp Asp Thr Ile Val Val Cys His Val Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile Pro Ala Ile Glu
1 5 10 15
Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu Ile Gly His Pro
20 25 30
Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala Ser His Gln Val
35 40 45
Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile Tyr Ala Phe Arg
50 55 60
Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu Pro Val Met Lys
65 70 75 80
Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr Val Thr Gly Asp
85 90 95
Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu Gln Glu Gly Asp
100 105 110
Asp Thr Ile Val Val Cys His Val Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

ttgattacat tattcatgga gatgatacct gtcttctacc tgatggcact gatgcatatg 60
cgctacgaag aaggtcgggc gttacaagca aatcaagcga acagaagggtg tctcgagcac 120
tgacatagtt gggaggatat tgctaacatt caggcagaaa gatgctggca ctgatttaag 180
tgttgctcgt gctgagaagt ctggagagaa atcaaagtat gaagtgaaaa gtcagctatc 240
tcatttcctt ccaacttctc gccgatcat gcagttttca aatgggcagg ctccttcgcc 300
aggtgctcgt gttgtctatg tagatggcac atttgatctt ttccacgctg gccatgttga 360
gttctcagc agtgccagac aacttggtga ctttcttctt gtcggtatct atgacgacga 420
gtctatcagg gatagaagag gctgccgtcc tataatgcat ctccatgagc g

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..41
(D) OTHER INFORMATION: / Ceres Seq. ID 1503779
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:
Asp Tyr Ile Ile His Gly Asp Asp Pro Cys Leu Leu Pro Asp Gly Thr
1 5 10 15
Asp Ala Tyr Ala Leu Arg Arg Arg Ser Gly Val Thr Ser Lys Ser Ser
20 25 30
Glu Gln Lys Val Ser Arg Ala Leu Thr
35 40

(2) INFORMATION FOR SEQ ID NO:2548:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..67
(D) OTHER INFORMATION: / Ceres Seq. ID 1503780
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:
Met Gln Phe Ser Asn Gly Gln Ala Pro Ser Pro Gly Ala Arg Val Val
1 5 10 15
Tyr Val Asp Gly Thr Phe Asp Leu Phe His Ala Gly His Val Glu Phe
20 25 30
Leu Arg Ser Ala Arg Gln Leu Gly Asp Phe Leu Leu Val Gly Ile Tyr
35 40 45
Asp Asp Glu Ser Ile Arg Asp Arg Arg Gly Cys Arg Pro Ile Met His
50 55 60
Leu His Glu
65

(2) INFORMATION FOR SEQ ID NO:2549:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: / Ceres Seq. ID 1503781
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:
Met Ala His Leu Ile Phe Ser Thr Leu Ala Met Leu Ser Ser Ser Gly
1 5 10 15
Val Pro Asp Asn Leu Val Thr Phe Phe Leu Ser Val Ser Met Thr Thr
20 25 30
Ser Leu Ser Gly Ile Glu Glu Ala Ala Val Leu
35 40

(2) INFORMATION FOR SEQ ID NO:2550:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1503796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

```
cacattaatt aaacattttt tgtgttttctt tttatacctt aatttttttc tttccctttt      60
tctctataag tatctgactc tactttctgct gttgcagaat cattcgagat atcattcaga      120
atcattttact gcaggttttc tgtttggttg caatggaaaa gcctgtctcc cttaagcctg      180
agcacatcag agatkagaaa gtcaagggttc tgcaatctgt gaaccctatt aagcctgaag      240
aggtagtcct tgggcaatac gatggtctac aaggatgacc ctacagtgcc agatgacttg      300
aataactccaa cttttgcatac tgttgttctt cgggtacaca atgaaagatg ggaaggtgtt      360
cctttcattc ttaaagctgg taaagcattg agttc
```

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

```
Thr Leu Ile Lys His Phe Leu Cys Phe Phe Leu Tyr Leu Asn Phe Phe
1           5           10           15
Leu Ser Leu Phe Leu Tyr Lys Tyr Leu Thr Leu Leu Leu Leu Gln
20           25           30
Asn His Ser Arg Tyr His Ser Glu Ser Phe Thr Ala Gly Phe Leu Phe
35           40           45
Gly Cys Asn Gly Lys Ala Cys Leu Pro
50           55
```

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1503798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

```
Met Glu Lys Pro Val Ser Leu Lys Pro Glu His Ile Arg Asp Xaa Lys
1           5           10           15
Val Lys Val Leu Gln Ser Val Asn Pro Ile Lys Pro Glu Glu Val Val
20           25           30
Leu Gly Gln Tyr Asp Gly Leu Gln Gly
35           40
```

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1503799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

```
Met Val Tyr Lys Asp Asp Pro Thr Val Pro Asp Asp Leu Asn Thr Pro
1           5           10           15
Thr Phe Ala Ser Val Val Leu Arg Val His Asn Glu Arg Trp Glu Gly
20           25           30
Val Pro Phe Ile Leu Lys Ala Gly Lys Ala Leu Ser
35           40
```

(2) INFORMATION FOR SEQ ID NO:2554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1503810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

```
gaagtttctcg cggcggtcgta ggtagcggcg gtgtgcttgt gatctcaatc tcaaccccag      60
gcgagctcgg ctccggtcac ccgtcgatcc acgcaaccat gtcgaggagg aagaccaggg      120
agcccaagga ggagaacgtt acccttggac ccactgtccg tgaaggagag tttgtctttg      180
gtgttgctca catctttgca tccttcaatg acaccttcat tgtgagtgt atagtgtttt      240
ccctgtggat gggccttttc attatctttc ccattgtaac tgtgatggtg taatatgcag      300
catgtcactg atttgtcttg gagggaaact ttggttcgga tcactggtgg catgaagggt      360
aaggctgac gtgatgagtc gtctccttat gctgctatgc ttgctgcca agatgttgca      420
cagcgttgca aggagctcgg tatcacagcg ctgcacatta agcttcgtgc cactggaggc      480
aacaagacca atgacctctg gacct
```

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1503811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

```
Ser Phe Gly Gly Gly Val Gly Ser Gly Gly Val Leu Val Ile Ser Ile
1           5           10           15
Ser Thr Pro Gly Glu Leu Gly Ser Gly His Pro Ser Ile His Ala Thr
20           25           30
Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu
35           40           45
Gly Pro Thr Val Arg Glu Gly Glu Phe Val Phe Gly Val Ala His Ile
50           55           60
Phe Ala Ser Phe Asn Asp Thr Phe Ile Val Ser Ala Ile Cys Phe Ser
65           70           75           80
Leu Trp Met Gly Leu Phe Ile Ile Phe Pro Ile Val Thr Val Met Val
85           90           95
```

(2) INFORMATION FOR SEQ ID NO:2556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..64
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503812
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

```
Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu
1      5      10      15
Gly Pro Thr Val Arg Glu Gly Glu Phe Val Phe Gly Val Ala His Ile
      20      25      30
Phe Ala Ser Phe Asn Asp Thr Phe Ile Val Ser Ala Ile Cys Phe Ser
      35      40      45
Leu Trp Met Gly Leu Phe Ile Ile Phe Pro Ile Val Thr Val Met Val
50      55      60
```

(2) INFORMATION FOR SEQ ID NO:2557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..70
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

```
Met Gln His Val Thr Asp Leu Ser Gly Arg Glu Thr Leu Val Arg Ile
1      5      10      15
Thr Gly Gly Met Lys Val Lys Ala Asp Arg Asp Glu Ser Ser Pro Tyr
      20      25      30
Ala Ala Met Leu Ala Ala Gln Asp Val Ala Gln Arg Cys Lys Glu Leu
      35      40      45
Gly Ile Thr Ala Leu His Ile Lys Leu Arg Ala Thr Gly Gly Asn Lys
50      55      60
Thr Asn Asp Pro Trp Thr
65      70
```

(2) INFORMATION FOR SEQ ID NO:2558:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..456
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

```
gcnkccgccc cctacaacag gtgccccagg tcttcgctgc gccattcgcc agcgacgagc      60
acccaacagc atggtcaacc gcaatgacct catgtactgg attgtcgcgg cactctgatg      120
tggttgccck ckckgkgcac cagaagtga tggggcttt gaacaacaac gaggkactca      180
tgtttggggg ggttggtggc ckgttcaacg aggtcgtgac aaatttggtta ctacaggggtg      240
ccctggaaac ttctgagcga tactctgtta aagcagaaaa tataacagtt gttagtgttc      300
ctggaagctt tgaagttcct ataacgkcac aaaagcttgg gaaatctgga aaatttgatg      360
caattctgtg cattggagct gtgattagag gtgacacaac ccactatgat gccgttgcaa      420
actcagctgc atcaggtgta ctcaatgctg gattat
```

(2) INFORMATION FOR SEQ ID NO:2559:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..151
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503823
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:

Xaa	Arg	Arg	Leu	Gln	Val	Pro	Gln	Val	Phe	Ala	Ala	Pro	Phe	Ala
1			5				10						15	
Ser	Asp	Glu	His	Pro	Thr	Ala	Trp	Ser	Thr	Ala	Met	Thr	Ser	Cys
			20				25					30	Thr	
Gly	Leu	Ser	Arg	His	Ser	Asp	Val	Val	Ala	Xaa	Xaa	Xaa	His	Gln
			35				40					45	Lys	
Leu	Met	Gly	Ser	Leu	Asn	Asn	Asn	Glu	Xaa	Leu	Met	Phe	Gly	Val
			50			55					60		Val	
Val	Ala	Xaa	Phe	Asn	Glu	Val	Val	Thr	Asn	Leu	Leu	Gln	Gly	Ala
65					70					75				80
Leu	Glu	Thr	Phe	Glu	Arg	Tyr	Ser	Val	Lys	Ala	Glu	Asn	Ile	Thr
			85						90				95	Val
Val	Ser	Val	Pro	Gly	Ser	Phe	Glu	Val	Pro	Ile	Thr	Xaa	Gln	Lys
			100					105					110	Leu
Gly	Lys	Ser	Gly	Lys	Phe	Asp	Ala	Ile	Leu	Cys	Ile	Gly	Ala	Val
			115				120					125	Ile	
Arg	Gly	Asp	Thr	Thr	His	Tyr	Asp	Ala	Val	Ala	Asn	Ser	Ala	Ala
			130				135					140	Ser	
Gly	Val	Leu	Asn	Ala	Gly	Leu								
145					150									

(2) INFORMATION FOR SEQ ID NO:2560:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:

Met	Thr	Ser	Cys	Thr	Gly	Leu	Ser	Arg	His	Ser	Asp	Val	Val	Ala	Xaa
1				5				10						15	
Xaa	Xaa	His	Gln	Lys	Leu	Met	Gly	Ser	Leu	Asn	Asn	Asn	Glu	Xaa	Leu
			20					25					30		
Met	Phe	Gly	Val	Val	Val	Ala	Xaa	Phe	Asn	Glu	Val	Val	Thr	Asn	Leu
			35				40					45			
Leu	Leu	Gln	Gly	Ala	Leu	Glu	Thr	Phe	Glu	Arg	Tyr	Ser	Val	Lys	Ala
			50				55				60				
Glu	Asn	Ile	Thr	Val	Val	Ser	Val	Pro	Gly	Ser	Phe	Glu	Val	Pro	Ile
65					70					75				80	
Thr	Xaa	Gln	Lys	Leu	Gly	Lys	Ser	Gly	Lys	Phe	Asp	Ala	Ile	Leu	Cys
			85					90					95		
Ile	Gly	Ala	Val	Ile	Arg	Gly	Asp	Thr	Thr	His	Tyr	Asp	Ala	Val	Ala
			100					105					110		
Asn	Ser	Ala	Ala	Ser	Gly	Val	Leu	Asn	Ala	Gly	Leu				
			115				120								

(2) INFORMATION FOR SEQ ID NO:2561:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1503825
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:
Met Gly Ser Leu Asn Asn Glu Xaa Leu Met Phe Gly Val Val Val
1 5 10 15
Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Leu Gln Gly Ala Leu
20 25 30
Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val Val
35 40 45
Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu Gly
50 55 60
Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile Arg
65 70 75 80
Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser Gly
85 90 95
Val Leu Asn Ala Gly Leu
100

(2) INFORMATION FOR SEQ ID NO:2562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..392
(D) OTHER INFORMATION: / Ceres Seq. ID 1503826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

gaagtgcgag tcaatgctat catgatcacc agcacagtta ttgttggttct attcagcaca 60
atgggttttcg gcctkctgac gaagccgctg ctcagtctcc tcatcccacc aaggactgga 120
ctgaacacgt cgtctctgct ctcaagccag tctatgctgg acccactcct tactagcatg 180
atgggggtctg actttgatgt agggcagatc aactccctc aatacaacct ccagttcatt 240
ctcaccgcgc casstcgctc cgtccatcgc ctttgkycaa gtttgacgat cggtttcatg 300
cgccccgtgt tcggggggcg aggtttcgtc ccctttgtgc ctggttcgcc kktkkagagk 360
agtgtccctg aatctcacct gggcactgtg ac

(2) INFORMATION FOR SEQ ID NO:2563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1503827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

Glu Val Arg Val Asn Ala Ile Met Ile Thr Ser Thr Val Ile Val Val
1 5 10 15
Leu Phe Ser Thr Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser
20 25 30
Leu Leu Ile Pro Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser
35 40 45
Ser Gln Ser Met Leu Asp Pro Leu Leu Thr Ser Met Met Gly Ser Asp
50 55 60

Phe Asp Val Gly Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile
65 70 75 80
Leu Thr Ala Pro Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr
85 90 95
Ile Gly Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe
100 105 110
Val Pro Gly Ser Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly
115 120 125
Thr Val
130

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..123

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met Val Phe
1 5 10 15
Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro Pro Arg Thr
20 25 30
Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met Leu Asp Pro
35 40 45
Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly Gln Ile Asn
50 55 60
Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro Xaa Arg Ser
65 70 75 80
Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met Arg Pro Val
85 90 95
Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Xaa Xaa Xaa
100 105 110
Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val
115 120

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..110

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro
1 5 10 15
Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met
20 25 30
Leu Asp Pro Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly
35 40 45
Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro
50 55 60
Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met
65 70 75 80
Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser

85 90 95
Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

```
gtagtgggaa ggggtacgtt agcktttgck ggcggtmrac tccccacgca aagccgccgc      60
cgttccctct cgtcttcccc agttccccta cgccggtaat cccacgtcct atcagccgnc      120
gatccagcct tgcttccatc catccatcca tccatccatc catctcgtcg cttctctctg      180
ttccgcgtgc gatcgagtag atcaaaagga ggaggaggat ggcgaggagt tcgttcaagt      240
tggagcacc cttcgaaagg aggcaagctg aggctaaccg catcaggag aaataccctg      300
acagaatccc tgtcattgtt gagaaggccg agaggagtga catcccagac attgacaaga      360
aaaagtacct tgttctctgcc gacctcacag tcggacagtt tgtgtatgtg gtacggaagc      420
ggatcaagct aagcgctgag aaggcaatct tcattctcgt aaag
```

(2) INFORMATION FOR SEQ ID NO:2567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

```
Ser Gly Lys Gly Tyr Val Ser Xaa Cys Xaa Ala Xaa Thr Pro His Ala
1      5      10      15
Lys Pro Pro Pro Phe Pro Leu Val Phe Pro Ser Ser Pro Thr Pro Val
20     25     30
Ile Pro Arg Pro Ile Ser Xaa Arg Ser Ser Leu Ala Ser Ile His Pro
35     40     45
Ser Ile His Pro Ser Ile Ser Ser Leu Leu Ser Val Pro Arg Ala Ile
50     55     60
Glu
65
```

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

```
Met Ala Arg Ser Ser Phe Lys Leu Glu His Pro Phe Glu Arg Arg Gln
1      5      10      15
Ala Glu Ala Asn Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro Val
20     25     30
```

Ile Val Glu Lys Ala Glu Arg Ser Asp Ile Pro Asp Ile Asp Lys Lys
35 40 45
Lys Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val
50 55 60
Val Arg Lys Arg Ile Lys Leu Ser Ala Glu Lys Ala Ile Phe Ile Phe
65 70 75 80
Val Lys

(2) INFORMATION FOR SEQ ID NO:2569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

cccagtcattg atgcacccga tccatgagat cgtcgagaca aggttcagat ccaacagatg	60
ctttcggaag ctcagccaca acgatggcgg cgcggagtgg ataggcttgc acgcwagyg	120
tgctctcgtg gtggcggtcc tcaactgtgtt ggcgtccttc atccccctct ttgggtcctt	180
catctcgttc gtcgggagca ccatgtggcg cttctctcct ttgtgctgcc ggctctcttc	240
catctcagca ttgtaggctc gtcaataccc ttgtggaggc gggttgctgg actacggcat	300
ccttctcttt ggtctggctt tcgctggata tggctctgtc actgctctct cctcgcattg	360
aacaatggcc caaacagtca aaaaagtga gagatcagga tatcttgtga tgacakgagt	420
caaattggatg ctaggagcac catatatcag atagcacggc tcggattagt gcgtgattg	

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

Pro Val Met Met His Pro Ile His Glu Ile Val Glu Thr Arg Phe Arg	
1 5 10 15	
Ser Asn Arg Cys Phe Arg Lys Leu Ser His Asn Asp Gly Gly Ala Glu	
20 25 30	
Trp Ile Gly Leu His Xaa Xaa Ala Val Leu Val Val Ala Val Leu Thr	
35 40 45	
Val Val Ala Ser Phe Ile Pro Phe Phe Gly Ser Phe Ile Ser Phe Val	
50 55 60	
Gly Ser Thr Met Trp Arg Phe Ser Pro Leu Cys Cys Arg Leu Ser Ser	
65 70 75 80	
Ile Ser Ala Leu	

(2) INFORMATION FOR SEQ ID NO:2571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1503875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

Met Met His Pro Ile His Glu Ile Val Glu Thr Arg Phe Arg Ser Asn
1 5 10 15
Arg Cys Phe Arg Lys Leu Ser His Asn Asp Gly Gly Ala Glu Trp Ile
20 25 30
Gly Leu His Xaa Xaa Ala Val Leu Val Val Ala Val Leu Thr Val Val
35 40 45
Ala Ser Phe Ile Pro Phe Phe Gly Ser Phe Ile Ser Phe Val Gly Ser
50 55 60
Thr Met Trp Arg Phe Ser Pro Leu Cys Cys Arg Leu Ser Ser Ile Ser
65 70 75 80
Ala Leu

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1503876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Met Leu Ser Glu Ala Gln Pro Gln Arg Trp Arg Arg Gly Val Asp Arg
1 5 10 15
Leu Ala Arg Xaa Xaa Cys Pro Arg Gly Gly Pro His Cys Gly Gly
20 25 30
Val Leu His Pro Leu Leu Trp Val Leu His Leu Val Arg Arg Glu His
35 40 45
His Val Ala Leu Leu Ser Phe Val Leu Pro Ala Leu Phe His Leu Ser
50 55 60
Ile Val Gly Ser Ser Ile Pro Leu Trp Arg Arg Val Ala Gly Leu Arg
65 70 75 80
His Pro Ser Leu Trp Ser Gly Phe Arg Trp Ile Trp Ser Cys His Cys
85 90 95
Ser Leu Leu Ala Leu Asn Asn Gly Pro Asn Ser Gln Lys Ser Ala Glu
100 105 110
Ile Arg Ile Ser Cys Asp Asp Xaa Ser Gln Met Asp Ala Arg Ser Thr
115 120 125
Ile Tyr Gln Ile Ala Arg Leu Gly Leu Val Arg Asp
130 135 140

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1503886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

aaaccttccc accacctcct cccctcctc ccaacagtca ccacgtcgca ctaccgagcc 60
atgtcctccg ctaccaacct cggttattg tcgtgggact gcgccgagga cccgctggat 120
ttcgggtgctg tcgccgacac cgcgtttctc ccgtccagc

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503887
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:
Lys Pro Ser His His Leu Leu Pro Leu Leu Pro Thr Val Thr Thr Ser
1 5 10 15
His Tyr Arg Ala Met Ser Ser Ala Thr Asn Leu Arg Leu Leu Ser Trp
 20 25 30
Asp Cys Ala Glu Asp Pro Leu Asp Phe Gly Ala Phe Ala Asp Thr Ala
 35 40 45
Phe Leu Pro Leu Gln
50

(2) INFORMATION FOR SEQ ID NO:2575:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503888
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:
Asn Leu Pro Thr Thr Ser Ser Pro Ser Ser Gln Gln Ser Pro Arg Arg
1 5 10 15
Thr Thr Glu Pro Cys Pro Pro Leu Pro Thr Ser Val Tyr Cys Arg Gly
 20 25 30
Thr Ala Pro Arg Thr Arg Trp Ile Ser Val Arg Ser Pro Thr Pro Arg
 35 40 45
Phe Ser Arg Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2576:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..52
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503889
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:
Thr Phe Pro Pro Pro Pro Pro Pro Pro Pro Asn Ser His His Val Ala
1 5 10 15
Leu Pro Ser His Val Leu Arg Tyr Gln Pro Pro Phe Ile Val Val Gly
 20 25 30
Leu Arg Arg Gly Pro Ala Gly Phe Arg Cys Val Arg Arg His Arg Val
 35 40 45
Ser Pro Ala Pro
50

(2) INFORMATION FOR SEQ ID NO:2577:
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..338
(D) OTHER INFORMATION: / Ceres Seq. ID 1503890
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:
agctcgctct gggagagggt aatggcggca agtctccagc tcgccatttt catgtccgcc 60
gccatcgcgc tcgggttcgg cggcgtccag gccggcgcg cgcasstgtg cagcgagtac 120
tacgaccgga cgtgccccgt cgtgcaccgg gtcgtgcggc ggggtgtgaa gaaggcgcac 180
gagtcggacg tccgcatcta cgccagctc acccgctcc acttccacga ctgcttcgtg 240
caaggctgcg acggctccat cctgctggac aacagctcca gcatcgtgtc ggagaagttc 300
gccacgcccc acaacaactc ggcgcgcggg taccctcg

(2) INFORMATION FOR SEQ ID NO:2578:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1503891
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:
Ser Ser Leu Trp Glu Arg Leu Met Ala Ala Ser Leu Gln Leu Ala Ile
1 5 10 15
Phe Met Ser Ala Ala Ile Ala Leu Gly Phe Gly Gly Val Gln Ala Gly
20 25 30
Ala Ala Xaa Xaa Cys Ser Glu Tyr Tyr Asp Arg Thr Cys Pro Val Val
35 40 45
His Arg Val Val Arg Arg Val Leu Lys Lys Ala His Glu Ser Asp Val
50 55 60
Arg Ile Tyr Ala Ser Leu Thr Arg Leu His Phe His Asp Cys Phe Val
65 70 75 80
Gln Gly Cys Asp Gly Ser Ile Leu Leu Asp Asn Ser Ser Ser Ile Val
85 90 95
Ser Glu Lys Phe Ala Thr Pro Asn Asn Asn Ser Ala Arg Gly Tyr Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1503892
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:
Leu Ala Leu Gly Glu Val Asn Gly Gly Lys Ser Pro Ala Arg His Phe
1 5 10 15
His Val Arg Arg His Arg Ala Arg Val Arg Arg Arg Pro Gly Arg Arg
20 25 30
Gly Ala Xaa Val Gln Arg Val Leu Arg Pro Asp Val Pro Arg Arg Ala

35	40	45
Pro Gly Arg Ala Ala Gly	Ala Glu Glu Gly Ala Arg	Val Arg Arg Pro
50	55	60
His Leu Arg Gln Pro His	Pro Pro Pro Leu Pro Arg	Leu Leu Arg Ala
65	70	75
Arg Leu Arg Arg Leu His	Pro Ala Gly Gln Gln Leu	Gln His Arg Val
85	90	95
Gly Glu Val Arg His Ala	Gln Gln Gln Leu Gly Ala	Arg Val Pro Arg
100	105	110

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

Met	Ala	Ala	Ser	Leu	Gln	Leu	Ala	Ile	Phe	Met	Ser	Ala	Ala	Ile	Ala
1				5					10					15	
Leu	Gly	Phe	Gly	Gly	Val	Gln	Ala	Gly	Ala	Ala	Xaa	Xaa	Cys	Ser	Glu
			20					25						30	
Tyr	Tyr	Asp	Arg	Thr	Cys	Pro	Val	Val	His	Arg	Val	Val	Arg	Arg	Val
			35				40					45			
Leu	Lys	Lys	Ala	His	Glu	Ser	Asp	Val	Arg	Ile	Tyr	Ala	Ser	Leu	Thr
			50				55					60			
Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	Gln	Gly	Cys	Asp	Gly	Ser	Ile
65					70					75					80
Leu	Leu	Asp	Asn	Ser	Ser	Ser	Ile	Val	Ser	Glu	Lys	Phe	Ala	Thr	Pro
			85						90						95
Asn	Asn	Asn	Ser	Ala	Arg	Gly	Tyr	Pro							
			100				105								

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

agggtttttt	gccaagtcgc	cgccgtcgt	ctgcccgc	at tcccttccac	aacaccgaga	60
cgccaggatg	acggcgagc	ctgcggagga	gctcgccacc	cagatcgagc	agcagaagct	120
cgaggagcag	aagaccgagg	cagaggaggt	tgtggtggag	gatgaggagg	acgacgacga	180
tgaggacgat	gaggatgatg	atgaacttga	cggacaagaa	ggggatgcca	gcggcaagtc	240
aaagcaaagc	aggagtgaga	agaagagccg	caaagccatg	ctgaagcttg	gcatgaagcc	300
catcactggt	gtcagccgtg	tactgtgaa	gaaaagcaag	aatatactgt	ttgtcatctc	360
gaagccagat	gtgttcaaga	gcccgaactc	agacacatac	gtcatattcg	gcgaggccaa	420
gatcgaggac	ctcagctccc	agctgcagac	ccaggccgca	gaacagttca	aggccccttg	480
acttgagcca	gatcacgagt	ccagagactt				

(2) INFORMATION FOR SEQ ID NO:2582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1503895
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

Gly Phe Phe Ala Lys Ser Pro Pro Ser Leu Cys Pro His Ser Leu Pro
1 5 10 15
Gln His Arg Asp Ala Arg Met Thr Ala Gln Thr Ala Glu Glu Leu Ala
20 25 30
Thr Gln Ile Glu Gln Gln Lys Leu Glu Glu Gln Lys Thr Glu Ala Glu
35 40 45
Glu Val Val Val Glu Asp Glu Glu Asp Asp Asp Asp Glu Asp Asp Glu
50 55 60
Asp Asp Asp Glu Leu Asp Gly Gln Glu Gly Asp Ala Ser Gly Lys Ser
65 70 75 80
Lys Gln Ser Arg Ser Glu Lys Lys Ser Arg Lys Ala Met Leu Lys Leu
85 90 95
Gly Met Lys Pro Ile Thr Gly Val Ser Arg Val Thr Val Lys Lys Ser
100 105 110
Lys Asn Ile Leu Phe Val Ile Ser Lys Pro Asp Val Phe Lys Ser Pro
115 120 125
Asn Ser Asp Thr Tyr Val Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu
130 135 140
Ser Ser Gln Leu Gln Thr Gln Ala Ala Glu Gln Phe Lys Ala Pro
145 150 155

(2) INFORMATION FOR SEQ ID NO:2583:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1503896
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

Met Thr Ala Gln Thr Ala Glu Glu Leu Ala Thr Gln Ile Glu Gln Gln
1 5 10 15
Lys Leu Glu Glu Gln Lys Thr Glu Ala Glu Glu Val Val Val Glu Asp
20 25 30
Glu Glu Asp Asp Asp Asp Glu Asp Asp Glu Asp Asp Asp Glu Leu Asp
35 40 45
Gly Gln Glu Gly Asp Ala Ser Gly Lys Ser Lys Gln Ser Arg Ser Glu
50 55 60
Lys Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr
65 70 75 80
Gly Val Ser Arg Val Thr Val Lys Lys Ser Lys Asn Ile Leu Phe Val
85 90 95
Ile Ser Lys Pro Asp Val Phe Lys Ser Pro Asn Ser Asp Thr Tyr Val
100 105 110
Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr
115 120 125
Gln Ala Ala Glu Gln Phe Lys Ala Pro
130 135

(2) INFORMATION FOR SEQ ID NO:2584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

acaactttac agctaacatg gagacagagc tagataatgt ctctgctggg tcaactgaat	60
ggaagggtct tctgaaagac tactgggaac gattcagcaa atattgtgca gatgtgagta	120
aactggatgg cagaaaggta gagagaatgc ttgaagaaaa atttggtcct atcctctttt	180
ccgatgttta caaggattgt agaatttgcc ctgattgttc tgaaggaacc ttgagattca	240
aagttagtag gtacggtgaa ggctattttg taggttgatga tcgacatcca aaatgcaagt	300
acattgctcg ctactgtca cagcaagaag atgaaactga acccatagaa gaaaatgcaa	360
aatcttttga acccagggtta cttggtgtca tgcctgattc tgatcaaaaag gtgtttttga	420
aacaaggggcc atatggctac tatgttcaag ttggagagg	

(2) INFORMATION FOR SEQ ID NO:2585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

Asn Phe Thr Ala Asn Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly	
1 5 10 15	
Ser Thr Glu Trp Lys Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser	
20 25 30	
Lys Tyr Cys Ala Asp Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg	
35 40 45	
Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys	
50 55 60	
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys	
65 70 75 80	
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro	
85 90 95	
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr	
100 105 110	
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly	
115 120 125	
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr	
130 135 140	
Gly Tyr Tyr Val Gln Val Gly Glu	
145 150	

(2) INFORMATION FOR SEQ ID NO:2586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly Ser Thr Glu Trp Lys
1 5 10 15
Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser Lys Tyr Cys Ala Asp
20 25 30
Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg Met Leu Glu Glu Lys
35 40 45
Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys Asp Cys Arg Ile Cys
50 55 60
Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys Val Ser Arg Tyr Gly
65 70 75 80
Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro Lys Cys Lys Tyr Ile
85 90 95
Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr Glu Pro Ile Glu Glu
100 105 110
Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly Val Met Pro Asp Ser
115 120 125
Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr Gly Tyr Tyr Val Gln
130 135 140
Val Gly Glu
145

(2) INFORMATION FOR SEQ ID NO:2587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys
1 5 10 15
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys
20 25 30
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro
35 40 45
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr
50 55 60
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly
65 70 75 80
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr
85 90 95
Gly Tyr Tyr Val Gln Val Gly Glu
100

(2) INFORMATION FOR SEQ ID NO:2588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

cggaagaatt ttgatatttg gcggtcagtg ggcaggtctt cactcagcgt cacagcttta 60
tctgttgat ccaactgaag aaaakccgac ctggagaata ttgaatatc ctggctgcgc 120

```
tccccgtttc gcctggggcc acagcacctg tgttggttga ggaacaaagg cgatagtgtc 180
tgggtggacaa actggagaag agtggatgct tacagaaata catgagcttt ctttggtcag 240
ccgctcagtt tgagttctgg aatggtttgt agtcatgttc cttgcaaatt agatgcggct 300
tcttatgcaa cctgaagttt gattgccgtc ttcagaagaa ctagaagaat gaatgctggg 360
catactgaat cttctggcag ctacctggcg gacttggaag atgaaatggc atcgactggt 420
ttgctcgctt tgtgtagaaa aggg
```

(2) INFORMATION FOR SEQ ID NO:2589:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1503925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

```
Gly Arg Ile Leu Phe Gly Gly Ser Val Ala Gly Leu His Ser Ala
1          5          10          15
Ser Gln Leu Tyr Leu Leu Asp Pro Thr Glu Glu Xaa Pro Thr Trp Arg
          20          25          30
Ile Leu Asn Ile Pro Gly Arg Pro Pro Arg Phe Ala Trp Gly His Ser
          35          40          45
Thr Cys Val Val Gly Gly Thr Lys Ala Ile Val Leu Gly Gly Gln Thr
          50          55          60
Gly Glu Glu Trp Met Leu Thr Glu Ile His Glu Leu Ser Leu Val Ser
65          70          75          80
Arg Ser Val
```

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

```
tctgtgcatc ttaaatatgg gggacagtag agctgtgctt gcttccatgc catatgtaga 60
aaatggtgct ttgaaggcta ctcaactgac agagaccac tcgcttgaaa atcctttgga 120
gtaccaaaaa cttttagctg aacatcccaa tgattcttca gttgtcaggg gtaacaaaat 180
aaaaggaaaag ctgaaggtta ctctgtgcttt tggagttggc tatctgaagc agaggaagtt 240
caacgatgca ctcatgggca ttctgagagt ccgcgatttg agcagccctc catatgttta 300
cacaaatcca cacacattga gccacaaagt tacagaagat gatttatttg ttgtgcttgg 360
tagtgatggc ttatttgatt tcttcagcaa tgatgaagtt gttcggttgg tttatcaatt 420
tatgcatgat aatccaatgg gggatcctgc aaaatatctt attgagcaac ttataactca 480
aagcagccaa gggagcagct ctaacagccg
```

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1503927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

Leu	Cys	Ile	Leu	Asn	Met	Gly	Asp	Ser	Arg	Ala	Val	Leu	Ala	Ser	Met
1				5					10					15	
Pro	Tyr	Val	Glu	Asn	Gly	Ala	Leu	Lys	Ala	Thr	Gln	Leu	Thr	Glu	Thr
			20					25					30		
His	Ser	Leu	Glu	Asn	Pro	Leu	Glu	Tyr	Gln	Lys	Leu	Leu	Ala	Glu	His
		35					40					45			
Pro	Asn	Asp	Ser	Ser	Val	Val	Arg	Gly	Asn	Lys	Ile	Lys	Gly	Lys	Leu
	50					55					60				
Lys	Val	Thr	Arg	Ala	Phe	Gly	Val	Gly	Tyr	Leu	Lys	Gln	Arg	Lys	Phe
65				70					75						80
Asn	Asp	Ala	Leu	Met	Gly	Ile	Leu	Arg	Val	Arg	Asp	Leu	Ser	Ser	Pro
			85					90					95		
Pro	Tyr	Val	Tyr	Thr	Asn	Pro	His	Thr	Leu	Ser	His	Lys	Val	Thr	Glu
		100						105					110		
Asp	Asp	Leu	Phe	Val	Val	Leu	Gly	Ser	Asp	Gly	Leu	Phe	Asp	Phe	Phe
	115					120						125			
Ser	Asn	Asp	Glu	Val	Val	Arg	Leu	Val	Tyr	Gln	Phe	Met	His	Asp	Asn
	130					135					140				
Pro	Met	Gly	Asp	Pro	Ala	Lys	Tyr	Leu	Ile	Glu	Gln	Leu	Tyr	Thr	Gln
145				150					155						160
Ser	Ser	Gln	Gly	Ser	Ser	Ser	Asn	Ser							
				165											

(2) INFORMATION FOR SEQ ID NO:2592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1503928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

Met	Gly	Asp	Ser	Arg	Ala	Val	Leu	Ala	Ser	Met	Pro	Tyr	Val	Glu	Asn
1				5					10					15	
Gly	Ala	Leu	Lys	Ala	Thr	Gln	Leu	Thr	Glu	Thr	His	Ser	Leu	Glu	Asn
		20						25					30		
Pro	Leu	Glu	Tyr	Gln	Lys	Leu	Leu	Ala	Glu	His	Pro	Asn	Asp	Ser	Ser
		35					40					45			
Val	Val	Arg	Gly	Asn	Lys	Ile	Lys	Gly	Lys	Leu	Lys	Val	Thr	Arg	Ala
	50					55					60				
Phe	Gly	Val	Gly	Tyr	Leu	Lys	Gln	Arg	Lys	Phe	Asn	Asp	Ala	Leu	Met
65				70					75						80
Gly	Ile	Leu	Arg	Val	Arg	Asp	Leu	Ser	Ser	Pro	Pro	Tyr	Val	Tyr	Thr
			85					90					95		
Asn	Pro	His	Thr	Leu	Ser	His	Lys	Val	Thr	Glu	Asp	Asp	Leu	Phe	Val
		100						105					110		
Val	Leu	Gly	Ser	Asp	Gly	Leu	Phe	Asp	Phe	Phe	Ser	Asn	Asp	Glu	Val
	115					120						125			
Val	Arg	Leu	Val	Tyr	Gln	Phe	Met	His	Asp	Asn	Pro	Met	Gly	Asp	Pro
	130					135					140				
Ala	Lys	Tyr	Leu	Ile	Glu	Gln	Leu	Tyr	Thr	Gln	Ser	Ser	Gln	Gly	Ser
145				150					155						160
Ser	Ser	Asn	Ser												

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..154
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503929
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:
Met Pro Tyr Val Glu Asn Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu
1 5 10 15
Thr His Ser Leu Glu Asn Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu
 20 25 30
His Pro Asn Asp Ser Ser Val Val Arg Gly Asn Lys Ile Lys Gly Lys
 35 40 45
Leu Lys Val Thr Arg Ala Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys
 50 55 60
Phe Asn Asp Ala Leu Met Gly Ile Leu Arg Val Arg Asp Leu Ser Ser
65 70 75 80
Pro Pro Tyr Val Tyr Thr Asn Pro His Thr Leu Ser His Lys Val Thr
 85 90 95
Glu Asp Asp Leu Phe Val Val Leu Gly Ser Asp Gly Leu Phe Asp Phe
 100 105 110
Phe Ser Asn Asp Glu Val Val Arg Leu Val Tyr Gln Phe Met His Asp
 115 120 125
Asn Pro Met Gly Asp Pro Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr
 130 135 140
Gln Ser Ser Gln Gly Ser Ser Ser Asn Ser
145 150

(2) INFORMATION FOR SEQ ID NO:2594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..161
(D) OTHER INFORMATION: / Ceres Seq. ID 1503934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

accgcaccca gaggaggcaa ggagcccata cacatccacc tggctcctgct ctcaccacac 60
cgccgcgcca attggggctc gcggcagcac cgccgcggct tcccgcctggt cccgctcctg 120
ctctccctcc tggccgcccgc cgcgtacggc cgcctcatct c

(2) INFORMATION FOR SEQ ID NO:2595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

Thr Ala Pro Arg Gly Gly Lys Glu Pro Ile His Ile His Leu Val Leu
1 5 10 15
Leu Ser Pro His Arg Arg Ala Asn Trp Gly Ser Arg Gln His Arg Arg
 20 25 30
Gly Phe Pro Leu Val Pro Leu Leu Leu Ser Leu Leu Ala Ala Ala Ala

35 40 45
Tyr Gly Arg Leu Ile
50
(2) INFORMATION FOR SEQ ID NO:2596:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503936
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:
Pro His Pro Glu Glu Ala Arg Ser Pro Ser Thr Ser Thr Trp Ser Cys
1 5 10 15
Ser His His Thr Ala Ala Pro Ile Gly Ala Arg Gly Ser Thr Ala Ala
20 25 30
Ala Ser Arg Trp Ser Arg Ser Cys Ser Pro Ser Trp Pro Pro Pro Arg
35 40 45
Thr Ala Ala Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2597:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503937
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:
Arg Thr Gln Arg Arg Gln Gly Ala His Pro His Pro Pro Gly Pro Ala
1 5 10 15
Leu Thr Thr Pro Pro Arg Gln Leu Gly Leu Ala Ala Ala Pro Pro Arg
20 25 30
Leu Pro Ala Gly Pro Ala Pro Ala Leu Pro Pro Gly Arg Arg Arg Val
35 40 45
Arg Pro Pro His Leu
50

(2) INFORMATION FOR SEQ ID NO:2598:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1503942
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:
gaaccacttc acagaagaag tgctttaccc tcacccgccc cagcgcgcggt agttcggttcg 60
acacagtcac agtcacagac cagtcgtttc tcccttctct cccccgggcc cggagaggag 120
aggatggccg gccggagcag cctctccatg gtcgctcgac accggctctt cagcccggtc 180
aaccagtg ggcggcgccga ccacggcggt ggagctcgac gaggccgacg tcctctgggg 240
cgccggcgcc ggatacccg cgtcgctcct accgtcgctg tcgccgttcc tgtcctccgc 300
ggtcgacccg tacgcgcggt cgccgcccgt ggccgcgcgc tccaagcaga agccgcggtg 360

gggtggtggcc ggcgctccgg ggccggcgta cggtgcccgt caacatcccg gactggtcca 420
agatcctggg cgccg

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

Glu	Pro	Leu	His	Arg	Arg	Ser	Ala	Leu	Pro	Ser	Pro	Ala	Pro	Arg	Ala
1				5					10					15	
Val	Val	Arg	Ser	Thr	Gln	Ser	Gln	Ser	Gln	Thr	Ser	Arg	Phe	Ser	Leu
			20					25					30		
Leu	Ser	Pro	Gly	Pro	Gly	Glu	Glu	Arg	Met	Ala	Gly	Arg	Ser	Ser	Leu
		35				40						45			
Ser	Met	Val	Ala	Ser	His	Arg	Leu	Phe	Thr	Pro	Val	Asn	Pro	Val	Gly
	50					55					60				
Gly	Ala	Asp	His	Gly	Val	Gly	Ala	Arg	Arg	Gly	Arg	Arg	His	Leu	Gly
65					70					75				80	
Arg	Arg	Arg	Arg	Ile	Pro	Gly	Val	Val	Leu	Thr	Val	Val	Val	Ala	Val
				85					90					95	
Pro	Val	Leu	Arg	Gly	Arg	Pro	Val	Arg	Ala	Val	Ala	Ala	Gly	Gly	Arg
			100					105					110		
Ala	Val	Gln	Ala	Glu	Ala	Ala	Trp	Gly	Gly	Gly	Arg	Arg	Ser	Gly	Ala
		115					120					125			
Gly	Val	Arg	Cys	Pro	Ser	Thr	Ser	Arg	Thr	Gly	Pro	Arg	Ser	Trp	Ala
	130					135					140				
Pro															
145															

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Thr	Thr	Ser	Gln	Lys	Cys	Phe	Thr	Leu	Thr	Arg	Pro	Thr	Arg	Gly	
1				5					10					15	
Ser	Ser	Phe	Asp	Thr	Val	Thr	Val	Thr	Asp	Gln	Ser	Phe	Leu	Pro	Ser
			20					25					30		
Leu	Pro	Arg	Ala	Arg	Arg	Gly	Glu	Asp	Gly	Arg	Pro	Glu	Gln	Pro	Leu
		35				40						45			
His	Gly	Arg	Val	Ala	Pro	Ala	Leu	His	Ala	Gly	Gln	Pro	Ser	Gly	Arg
	50					55					60				
Arg	Arg	Pro	Arg	Arg	Gly	Ser	Ser	Thr	Arg	Pro	Thr	Ser	Ser	Gly	Ala
65					70					75				80	
Ala	Ala	Ala	Asp	Thr	Arg	Arg	Arg	Pro	His	Arg	Arg	Arg	Arg	Arg	Ser
			85					90						95	
Cys	Pro	Pro	Arg	Ser	Thr	Arg	Thr	Arg	Gly	Arg	Arg	Arg	Trp	Pro	Arg
		100						105					110		
Arg	Pro	Ser	Arg	Ser	Arg	Val	Gly	Trp	Trp	Pro	Ala	Leu	Arg	Gly	Arg

(2) INFORMATION FOR SEQ ID NO:2601:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1503945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

Thr Gly Pro Arg Ser Trp Ala Pro
100

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1503946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 1						
tggtcagttg	caagaaagtg	tacggggctg	tgatgttttc	cttgtgcaac	cgtcgtgtcc	60
tccagcaaat	gaaaatctta	tggagcttct	gatcatgatt	gatgcctgta	ggagagcatc	120
tgctaagaat	atcactgcag	ttatccctta	ttttggttat	gcaagggctg	acaggaagtc	180
ccagggcagg	gaatctatag	ctgcaaaact	tgtagctaata	atgattaccg	aagctgggtgc	240
caacgtgtcc	ttgttttgtga	tcttcattct	agtcaagcaa	tgggatactt	tgacatccca	300
gtagatcacg	tttatggcca	gcctgtttatt	cttgattatc	tgcgcagcaa	gacaatatgt	360
tcagatgaact	tggtgattgt	atctcctgat	ggtggagggtg	ttgccagggc	acgtgccttt	420
gccaaaaagc	tgtcagatgc	acctctagct	attgtagata	aaagaaggca	aggacataat	480
gtcgcgtgagg	tgat					

(2) INFORMATION FOR SEQ ID NO:2603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1503947

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1503948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1503949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606:

gattttgaaa	ggggtttcat	atgcgctgag	gtaatgaagt	ttgaagatct	gaaagaactg	60
ggcagtgaat	ctgctgtaaa	ggctgctgga	aaatacaagc	aggaggggaa	aacctatgtg	120
gtccaggacg	gggacatcat	ctttttcaaa	ttcaacgtgt	ctgggtggcg	gaagaagtga	180
ataatgtatg	aagatggtag	catcaacagt	gttttacgtc	ttaccccgaa	tttctcattc	240
aacagtgttt	acaccttgcc	ccgtatttcc	acatttttga	ggtcgcttcc	cagtagctct	300
aggttccggt	atcgaaaact	tgtacaacaa	ggctccagac	cgttgaagga	tttgtattaa	360
taacatgcac	aattgtatgg	cttgctgctg	agctctcgct	gttaccagaa	gcttagaatc	420
gtttgagttc	tgtgg					

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

Asp	Phe	Glu	Arg	Gly	Phe	Ile	Cys	Ala	Glu	Val	Met	Lys	Phe	Glu	Asp
1				5					10					15	
Leu	Lys	Glu	Leu	Gly	Ser	Glu	Ser	Ala	Val	Lys	Ala	Ala	Gly	Lys	Tyr
			20					25					30		
Lys	Gln	Glu	Gly	Lys	Thr	Tyr	Val	Val	Gln	Asp	Gly	Asp	Ile	Ile	Phe
		35					40					45			
Phe	Lys	Phe	Asn	Val	Ser	Gly	Gly	Gly	Lys	Lys					
	50					55									

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

Met	Lys	Phe	Glu	Asp	Leu	Lys	Glu	Leu	Gly	Ser	Glu	Ser	Ala	Val	Lys
1					5				10					15	
Ala	Ala	Gly	Lys	Tyr	Lys	Gln	Glu	Gly	Lys	Thr	Tyr	Val	Val	Gln	Asp
			20					25					30		
Gly	Asp	Ile	Ile	Phe	Phe	Lys	Phe	Asn	Val	Ser	Gly	Gly	Gly	Lys	Lys
		35					40						45		

(2) INFORMATION FOR SEQ ID NO:2609:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..58
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503972
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:
Met Tyr Glu Asp Gly Ser Ile Asn Ser Val Leu Arg Leu Thr Pro Asn
1 5 10 15
Phe Ser Phe Asn Ser Val Tyr Thr Leu Pro Arg Ile Ser Thr Phe Leu
 20 25 30
Arg Ser Leu Pro Ser Ser Ser Arg Phe Arg Tyr Arg Lys Leu Val Gln
 35 40 45
Gln Gly Ser Arg Pro Leu Lys Asp Leu Tyr
50 55

(2) INFORMATION FOR SEQ ID NO:2610:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..506

(D) OTHER INFORMATION: / Ceres Seq. ID 1503989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

accgcgccct gatccactct ccgcttcccc ctccgatcga cctgctccct cccaccacc	60
gagcccatgg cggaccagct caccgacgac cagatcgccg agttcaagga ggccttcagc	120
ctcttcgaca aggacgggga tggttgcatc acgaccaagg agctggggcac tgatcatgcg	180
tcgctggggc aaaatcctac agaggctgag ctccaggaca tgatcaacga ggtcgatgct	240
gatggcaacg gcaccatcga tttcccagag tttctcaacc ttatggctcg caagatgaag	300
gacaccgact ctgaggaaga gctcaaggag gccttcctg tgtttgacaa ggaccagaac	360
ggcttcactc cggccgccga gctccgccat gtcatgacaa atcttggtga gaagctaact	420
gatgaggagg tggacgagat gatccgtgag gctgatgtcg atggtgatgg ccagatcaac	480
tacgaggagt ttgtcaagggt catgat	

(2) INFORMATION FOR SEQ ID NO:2611:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1503990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala	
1 5 10 15	
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu	
20 25 30	
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu	
35 40 45	
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile	
50 55 60	
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr	

(2) INFORMATION FOR SEQ ID NO:2612:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1503991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1503992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

(X1) SEQUENCE DESCRIPTION															
Met	Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro
1				5					10					15	
Glu	Phe	Leu	Asn	Leu	Met	Ala	Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu
			20					25					30		
Glu	Glu	Leu	Lys	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp	Gln	Asn	Gly
			35				40					45			
Phe	Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu
	50					55					60				
Lys	Leu	Thr	Asp	Glu	Glu	Val	Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Val
65				70					75					80	
Asp	Gly	Asp	Gly	Gln	Ile	Asn	Tyr	Glu	Glu	Phe	Val	Lys	Val	Met	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

tcaacgcaca tctccaccgt cgtccgccgc cgccgaagac ggaaggagaa gaggggtacgg	60
ccgtctcctc gcccccatgg cccacgagaa gaagctgtcc aaccgatgc gggagatcaa	120
ggtgcagaag ctgcgtcctca atatctccgt cggggagagc ggcgaccgtc tcaccgcgc	180
cgcaaaggtg ctgcagcagc tcagcggcca gaccccgctc ttctccaagg gtgagtactg	240
agttctcgcg gctccgtttc atgccttccg ctgacggggg gcttccttct gcctgctggc	300
ggtgttggtt cgtcttgagc cgaggtacac ggtgcgggtc ttcggcatcc ggcgtaacga	360
gaagatcgcc tgctacgtca cggtgagggg cgagaaggcc atgcagctgc ttgagagcgg	420
cctcaaggtc aaggagtacg agctgctcag gaggaacttc agcgacaccg ggtgctttg	

(2) INFORMATION FOR SEQ ID NO:2615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

Ser Thr His Ile Ser Thr Val Val Arg Arg Arg Arg Arg Arg Lys Glu	
1 5 10 15	
Lys Arg Val Arg Pro Ser Pro Arg Pro His Gly Pro Arg Glu Ala	
20 25 30	
Val Gln Pro Asp Ala Gly Asp Gln Gly Ala Glu Ala Arg Pro Gln Tyr	
35 40 45	
Leu Arg Arg Gly Glu Arg Arg Pro Ser His Pro Arg Arg Lys Gly Ala	
50 55 60	
Arg Ala Ala Gln Arg Pro Asp Pro Arg Leu Leu Gln Gly	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:2616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

Gln Arg Thr Ser Pro Ser Ser Ala Ala Glu Asp Gly Arg Arg	
1 5 10 15	
Arg Gly Tyr Gly Arg Leu Leu Ala Pro Met Ala His Glu Lys Lys Leu	
20 25 30	
Ser Asn Pro Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile	
35 40 45	
Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu	

50 55 60
Glu Gln Leu Ser Gly Gln Thr Pro Val Phe Ser Lys Gly Glu Tyr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

Asn Ala His Leu His Arg Arg Pro Pro Pro Lys Thr Glu Gly Glu
1 5 10 15
Glu Gly Thr Ala Val Ser Ser Pro Pro Trp Pro Thr Arg Arg Ser Cys
20 25 30
Pro Thr Arg Cys Gly Arg Ser Arg Cys Arg Ser Ser Ser Ile Ser
35 40 45
Pro Ser Gly Arg Ala Ala Thr Val Ser Pro Ala Pro Gln Arg Cys Ser
50 55 60
Ser Ser Ser Ala Ala Arg Pro Pro Ser Ser Pro Arg Val Ser Thr Glu
65 70 75 80
Phe Ser Arg Leu Arg Phe Met Pro Ser Ala Asp Gly Val Leu Pro Ser
85 90 95
Ala Cys Trp Arg Cys Trp Phe Val Leu Gln Arg Gly Thr Arg Cys Gly
100 105 110
Arg Ser Ala Ser Gly Val Thr Arg Arg Ser Pro Ala Thr Ser Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

atcgagacac acacagaact tctcctgtcg gcctactaat acagctagct agctgccctc 60
ttaggtatac tgtgatggcc acaaccttgt cctccacagt agtagttgca cttggtgacc 120
tctcttcttg ctctttgtaa cgtgtggctc gtgcgcgagg ccggtgagct ttaacgcctc 180
cgacctcacc gccgatcccg gctgggatgc tgccagggcc acctgttacg gtgcgcccac 240
cggcgcgggc ctgatgacga cgggtgggccc tgtggattca agaactgtaa tctgccgccg 300
ttctcgcaa tgacgtcgtg cggcaacgag cccctgttca aggacggcaa gggctgcggc 360
tctgtctacc agatacgatg ccaaaaccac ccggcctgct ccggcaaccc agagacggtg 420
atcatcactg acatgaacta ctaccccggtg gccaaagtacc acttcgacct yagcggc

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1504017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:

Arg Asp Thr His Arg Thr Ser Pro Val Gly Leu Leu Ile Gln Leu Ala
1 5 10 15
Ser Cys Pro Leu Arg Tyr Thr Val Met Ala Thr Thr Leu Ser Ser Thr
20 25 30
Val Val Val Ala Leu Gly Asp Leu Ser Ser Cys Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1504018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

Met Thr Ser Cys Gly Asn Glu Pro Leu Phe Lys Asp Gly Lys Gly Cys
1 5 10 15
Gly Ser Cys Tyr Gln Ile Arg Cys Gln Asn His Pro Ala Cys Ser Gly
20 25 30
Asn Pro Glu Thr Val Ile Ile Thr Asp Met Asn Tyr Tyr Pro Val Ala
35 40 45
Lys Tyr His Phe Asp Xaa Ser Gly
50 55

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1504025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

catgtggttg tgggcactgt gaaagctctt tggccactca cagaagccct agaataagaa 60
tattgctaatt gatgagaagt aactaaaaca atatcatata attgcagtgc tctctccaat 120
agtttgagg gtagtctcct tggaagattt ttggtaggaa cagggatggg attgggtcca 180
ccagtagctt cactttatat aacggagggt tctccttcta cagtggggg tacatatggt 240
agctttgttc agattgcaac ctgccttgga attatagtat cactactcat tggtagacct 300
gtcaaagata ttgatagatg gtggagagtg tgtttctggg ttgccgttat ccagcaact 360
ttacaagctc tcggtatgga gttttgtgct gagagccctc agtggcttta taagtgtgga 420
aaaataagtg

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1504026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

Met Leu Leu Gly Arg Phe Leu Val Gly Thr Gly Met Gly Leu Gly Pro

```

1           5           10           15
Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser Pro Ser Thr Val Arg
                20                25                30
Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr Cys Leu Gly Ile Ile
                35                40                45
Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp Ile Asp Arg Trp Trp
                50                55                60
Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala Thr Leu Gln Ala Leu
        65                70                75                80
Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp Leu Tyr Lys Cys Gly
                85                90                95
Lys Ile Ser
```

(2) INFORMATION FOR SEQ ID NO:2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

```

Met Gly Leu Gly Pro Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser
1           5           10           15
Pro Ser Thr Val Arg Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr
                20                25                30
Cys Leu Gly Ile Ile Val Ser Leu Ile Gly Thr Pro Val Lys Asp
                35                40                45
Ile Asp Arg Trp Trp Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala
        50                55                60
Thr Leu Gln Ala Leu Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp
        65                70                75                80
Leu Tyr Lys Cys Gly Lys Ile Ser
                85
```

(2) INFORMATION FOR SEQ ID NO:2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

```

tattatcaga gaaacaagag ctgtgcttct ctgttgctctc attgctctgg cagaagctca      60
tagcttctcc tgaaatgcag atgtctgcag aaagtacatc agctcaccaa ggatggagga      120
agggttggtga tgcactttgt gatgtcggtt cagcctcacc aaccaaggca tcagctgcta      180
tcgttctcca ggccgagaag gacttgcagc cttggattgc tagagatgac gaacaaggtc      240
agaagatgtg gagagtcaac cagcgtatag tgaagcttat agctgagctt atgaggaacc      300
atgacagccc tgaagcgttg gtgatactcg ctagtgcctc cgaccttcta cttcgtgcta      360
ccgatggaat gctcgtcgat ggtgaagctt gtactttgcc acagcttgag cttctggaag      420
tgaccgctcg ggctgtccat cttatcatcg aatggggaga tc
```

(2) INFORMATION FOR SEQ ID NO:2625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1504037
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Leu	Ser	Glu	Lys	Gln	Glu	Leu	Cys	Phe	Ser	Val	Val	Ser	Leu	Leu	Trp
1				5				10						15	
Gln	Lys	Leu	Ile	Ala	Ser	Pro	Glu	Met	Gln	Met	Ser	Ala	Glu	Ser	Thr
			20					25					30		
Ser	Ala	His	Gln	Gly	Trp	Arg	Lys	Val	Val	Asp	Ala	Leu	Cys	Asp	Val
		35					40					45			
Val	Ser	Ala	Ser	Pro	Thr	Lys	Ala	Ser	Ala	Ala	Ile	Val	Leu	Gln	Ala
		50				55					60				
Glu	Lys	Asp	Leu	Gln	Pro	Trp	Ile	Ala	Arg	Asp	Asp	Glu	Gln	Gly	Gln
65					70					75				80	
Lys	Met	Trp	Arg	Val	Asn	Gln	Arg	Ile	Val	Lys	Leu	Ile	Ala	Glu	Leu
			85					90					95		
Met	Arg	Asn	His	Asp	Ser	Pro	Glu	Ala	Leu	Val	Ile	Leu	Ala	Ser	Ala
			100					105					110		
Ser	Asp	Leu	Leu	Leu	Arg	Ala	Thr	Asp	Gly	Met	Leu	Val	Asp	Gly	Glu
		115				120						125			
Ala	Cys	Thr	Leu	Pro	Gln	Leu	Glu	Leu	Leu	Glu	Val	Thr	Ala	Arg	Ala
		130				135					140				
Val	His	Leu	Ile	Ile	Glu	Trp	Gly	Asp							
145					150										

(2) INFORMATION FOR SEQ ID NO:2626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
(D) OTHER INFORMATION: / Ceres Seq. ID 1504038
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met	Gln	Met	Ser	Ala	Glu	Ser	Thr	Ser	Ala	His	Gln	Gly	Trp	Arg	Lys
1				5				10						15	
Val	Val	Asp	Ala	Leu	Cys	Asp	Val	Val	Ser	Ala	Ser	Pro	Thr	Lys	Ala
			20					25					30		
Ser	Ala	Ala	Ile	Val	Leu	Gln	Ala	Glu	Lys	Asp	Leu	Gln	Pro	Trp	Ile
		35				40						45			
Ala	Arg	Asp	Asp	Glu	Gln	Gly	Gln	Lys	Met	Trp	Arg	Val	Asn	Gln	Arg
		50				55					60				
Ile	Val	Lys	Leu	Ile	Ala	Glu	Leu	Met	Arg	Asn	His	Asp	Ser	Pro	Glu
65					70					75				80	
Ala	Leu	Val	Ile	Leu	Ala	Ser	Ala	Ser	Asp	Leu	Leu	Leu	Arg	Ala	Thr
			85					90					95		
Asp	Gly	Met	Leu	Val	Asp	Gly	Glu	Ala	Cys	Thr	Leu	Pro	Gln	Leu	Glu
		100						105					110		
Leu	Leu	Glu	Val	Thr	Ala	Arg	Ala	Val	His	Leu	Ile	Ile	Glu	Trp	Gly
		115				120						125			

Asp

(2) INFORMATION FOR SEQ ID NO:2627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

```
Met Ser Ala Glu Ser Thr Ser Ala His Gln Gly Trp Arg Lys Val Val
1           5           10           15
Asp Ala Leu Cys Asp Val Val Ser Ala Ser Pro Thr Lys Ala Ser Ala
20           25           30
Ala Ile Val Leu Gln Ala Glu Lys Asp Leu Gln Pro Trp Ile Ala Arg
35           40           45
Asp Asp Glu Gln Gly Gln Lys Met Trp Arg Val Asn Gln Arg Ile Val
50           55           60
Lys Leu Ile Ala Glu Leu Met Arg Asn His Asp Ser Pro Glu Ala Leu
65           70           75           80
Val Ile Leu Ala Ser Ala Ser Asp Leu Leu Arg Ala Thr Asp Gly
85           90           95
Met Leu Val Asp Gly Glu Ala Cys Thr Leu Pro Gln Leu Glu Leu Leu
100          105          110
Glu Val Thr Ala Arg Ala Val His Leu Ile Ile Glu Trp Gly Asp
115          120          125
```

(2) INFORMATION FOR SEQ ID NO:2628:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

```
aaatctctct cttctcctcg cctcgcccttg gtgttcacgc cgtcgctagc gcctgckcct      60
gccssggcka asttcctgcc ctccccggcg ccgggctcgg gtcgtcgtcg gccaggaaga      120
tggttgggcg cttcagggtg ctgcatctgg tcaggccttt tctggctttc ttgccatakk      180
ttgcagagcg cggatagkaa gataccgttc agagaaaaag ttatctacac tggtatttcc      240
ctcttcattt tcttggtctg cagccagctc ccactctatg gcattcattc aacaactgga      300
gctgatcctt tctactggat gcgtgttatc ctgcgcatcaa accgtggcac tgtgatggag      360
ttgggtatta ctccaattgt gacatctggg atggtaatgc aacttcttgt tggatcgaag      420
atcatttgaa gttgacaaca gtgtgagaka ggatcgtgct ctg
```

(2) INFORMATION FOR SEQ ID NO:2629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

```
Lys Ser Leu Ser Ser Pro Arg Leu Ala Leu Val Phe Thr Pro Ser Leu
1           5           10           15
Ala Pro Xaa Pro Ala Xaa Xaa Xaa Phe Leu Pro Ser Pro Ala Pro Gly
20           25           30
```

Ser Gly Arg Arg Arg Pro Gly Arg Trp Leu Ala Ala Ser Gly Tyr Cys
35 40 45
Ile Trp Ser Gly Leu Phe Trp Leu Ser Cys His Xaa Leu Gln Ser Ala
50 55 60
Asp Xaa Lys Ile Pro Phe Arg Glu Lys Val Ile Tyr Thr Val Ile Ser
65 70 75 80
Leu Phe Ile Phe Leu Val Cys Ser Gln Leu Pro Leu Tyr Gly Ile His
85 90 95
Ser Thr Thr Gly Ala Asp Pro Phe Tyr Trp Met Arg Val Ile Leu Ala
100 105 110
Ser Asn Arg Gly Thr Val Met Glu Leu Gly Ile Thr Pro Ile Val Thr
115 120 125
Ser Gly Met Val Met Gln Leu Val Gly Ser Lys Ile Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

atctgaagga tatggcttat catggagtat ttttaaagag ggacatttgt taagtgggtc	60
tgacgatgct caaatttgc tgtgggacat taaagcaaat agtagaaaca aaagtcttga	120
cgccttgacg atttttaagc atcatgatgg tgtcgttgaa gatgttgctt ggcacttgag	180
gcatgagtac ttatttgggt cagttgggtga cgattatcat cttttgattt gggacctgcg	240
gtctcccgcc octactaaac ctgttcagtc agtggtggcg caccagggtg aggtgaactg	300
cctggctttt aaccggttca acgaatgggt tgttgcaact ggttctactg acaagactgt	360
caaattattt gatcttagga agattgatac ttctctgcac acctttgact gtcacaaaga	420
ggaagttttt caagttggat ggagtccaaa gaatgaaact gtacttgcac cctgttgtct	480
gggcagaagg ctcattgtct gg	

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

Ser Glu Gly Tyr Gly Leu Ser Trp Ser Ile Phe Lys Glu Gly His Leu
1 5 10 15
Leu Ser Gly Ser Asp Asp Ala Gln Ile Cys Leu Trp Asp Ile Lys Ala
20 25 30
Asn Ser Arg Asn Lys Ser Leu Asp Ala Leu Gln Ile Phe Lys His His
35 40 45
Asp Gly Val Val Glu Asp Val Ala Trp His Leu Arg His Glu Tyr Leu
50 55 60
Phe Gly Ser Val Gly Asp Asp Tyr His Leu Leu Ile Trp Asp Leu Arg
65 70 75 80
Ser Pro Ala Pro Thr Lys Pro Val Gln Ser Val Val Ala His Gln Gly
85 90 95
Glu Val Asn Cys Leu Ala Phe Asn Pro Phe Asn Glu Trp Val Val Ala
100 105 110

Thr Gly Ser Thr Asp Lys Thr Val Lys Leu Phe Asp Leu Arg Lys Ile
115 120 125
Asp Thr Ser Leu His Thr Phe Asp Cys His Lys Glu Glu Val Phe Gln
130 135 140
Val Gly Trp Ser Pro Lys Asn Glu Thr Val Leu Ala Ser Cys Cys Leu
145 150 155 160
Gly Arg Arg Leu Met Val Trp
165

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

attccggttc	gagagccaaa	aactccactg	ctttcatcaa	ctccggcgac	ttggagaaga	60
cgaaktccag	aatccgatcg	gaagtttggt	gctcgcgctt	tgacggattg	atttcggtgc	120
gccgatgggg	caggcggttc	gcaagctggt	cgattccttc	ttcggcacca	gcgagatgag	180
ggttgatgat	cttggtctgg	atgctgccgg	taaaaccacc	atattgtaca	agctgcatat	240
cggggaggtt	ttgtcgactg	ttcccacgat	tggtttcaac	gtcgagaaag	ttcaatacaa	300
gaatgtgatg	tttactgtgt	gggatgttgg	tggccaagaa	aagttgaggg	tgactacgtc	360
cgcaaaggag	atgagtttgg	gtattttctcc	tttggaggga	gtacagtgat	atgcgtcttc	420
gagaaggacg	ccatccaatt	tgacgctgat	ctcgtggcaa	acagcgaaag	gtcactggag	480
accaagtccc	ggatctgcag	aaagtttcgc	tcgg			

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

Met Gly Gln Ala Phe Arg Lys Leu Phe Asp Ser Phe Phe Gly Thr Ser	
1 5 10 15	
Glu Met Arg Val Val Met Leu Gly Leu Asp Ala Ala Gly Lys Thr Thr	
20 25 30	
Ile Leu Tyr Lys Leu His Ile Gly Glu Val Leu Ser Thr Val Pro Thr	
35 40 45	
Ile Gly Phe Asn Val Glu Lys Val Gln Tyr Lys Asn Val Met Phe Thr	
50 55 60	
Val Trp Asp Val Gly Gly Gln Glu Lys Leu Arg Val Thr Thr Ser Ala	
65 70 75 80	
Lys Glu Met Ser Leu Gly Ile Ser Pro Leu Glu Gly Val Gln	
85 90	

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile
1			5				10						15		
Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile
			20				25						30		
Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val
		35				40					45				
Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Val	Thr	Thr	Ser	Ala	Lys
	50				55						60				
Glu	Met	Ser	Leu	Gly	Ile	Ser	Pro	Leu	Glu	Gly	Val	Gln			
65			70							75					

(2) INFORMATION FOR SEQ ID NO:2635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1504101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile	Leu	Tyr	Lys	Leu
1			5				10						15		
His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile	Gly	Phe	Asn	Val
			20				25						30		
Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val	Trp	Asp	Val	Gly
		35				40					45				
Gly	Gln	Glu	Lys	Leu	Arg	Val	Thr	Thr	Ser	Ala	Lys	Glu	Met	Ser	Leu
	50				55						60				
Gly	Ile	Ser	Pro	Leu	Glu	Gly	Val	Gln							
65			70												

(2) INFORMATION FOR SEQ ID NO:2636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1504102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

atatatactc	ctgttgcgta	gaatcggcac	aagggtgcac	gttcaggagg	agctctcgtg	60
gcgtcctagt	ctgtggaagg	tccaaagaag	aagatggacg	gcgagatgga	cgaggacgtt	120
ctcacggaga	tcctcgcgag	gctgccgtgc	aggctcgttg	cgcggttcca	gtgcgtgtcc	180
acgtcgtgcg	gcgcatcatc	tccagcgact	acctccgccg	ccggctgccg	ctcatcacgt	240
cgggcgtgct	ctaccacgat	ggtggcagga	ggcagcagtc	gtacacgtac	gcgtgcgcgt	300
caggcggcgg	cggcggcggc	ggcgcatctg	cggaggccgc	ggacatgcgc	ttcttcccgc	360
gccacgagac	gtccaccatc	atcgacggct	gcaacggcct	gctgctctac	tacgcgtccc	420
gcccggcgcg	ttccacgtcg	tgagcccgac	cacgcggcgg			

(2) INFORMATION FOR SEQ ID NO:2637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504103
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:
Tyr Ile Leu Leu Leu Arg Arg Ile Gly Thr Arg Val His Val Gln Glu
1 5 10 15
Glu Leu Ser Trp Arg Pro Ser Leu Trp Lys Val Gln Arg Arg Arg Trp
 20 25 30
Thr Ala Arg Trp Thr Arg Thr Phe Ser Arg Arg Ser Ser Arg Gly Cys
 35 40 45
Arg Ala Gly Arg Trp Arg Gly Ser Ser Ala Cys Pro Arg Arg Ala Ala
 50 55 60
His His Leu Gln Arg Leu Pro Pro Pro Pro Ala Ala Ala His His Val
65 70 75 80
Gly Arg Ala Leu Pro Arg Trp Trp Gln Glu Ala Ala Val Val His Val
 85 90 95
Arg Val Arg Val Arg Arg Arg Arg Arg Arg Arg Arg Ile Gly Gly Gly
 100 105 110
Arg Gly His Ala Leu Leu Pro Ala Pro Arg Asp Val His His His Arg
 115 120 125
Arg Leu Gln Arg Pro Ala Ala Leu Leu Arg Val Pro Pro Gly Ala Phe
 130 135 140
His Val Val Ser Pro Thr Thr Arg Arg
145 150

(2) INFORMATION FOR SEQ ID NO:2638:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1504104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:

Ile Tyr Ser Cys Cys Val Glu Ser Ala Gln Gly Cys Thr Phe Arg Arg
1 5 10 15
Ser Ser Arg Gly Val Leu Val Cys Gly Arg Ser Lys Glu Glu Asp Gly
 20 25 30
Arg Arg Asp Gly Arg Gly Arg Ser His Gly Asp Pro Arg Glu Ala Ala
 35 40 45
Val Gln Val Ala Gly Ala Val Pro Val Arg Val His Val Val Arg Arg
 50 55 60
Ile Ile Ser Ser Asp Tyr Leu Arg Arg Arg Leu Pro Leu Ile Thr Ser
65 70 75 80
Gly Val Leu Tyr His Asp Gly Gly Arg Arg Gln Gln Ser Tyr Thr Tyr
 85 90 95
Ala Cys Ala Ser Gly Gly Gly Gly Gly Gly Gly Ala Leu Ala Glu Ala
 100 105 110
Ala Asp Met Arg Phe Phe Pro Arg His Glu Thr Ser Thr Ile Ile Asp
 115 120 125
Gly Cys Asn Gly Leu Leu Leu Tyr Tyr Ala Ser Arg Pro Ala Arg Ser
 130 135 140
Thr Ser
145

(2) INFORMATION FOR SEQ ID NO:2639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

```
Met Asp Gly Glu Met Asp Glu Asp Val Leu Thr Glu Ile Leu Ala Arg
1           5           10           15
Leu Pro Cys Arg Ser Leu Ala Arg Phe Gln Cys Val Ser Thr Ser Cys
20           25           30
Gly Ala Ser Ser Pro Ala Thr Thr Ser Ala Ala Gly Cys Arg Ser Ser
35           40           45
Arg Arg Ala Cys Ser Thr Thr Met Val Ala Gly Gly Ser Ser Arg Thr
50           55           60
Arg Thr Arg Ala Arg Gln Ala Ala Ala Ala Ala Ala His Trp Arg
65           70           75           80
Arg Pro Arg Thr Cys Ala Ser Ser Arg Ala Thr Arg Arg Pro Pro Ser
85           90           95
Ser Thr Ala Ala Thr Ala Cys Cys Ser Thr Thr Arg Pro Ala Arg Arg
100          105          110
Val Pro Arg Arg Glu Pro Asp His Ala Ala
115          120
```

(2) INFORMATION FOR SEQ ID NO:2640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..469
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504107
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

```
aactgcggtt gtgcgcttcg ttcagttcag ttcattccgt ttcttggttg cgaggctcag 60
agagactgag agaggatgtc gtgctgcgga ggcaactgcg ggtgcggctc cggtgcgaag 120
tgccggcaacg gctgcggagg gtgcagcaag atgtaccgcg agaatgggta tcgacctcgt 180
cgccgggtggg aggaataaga agaccaagcg cactgcgccc aagtctgacg atgtctacct 240
caagctcctc gtcaagctct accgtttctt ggtcaggagg accaagagca atttcaacgc 300
tgtcattctc aagaggcttt tcatgagtaa aaccaaccga ccaccaatct ccatgcgccg 360
ccttggtcaag tttatggaag gaaaggagaa gaacattgct gtcattgttg gcacagtcac 420
agatgacaaa aggatccagg aggttcagc aatgaagggt actgccctg
```

(2) INFORMATION FOR SEQ ID NO:2641:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..156
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504108
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

```
Thr Ala Ala Val Arg Phe Val Gln Phe Ser Ser Ser Val Phe Leu Phe
1           5           10           15
Ala Arg Ser Arg Glu Thr Glu Arg Gly Cys Arg Ala Ala Glu Ala Thr
```

	20		25		30
Ala Gly	Ala Ala Pro Ala Ala Ser	Ala Ala Thr Ala Ala Glu Gly	Ala		
	35		40		45
Ala Arg	Cys Thr Arg Arg Met Gly	Ile Asp Leu Val Ala Gly Gly	Arg		
	50		55		60
Asn Lys	Lys Thr Lys Arg Thr Ala Pro	Lys Ser Asp Asp Val Tyr Leu			
65		70		75	80
Lys Leu	Leu Val Lys Leu Tyr Arg Phe	Leu Val Arg Arg Thr Lys Ser			
		85		90	95
Asn Phe	Asn Ala Val Ile Leu Lys Arg	Leu Phe Met Ser Lys Thr Asn			
		100		105	110
Arg Pro	Pro Ile Ser Met Arg Arg Leu	Val Lys Phe Met Glu Gly Lys			
		115		120	125
Glu Lys	Asn Ile Ala Val Ile Val Gly	Thr Val Thr Asp Asp Lys Arg			
		130		135	140
Ile Gln	Glu Val Pro Ala Met Lys Val	Thr Ala Leu			
145		150		155	

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

Leu Arg	Leu Cys Ala Ser Phe Ser Ser	Val His Pro Cys Ser Cys Leu			
1		5		10	15
Arg Gly	Arg Glu Arg Leu Arg Glu Asp	Val Val Leu Arg Arg Gln Leu			
		20		25	30
Arg Val	Arg Leu Arg Leu Gln Val Arg	Gln Arg Leu Arg Arg Val Gln			
		35		40	45
Gln Asp	Val Pro Ala Glu Trp Val Ser	Thr Ser Ser Pro Val Gly Gly			
		50		55	60
Ile Arg	Arg Pro Ser Ala Leu Arg Pro	Ser Leu Thr Met Ser Thr Ser			
65		70		75	80
Ser Ser	Ser Ser Ser Thr Val Ser Trp	Ser Gly Gly Pro Arg Ala			
		85		90	95
Ile Ser	Thr Leu Ser Phe Ser Arg Gly	Phe Ser			
		100		105	

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

Met Gly	Ile Asp Leu Val Ala Gly Gly	Arg Asn Lys Lys Thr Lys Arg			
1		5		10	15
Thr Ala	Pro Lys Ser Asp Asp Val Tyr	Leu Lys Leu Leu Val Lys Leu			
		20		25	30
Tyr Arg	Phe Leu Val Arg Arg Thr Lys	Ser Asn Phe Asn Ala Val Ile			
		35		40	45

Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met
50 55 60
Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val
65 70 75 80
Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala
85 90 95
Met Lys Val Thr Ala Leu
100

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

acatcaccag cgcacagctt tcctcatcga ggcccgagtc ctgctctgat ggcgaccgac	60
gtggctgaga ctcccgcgcc gttggtggat gcggcccctg aggcgcccgc ggacacccccg	120
gcggcgctgc tgttgacgcg amscggccaa ggccaagaag gccacagcgc cgaagaagcg	180
cgccassccg acccatccgc cgtacgccga gatggtctcg gaggcgatcg cgtcgctcaa	240
ggagaggacg ggggtccagca gctttgctat tgccaagttc ttggaggaca agcacaagga	300
caagctcccc cccaacttcc gcaagcttct gaacgttcag ctcaagaagc tcgtcgccgg	360
cggcaagctg accaaggtga agaactcgta caagctgtcg tccgccacca agccaaaagg	420
ccgccccgaa gaagacc	

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Thr Ser Pro Ala His Ser Phe Pro His Arg Gly Pro Ser Pro Ala Leu	
1 5 10 15	
Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala	
20 25 30	
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa	
35 40 45	
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp	
50 55 60	
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln	
65 70 75 80	
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly	
85 90 95	
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg	
100 105 110	
Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu	
115 120 125	
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg	
130 135 140	
Arg	
145	

(2) INFORMATION FOR SEQ ID NO:2646:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..129
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504113
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

```
Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala
1           5           10           15
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa
          20           25           30
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp
          35           40           45
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln
          50           55           60
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly
65           70           75           80
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg
          85           90           95
Ser Ala Gln Glu Ala Arg Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu
          100          105          110
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg
          115          120          125
Arg
```

- (2) INFORMATION FOR SEQ ID NO:2647:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..75
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504114
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

```
Met Val Ser Glu Ala Ile Ala Ser Leu Lys Glu Arg Thr Gly Ser Ser
1           5           10           15
Ser Phe Ala Ile Ala Lys Phe Leu Glu Asp Lys His Lys Asp Lys Leu
          20           25           30
Pro Pro Asn Phe Arg Lys Leu Leu Asn Val Gln Leu Lys Lys Leu Val
          35           40           45
Ala Gly Gly Lys Leu Thr Lys Val Lys Asn Ser Tyr Lys Leu Ser Ser
          50           55           60
Ala Thr Lys Pro Lys Gly Arg Pro Glu Glu Asp
65           70           75
```

- (2) INFORMATION FOR SEQ ID NO:2648:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1504119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

cacccaaaag	cgagagscgn	gggctggtgg	ctgctgacca	aaacgaatcc	ctcgccgccc	60
cttcccgaaa	tcccccaa	atccggagccaa	tgccgcccgtc	ccctcccacc	ccggcggcac	120
ncaaaactat	cgccgacttc	ttcgcgcgcc	ccgccaagcg	cctgtgcgtg	ccccggccgc	180
ctccctctcc	tccaactcct	ctccctcctc	gctgtcgccg	gagcagcgcc	gtcgcgscga	240
caccaacctg	gcgctcg					

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

His	Pro	Lys	Ala	Arg	Xaa	Xaa	Gly	Trp	Leu	Leu	Thr	Lys	Thr	Asn	
1					5				10					15	
Pro	Ser	Pro	Pro	Leu	Pro	Glu	Ile	Pro	Gln	Ile	Arg	Ser	Gln	Cys	Arg
				20				25						30	
Arg	Pro	Leu	Pro	Pro	Arg	Arg	His	Xaa	Lys	Leu	Ser	Pro	Thr	Ser	Ser
				35			40					45			
Arg	Ala	Pro	Pro	Ser	Ala	Cys	Ala	Cys	Pro	Gly	Arg	Leu	Pro	Leu	Leu
	50					55				60					
Gln	Leu	Leu	Ser	Leu	Leu	Ala	Val	Ala	Gly	Ala	Ala	Pro	Ser	Xaa	Arg
65					70				75						80
His	Gln	Pro	Gly	Ala											
				85											

(2) INFORMATION FOR SEQ ID NO:2650:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Pro	Lys	Ser	Glu	Xaa	Xaa	Gly	Leu	Val	Ala	Ala	Asp	Gln	Asn	Glu	Ser
1				5					10					15	
Leu	Ala	Ala	Ala	Ser	Arg	Asn	Pro	Pro	Asn	Pro	Glu	Pro	Met	Pro	Pro
				20				25					30		
Ser	Pro	Pro	Thr	Pro	Ala	Ala	Xaa	Lys	Thr	Ile	Ala	Asp	Phe	Phe	Ala
				35			40				45				
Arg	Pro	Ala	Lys	Arg	Leu	Cys	Val	Pro	Arg	Pro	Pro	Pro	Ser	Pro	Pro
	50					55				60					
Thr	Pro	Leu	Pro	Pro	Arg	Cys	Arg	Arg	Ser	Ser	Ala	Val	Ala	Xaa	Thr
65					70				75						80
Pro	Thr	Trp	Arg	Ser											
				85											

(2) INFORMATION FOR SEQ ID NO:2651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1504122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

```
Met Pro Pro Ser Pro Pro Thr Pro Ala Ala Xaa Lys Thr Ile Ala Asp
1          5          10          15
Phe Phe Ala Arg Pro Ala Lys Arg Leu Cys Val Pro Arg Pro Pro Pro
20          25          30
Ser Pro Pro Thr Pro Leu Pro Pro Arg Cys Arg Arg Ser Ser Ala Val
35          40          45
Ala Xaa Thr Pro Thr Trp Arg Ser
50          55
```

(2) INFORMATION FOR SEQ ID NO:2652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1504161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:

```
acgcgcctcc tctcgccctc gctcgcgcgc cgccgcgcgc gccgcatcaw gcacccgccc      60
cgccgtcgcc tgaggtagac accaatccgc cgccatgdgg sstatgcaca gccgcgggaa      120
ctggaggaac tgagcgggtg ggcccnccgc gccaaagttat cctgttcgct accgtgttgt      180
ttaccctagt ccagagtgtt tatcttcggt cgtctcgtgt ttgttggtgc ccattctgtgt      240
ttttgattga aggtcgctct gtgtcagttg ttagtgctgt gttcatcctc ggctccagca      300
gacccatgca tcaaccagca tggactgcgg atcgatgggt gctgttacc cgtcagctt      360
tattctaagt taaatcctaa ggaaaaaat ggtgcttctt ggtgctgcaa aatggttgtg      420
ctcatg
```

(2) INFORMATION FOR SEQ ID NO:2653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1504162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

```
Ala Pro Pro Leu Ala Leu Ala Pro Pro Pro Pro Pro Pro His Xaa
1          5          10          15
Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro Xaa
20          25          30
Xaa Xaa Cys Thr Ala Ala Gly Thr Gly Gly Thr Glu Arg Trp Gly Xaa
35          40          45
Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln
50          55          60
Ser Val Tyr Leu Arg Ser Ser Arg Val Cys Cys Cys Pro Ser Val Phe
65          70          75          80
Leu Ile Glu Gly Arg Ser Val Ser Val Val Ser Ala Val Phe Ile Leu
85          90          95
Gly Ser Ser Arg Pro Met His Gln Pro Ala Trp Thr Ala Asp Arg Trp
100         105         110
Val Leu Leu Pro Pro Ser Ala Leu Phe
```

115 120
(2) INFORMATION FOR SEQ ID NO:2654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..194
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:

acccaccccca	tccaaggccc	tcccaaagtc	ccaaaggccg	ccgccgccc	ccagcccacc	60
atggccgcgc	agtccttcct	cctcgccgcc	actgccgccg	ccagtcccc	gcggtcttcg	120
ccgctcccta	ttcctccgca	cgccctttcc	actcggtcca	cttcgtcgcc	ggcccgtggg	180
gcgccgcgcg	cgcc					

(2) INFORMATION FOR SEQ ID NO:2655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:

Thr	His	Pro	Ile	Gln	Gly	Pro	Pro	Lys	Val	Pro	Lys	Ala	Ala	Ala	Ala
1			5					10						15	
Arg	Gln	Pro	Thr	Met	Ala	Ala	Gln	Ser	Phe	Leu	Leu	Ala	Ala	Thr	Ala
			20					25						30	
Ala	Ala	Ser	Pro	Pro	Arg	Ser	Ser	Pro	Leu	Pro	Ile	Pro	Pro	His	Ala
			35				40					45			
Leu	Ser	Thr	Arg	Ser	Thr	Ser	Ser	Pro	Ala	Arg	Gly	Ala	Pro	Pro	Pro
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:2656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:

Pro	Thr	Pro	Ser	Lys	Ala	Leu	Pro	Lys	Ser	Gln	Arg	Pro	Pro	Pro	Pro
1			5					10						15	
Ala	Ser	Pro	Pro	Trp	Pro	Arg	Ser	Pro	Ser	Ser	Ser	Pro	Pro	Leu	Pro
			20					25						30	
Pro	Pro	Val	Pro	Arg	Gly	Leu	Arg	Arg	Ser	Leu	Phe	Leu	Arg	Thr	Pro
			35				40					45			
Phe	Pro	Leu	Gly	Pro	Leu	Arg	Arg	Arg	Pro	Val	Gly	Arg	Arg	Arg	Arg
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

Pro	Pro	His	Pro	Arg	Pro	Ser	Gln	Ser	Pro	Lys	Gly	Arg	Arg	Arg	Pro	
1				5					10					15		
Pro	Ala	His	His	Gly	Arg	Ala	Val	Leu	Pro	Pro	Arg	Arg	His	Cys	Arg	
			20					25					30			
Arg	Gln	Ser	Pro	Ala	Val	Phe	Ala	Ala	Pro	Tyr	Ser	Ser	Ala	Arg	Pro	
		35					40					45				
Phe	His	Ser	Val	His	Phe	Val	Ala	Gly	Pro	Trp	Gly	Ala	Ala	Ala	Ala	
	50					55					60					

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:

tagcaaaata	tggtttaagt	gatgatacag	tggatttcat	tggacatgca	cttgctcttc	60
atagagatga	tcgctatctt	gatgaaccgg	cacttgatac	agtgaaaagg	atgaaactat	120
attcagagtc	tcttgcgcg	tttcaaggag	gctcgccata	tatctatcca	wtgtatggtc	180
ygggt						

(2) INFORMATION FOR SEQ ID NO:2659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:

Ala	Lys	Tyr	Gly	Leu	Ser	Asp	Asp	Thr	Val	Asp	Phe	Ile	Gly	His	Ala	
1				5				10					15			
Leu	Ala	Leu	His	Arg	Asp	Asp	Arg	Tyr	Leu	Asp	Glu	Pro	Ala	Leu	Asp	
			20				25				30					
Thr	Val	Lys	Arg	Met	Lys	Leu	Tyr	Ser	Glu	Ser	Leu	Ala	Arg	Phe	Gln	
		35				40					45					
Gly	Gly	Ser	Pro	Tyr	Ile	Tyr	Pro	Xaa	Tyr	Gly	Xaa	Gly				
	50					55					60					

(2) INFORMATION FOR SEQ ID NO:2660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..509
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:

caattccaat	cccaatccca	ccagtgtcca	gtgctcgggg	aacgacacag	ctcctcagca	60
gagaagccag	cacgacaagc	ccgatcagca	gacagcaggc	atggcgctcg	cggaggccga	120
cgacggcgcg	gtggtcttcg	gcgaggagca	ggaggcgctg	gtgctcaagt	cgtgggccgt	180
catgaagaag	gacgccgcca	acctgggcct	ccgcttcttc	ctcaaggtct	tcgagatcgc	240
gccgtcggaa	gcagatgttc	tcgttcctgc	gcgactccga	cgtgccgctg	gagaagaacc	300
ccaagctcaa	gacgcacgcc	atgtccgtct	tcgtcatgac	ctgcgaggcg	gcggcgcast	360
tccgcaaggc	cgggaaggtc	accgtgagga	gaccacgctc	aagaggctgg	gcgccacgca	420
cttgaggtac	ggcgctcgag	atggacactt	cgagggtgacg	gggttcgcgc	tgcttgagac	480
gatcaaggag	gcgctccccg	ctgacatgt				

(2) INFORMATION FOR SEQ ID NO:2661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:

Gln	Phe	Gln	Ser	Gln	Ser	His	Gln	Cys	Pro	Val	Leu	Gly	Glu	Arg	His
1			5						10				15		
Ser	Ser	Ser	Ala	Glu	Lys	Pro	Ala	Arg	Gln	Ala	Arg	Ser	Ala	Asp	Ser
			20					25					30		
Arg	His	Gly	Ala	Arg	Gly	Gly	Arg	Arg	Arg	Arg	Gly	Gly	Leu	Arg	Arg
		35					40					45			
Gly	Ala	Gly	Gly	Ala	Gly	Ala	Gln	Val	Val	Gly	Arg	His	Glu	Glu	Gly
	50					55				60					
Arg	Arg	Gln	Pro	Gly	Pro	Pro	Leu	Leu	Pro	Gln	Gly	Leu	Arg	Asp	Arg
65					70					75				80	
Ala	Val	Gly	Ser	Arg	Cys	Ser	Arg	Ser	Cys	Ala	Thr	Pro	Thr	Cys	Arg
			85						90					95	
Trp	Arg	Arg	Thr	Pro	Ser	Ser	Arg	Arg	Thr	Pro	Cys	Pro	Ser	Ser	Ser
			100						105					110	

(2) INFORMATION FOR SEQ ID NO:2662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..169
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

Asn	Ser	Asn	Pro	Asn	Pro	Thr	Ser	Val	Gln	Cys	Ser	Gly	Asn	Asp	Thr
1			5						10				15		
Ala	Pro	Gln	Gln	Arg	Ser	Gln	His	Asp	Lys	Pro	Asp	Gln	Gln	Thr	Ala

	20		25		30
Gly Met Ala	Leu Ala Glu Ala Asp	Gly Ala Val Val Phe	Gly Glu		
35	40	45			
Glu Gln Glu	Ala Leu Val Leu Lys Ser Trp	Ala Val Met Lys Lys Asp			
50	55	60			
Ala Ala Asn	Leu Gly Leu Arg Phe Phe Leu Lys	Val Phe Glu Ile Ala			
65	70	75			80
Pro Ser Glu	Ala Asp Val Leu Val Pro Ala Arg	Leu Arg Arg Ala Ala			
	85	90			95
Gly Glu Glu	Pro Gln Ala Gln Asp Ala Arg His	Val Arg Leu Arg His			
	100	105			110
Asp Leu Arg	Gly Gly Gly Ala Xaa Pro Gln Gly Arg	Glu Gly His Arg			
	115	120			125
Glu Glu Thr	Thr Leu Lys Arg Leu Gly Ala Thr His	Leu Arg Tyr Gly			
	130	135			140
Val Ala Asp	Gly His Phe Glu Val Thr Gly Phe Ala	Leu Leu Glu Thr			
145	150	155			160
Ile Lys Glu	Ala Leu Pro Ala Asp Met				
	165				

(2) INFORMATION FOR SEQ ID NO:2663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

Met Ala Leu	Ala Glu Ala Asp Asp	Gly Ala Val Val Phe	Gly Glu Glu
1	5	10	15
Gln Glu Ala	Leu Val Leu Lys Ser Trp	Ala Val Met Lys Lys Asp	Ala
	20	25	30
Ala Asn Leu	Gly Leu Arg Phe Phe Leu Lys	Val Phe Glu Ile Ala Pro	
	35	40	45
Ser Glu Ala	Asp Val Leu Val Pro Ala Arg	Leu Arg Arg Ala Ala Gly	
	50	55	60
Glu Glu Pro	Gln Ala Gln Asp Ala Arg His	Val Arg Leu Arg His Asp	
65	70	75	80
Leu Arg Gly	Gly Gly Ala Xaa Pro Gln Gly	Arg Glu Gly His Arg Glu	
	85	90	95
Glu Thr Thr	Leu Lys Arg Leu Gly Ala Thr His	Leu Arg Tyr Gly Val	
	100	105	110
Ala Asp Gly	His Phe Glu Val Thr Gly Phe Ala	Leu Leu Glu Thr Ile	
	115	120	125
Lys Glu Ala	Leu Pro Ala Asp Met		
130	135		

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

```
ttagcatgcc tacaattggt catcgagatc tgaaatctcc aaacttgctg gttgacaata      60
attggaatgt taaggtttgt gactttggac tttcgcggtt gaagcacagt acatttttgt      120
catccaaatc tacagctggw acacctgagt ggatggcacc tgaggttctg cggaatgaac      180
aatcgaatga aaagtgtgat gtttatagct ttggtgtcat cttatgggaa ctggcaacac      240
ttagaatgcc atggagtggg atgaatccaa tgcaagttgt gggggcagtt ggtttccagg      300
atagacggct tgatattccc aaggaagttg atcctctggt cgcaaggata atatttgaat      360
gctggcagaa ggatccaaat ttgcgcccggt catttgcaca gttaacaagt gccctgaaga      420
ctgttcaaag actagtgacc ctttgtcacc aggagaacca gagcccatg ttcaacaaga      480
aatctcagtg c
```

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1504185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

```
Ser Met Pro Thr Ile Val His Arg Asp Leu Lys Ser Pro Asn Leu Leu
1           5           10           15
Val Asp Asn Asn Trp Asn Val Lys Val Cys Asp Phe Gly Leu Ser Arg
          20          25          30
Leu Lys His Ser Thr Phe Leu Ser Ser Lys Ser Thr Ala Xaa Thr Pro
          35          40          45
Glu Trp Met Ala Pro Glu Val Leu Arg Asn Glu Gln Ser Asn Glu Lys
          50          55          60
Cys Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu Leu Ala Thr Leu
          65          70          75          80
Arg Met Pro Trp Ser Gly Met Asn Pro Met Gln Val Val Gly Ala Val
          85          90          95
Gly Phe Gln Asp Arg Arg Leu Asp Ile Pro Lys Glu Val Asp Pro Leu
          100         105         110
Val Ala Arg Ile Ile Phe Glu Cys Trp Gln Lys Asp Pro Asn Leu Arg
          115         120         125
Pro Ser Phe Ala Gln Leu Thr Ser Ala Leu Lys Thr Val Gln Arg Leu
          130         135         140
Val Thr Leu Cys His Gln Glu Asn Gln Ser Pro Met Phe Asn Lys Lys
          145         150         155         160
Ser Gln Cys
```

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1504186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

```
Met Pro Thr Ile Val His Arg Asp Leu Lys Ser Pro Asn Leu Leu Val
1           5           10           15
Asp Asn Asn Trp Asn Val Lys Val Cys Asp Phe Gly Leu Ser Arg Leu
          20          25          30
Lys His Ser Thr Phe Leu Ser Ser Lys Ser Thr Ala Xaa Thr Pro Glu
          35          40          45
```

Trp Met Ala Pro Glu Val Leu Arg Asn Glu Gln Ser Asn Glu Lys Cys
50 55 60
Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu Leu Ala Thr Leu Arg
65 70 75 80
Met Pro Trp Ser Gly Met Asn Pro Met Gln Val Val Gly Ala Val Gly
85 90 95
Phe Gln Asp Arg Arg Leu Asp Ile Pro Lys Glu Val Asp Pro Leu Val
100 105 110
Ala Arg Ile Ile Phe Glu Cys Trp Gln Lys Asp Pro Asn Leu Arg Pro
115 120 125
Ser Phe Ala Gln Leu Thr Ser Ala Leu Lys Thr Val Gln Arg Leu Val
130 135 140
Thr Leu Cys His Gln Glu Asn Gln Ser Pro Met Phe Asn Lys Lys Ser
145 150 155 160
Gln Cys

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1504187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Met Ala Pro Glu Val Leu Arg Asn Glu Lys Cys Asp
1 5 10 15
Val Tyr Ser Phe Gly Val Ile Leu Trp Glu Leu Ala Thr Leu Arg Met
20 25 30
Pro Trp Ser Gly Met Asn Pro Met Gln Val Val Gly Ala Val Gly Phe
35 40 45
Gln Asp Arg Arg Leu Asp Ile Pro Lys Glu Val Asp Pro Leu Val Ala
50 55 60
Arg Ile Ile Phe Glu Cys Trp Gln Lys Asp Pro Asn Leu Arg Pro Ser
65 70 75 80
Phe Ala Gln Leu Thr Ser Ala Leu Lys Thr Val Gln Arg Leu Val Thr
85 90 95
Leu Cys His Gln Glu Asn Gln Ser Pro Met Phe Asn Lys Lys Ser Gln
100 105 110
Cys

(2) INFORMATION FOR SEQ ID NO:2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1504192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

aaagctggag tgaatccagc aggctgcttc tgaaaaaaaaa agtagcagat gcaacgagt	60
cactccaatg ctgcagttac aatgcaatga cggggtttgt tagtgagcta gcacgcgtcg	120
sggctcctgg agggacaata atcatcgtga catggtgcc a taggaacctg gatccatccg	180
aaacctcgct aaagcccgat gaactgagcc tcttgaggag gatatgcgac gcgtactacc	240
tcccggactg gtgctcacc tcaactatg tgaacattgc caagtcactg tctctcgagg	300

```
atatcaagac agctgactgg tcggagaacg tggccccgtt ttggcccgcc gtgataaaat 360
cagcgctaac atggaagggc ttcacctctc tgctgacgac cggatggaag acgatcagag 420
gcgcgatggt gatgccgcta atgatccagg gctacaagaa ggggctcatc aaattcacca 480
tc
```

(2) INFORMATION FOR SEQ ID NO:2669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

```
Ser Trp Ser Glu Ser Ser Arg Leu Leu Lys Lys Lys Val Ala Asp
1          5          10          15
Ala Thr Ser Ala Leu Gln Cys Cys Ser Tyr Asn Ala Met Thr Gly Phe
20          25          30
Val Ser Glu Leu Ala Arg Val Xaa Ala Pro Gly Gly Thr Ile Ile Ile
35          40          45
Val Thr Trp Cys His Arg Asn Leu Asp Pro Ser Glu Thr Ser Leu Lys
50          55          60
Pro Asp Glu Leu Ser Leu Leu Arg Arg Ile Cys Asp Ala Tyr Tyr Leu
65          70          75          80
Pro Asp Trp Cys Ser Pro Ser Asp Tyr Val Asn Ile Ala Lys Ser Leu
85          90          95
Ser Leu Glu Asp Ile Lys Thr Ala Asp Trp Ser Glu Asn Val Ala Pro
100         105         110
Phe Trp Pro Ala Val Ile Lys Ser Ala Leu Thr Trp Lys Gly Phe Thr
115         120         125
Ser Leu Leu Thr Thr Gly Trp Lys Thr Ile Arg Gly Ala Met Val Met
130         135         140
Pro Leu Met Ile Gln Gly Tyr Lys Lys Gly Leu Ile Lys Phe Thr Ile
145         150         155         160
```

(2) INFORMATION FOR SEQ ID NO:2670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

```
Met Thr Gly Phe Val Ser Glu Leu Ala Arg Val Xaa Ala Pro Gly Gly
1          5          10          15
Thr Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Asp Pro Ser Glu
20          25          30
Thr Ser Leu Lys Pro Asp Glu Leu Ser Leu Leu Arg Arg Ile Cys Asp
35          40          45
Ala Tyr Tyr Leu Pro Asp Trp Cys Ser Pro Ser Asp Tyr Val Asn Ile
50          55          60
Ala Lys Ser Leu Ser Leu Glu Asp Ile Lys Thr Ala Asp Trp Ser Glu
65          70          75          80
Asn Val Ala Pro Phe Trp Pro Ala Val Ile Lys Ser Ala Leu Thr Trp
```

85 90 95
Lys Gly Phe Thr Ser Leu Leu Thr Thr Gly Trp Lys Thr Ile Arg Gly
100 105 110
Ala Met Val Met Pro Leu Met Ile Gln Gly Tyr Lys Lys Gly Leu Ile
115 120 125
Lys Phe Thr Ile
130

(2) INFORMATION FOR SEQ ID NO:2671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

agcggttaga	gagagagaag	acagggagaa	ggaggaagag	ccgccgcgnt	ggaccgggtg	60
atttgtcagg	gttgtcaggg	gagtcgtcag	gacacgggca	agctttgtac	gctaccaatt	120
cagcgaataa	ccgacggggg	tgcgtggaat	tgctcaccgg	agcaaaccct	ccgccgccga	180
accaccatcc	ttctgagcag	cgcacgctag	cgtcccggtt	ctggacgcac	gccgtgaact	240
cgaagtccac	cgctctgtga	gcatcaagcg	ccggcatcgc	tagggtttca	cgcctccatc	300
cccccagggc	gccgtcgatc	ccggtcggcc	atctcccggg	gcctggtaac	tgatcggtta	360
tttcatcgat	gggtgccatg	gaggaccgca	gctccaagca	ggcagggcgc	ggcttggtgg	420
cccacctcca	cgacgacctc	cttgtggaga	tcctctcccc	cgtccccgcc	aagtccgtct	480
gccggttcaa	gtgcgtgtcc	aaggcctggc	t			

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

Arg	Leu	Glu	Arg	Glu	Lys	Thr	Gly	Arg	Arg	Arg	Lys	Ser	Arg	Arg	Xaa
1				5				10						15	
Gly	Pro	Gly	Asp	Leu	Ser	Gly	Leu	Ser	Gly	Glu	Ser	Ser	Gly	His	Gly
			20					25					30		
Gln	Ala	Leu	Tyr	Ala	Thr	Asn	Ser	Ala	Asn	Asn	Arg	Arg	Gly	Cys	Val
			35				40					45			
Glu	Leu	Leu	Thr	Gly	Ala	Asn	Pro	Pro	Pro	Pro	Asn	His	His	Pro	Ser
			50				55				60				
Glu	Gln	Arg	Thr	Leu	Ala	Ser	Gly	Ser	Trp	Thr	His	Ala	Val	Asn	Ser
65						70				75				80	
Lys	Ser	Thr	Ala	Leu											

85

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1504203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

Met	Gly	Ala	Met	Glu	Asp	Arg	Ser	Ser	Lys	Gln	Ala	Gly	Ala	Gly	Leu
1			5						10					15	
Val	Ala	His	Leu	His	Asp	Asp	Leu	Leu	Val	Glu	Ile	Leu	Ser	Arg	Val
			20					25					30		
Pro	Ala	Lys	Ser	Val	Cys	Arg	Phe	Lys	Cys	Val	Ser	Lys	Ala	Trp	
			35					40					45		

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1504204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

Met	Glu	Asp	Arg	Ser	Ser	Lys	Gln	Ala	Gly	Ala	Gly	Leu	Val	Ala	His
1				5					10					15	
Leu	His	Asp	Asp	Leu	Leu	Val	Glu	Ile	Leu	Ser	Arg	Val	Pro	Ala	Lys
				20				25					30		
Ser	Val	Cys	Arg	Phe	Lys	Cys	Val	Ser	Lys	Ala	Trp				
				35				40							

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..436

(D) OTHER INFORMATION: / Ceres Seq. ID 1504231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

cattgtcaat	ttctcccagg	ataaatcatg	gcgtgttcgt	tatatgggtcg	ccaatcagtt	60
atatgagctc	tgtgaggctg	ttggccctga	gccacaaga	gctgatttgg	tgctgcata	120
tgttcgtctc	cttcgcgata	atgaggctga	agtgcggaata	gcggctgctg	gaaaagtaac	180
taagttctgc	cgcataattaa	atccacagct	ttcaatccaa	catattcttc	cgtgcgttaa	240
ggaattgtca	tcatattcat	cccagcatgt	tcgttcagct	ttagcctcag	tcattatggg	300
aatggctcct	gtactgggaa	aggatgctac	catggaacag	cttcttccaa	tttttctctc	360
tttgctgaag	gatgaatttc	cagatgttcg	gcttaacata	atcagcaagc	ttgatcaggt	420
taatcaggtt	attggc					

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1504232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Ile	Val	Asn	Phe	Ser	Gln	Asp	Lys	Ser	Trp	Arg	Val	Arg	Tyr	Met	Val
1				5					10					15	

Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu Pro Thr
20 25 30
Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp Asn Glu
35 40 45
Ala Glu Val Arg Ile Ala Ala Ala Gly Lys Val Thr Lys Phe Cys Arg
50 55 60
Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys Val Lys
65 70 75 80
Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu Ala Ser
85 90 95
Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr Met Glu
100 105 110
Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe Pro Asp
115 120 125
Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln Val Ile
130 135 140
Gly
145

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met Val Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu
1 5 10 15
Pro Thr Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp
20 25 30
Asn Glu Ala Glu Val Arg Ile Ala Ala Ala Gly Lys Val Thr Lys Phe
35 40 45
Cys Arg Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys
50 55 60
Val Lys Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu
65 70 75 80
Ala Ser Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr
85 90 95
Met Glu Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe
100 105 110
Pro Asp Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln
115 120 125
Val Ile Gly
130

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

cgatcctttt atccgtaact atattgagga cttattgaag aacatcagaa cccaagtgc

gctcaagctt attaaacccat atactcgaat caggatacca ttcatattcac aggaactcaa	120
ttttccagaa aaggatgtcg agcagctgtt ggtgtcactc attctggaca accgtatcca	180
aggccacata gatcaggtta acaagctgct agaacgtgga gaaaggcca aggggatgag	240
gaagtacaat gctatcgaca agtgaatac tcagctgaag tccatttacc aaacattgtc	300
caacagagtt tgatgaggag gatcgctgct gctgctgcgt gcattgcaca cctagaattg	360
ttgatagcct gttttgtgga tttgagggca actgcaaaga actgtctggt gacgcttgcg	420
atagaatcct ggatctgggt aaagtt	

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1504240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Asp	Pro	Phe	Ile	Arg	Asn	Tyr	Ile	Glu	Asp	Leu	Leu	Lys	Asn	Ile	Arg
1					5					10				15	
Thr	Gln	Val	Leu	Leu	Lys	Leu	Ile	Lys	Pro	Tyr	Thr	Arg	Ile	Arg	Ile
			20					25					30		
Pro	Phe	Ile	Ser	Gln	Glu	Leu	Asn	Phe	Pro	Glu	Lys	Asp	Val	Glu	Gln
			35				40					45			
Leu	Leu	Val	Ser	Leu	Ile	Leu	Asp	Asn	Arg	Ile	Gln	Gly	His	Ile	Asp
			50				55				60				
Gln	Val	Asn	Lys	Leu	Leu	Glu	Arg	Gly	Glu	Arg	Ser	Lys	Gly	Met	Arg
			65			70				75				80	
Lys	Tyr	Asn	Ala	Ile	Asp	Lys	Trp	Asn	Thr	Gln	Leu	Lys	Ser	Ile	Tyr
			85					90						95	
Gln	Thr	Leu	Ser	Asn	Arg	Val									
						100									

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1504254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

gtttttctctt gatcgctttg tcacttgaat ccgtgcctgc tctaacagag agcggagacg	60
accacgacga cggcgaggcc aggtcttgcg atggagcagg agccgcaccg gcccatggag	120
ctgcccccg gcttccgctt ccaccgcacc gacgaggagn tcatcacgca ctacctggcc	180
cgcaaggcgc cgacgcccgc ttgcgcgcgc ttgccgtcgc cgaggccgac ctcaacaagt	240
gcgagccctg ggacctgcca tcgctggcga ggatggggga gaaggagtgg tacttcttct	300
gcctcaagga ccgcaagtac ccgacg	

(2) INFORMATION FOR SEQ ID NO:2681:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1504255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

```
Phe Leu Leu Ile Ala Leu Ser Leu Glu Ser Val Pro Ala Leu Thr Glu
1           5           10           15
Ser Gly Asp Asp His Asp Asp Gly Glu Ala Arg Leu Cys Asp Gly Ala
20           25           30
Gly Ala Ala Pro Ala His Gly Ala Ala Pro Gly Leu Pro Leu Pro Pro
35           40           45
Asp Arg Arg Gly Xaa His His Ala Leu Pro Gly Pro Gln Gly Ala Asp
50           55           60
Ala Arg Phe Ala Ala Leu Ala Val Ala Glu Ala Asp Leu Asn Lys Cys
65           70           75           80
Glu Pro Trp Asp Leu Pro Ser Leu Ala Arg Met Gly Glu Lys Glu Trp
85           90           95
Tyr Phe Phe Cys Leu Lys Asp Arg Lys Tyr Pro Thr
100          105
```

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1504256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

```
Met Glu Gln Glu Pro His Arg Pro Met Glu Leu Pro Pro Gly Phe Arg
1           5           10           15
Phe His Pro Thr Asp Glu Glu Xaa Ile Thr His Tyr Leu Ala Arg Lys
20           25           30
Ala Pro Thr Pro Ala Ser Pro Arg Leu Pro Ser Pro Arg Pro Thr Ser
35           40           45
Thr Ser Ala Ser Pro Gly Thr Cys His Arg Trp Arg Gly Trp Gly Arg
50           55           60
Arg Ser Gly Thr Ser Ser Ala Ser Arg Thr Ala Ser Thr Arg
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1504257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

```
Met Glu Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Xaa
1           5           10           15
Ile Thr His Tyr Leu Ala Arg Lys Ala Pro Thr Pro Ala Ser Pro Arg
20           25           30
Leu Pro Ser Pro Arg Pro Thr Ser Thr Ser Ala Ser Pro Gly Thr Cys
35           40           45
His Arg Trp Arg Gly Trp Gly Arg Arg Ser Gly Thr Ser Ser Ala Ser
50           55           60
Arg Thr Ala Ser Thr Arg
65           70
```

(2) INFORMATION FOR SEQ ID NO:2684:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..307
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

aattccccctc	cctgtcgtc	gtctcccctc	acccgaagcc	ccgdttcgaa	accggcggcg	60
ttcgatttgg	ggatttcggc	gtctcgctcc	ccggaatttc	ttggatctga	gtctgtccgc	120
cgtcttcgat	ttgcggctgc	agtgagcctg	cgagttttcc	ggctctgatt	tggwcggggh	180
cttcgatttc	gggatggcg	tcgtctccgg	tgtcctactg	gtgctacagc	tgcagccgct	240
tcgtgagggt	atctccgtcc	accgtygtct	gcccgagtg	cgatggcggc	ttcctggagc	300
agtttac						

- (2) INFORMATION FOR SEQ ID NO:2685:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..55
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504259
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:

Asn	Ser	Pro	Pro	Leu	Ser	Ser	Ser	Pro	Leu	Thr	Arg	Ser	Pro	Xaa	Ser
1				5					10					15	
Lys	Pro	Ala	Ala	Phe	Asp	Leu	Gly	Ile	Ser	Ala	Ser	Arg	Ser	Pro	Glu
				20				25					30		
Phe	Leu	Gly	Ser	Glu	Ser	Val	Arg	Arg	Leu	Arg	Phe	Ala	Ala	Ala	Val
				35				40				45			
Ser	Leu	Arg	Val	Phe	Arg	Leu									
				50				55							

- (2) INFORMATION FOR SEQ ID NO:2686:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..47
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504260
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:

Ile	Pro	Leu	Pro	Cys	Arg	Arg	Leu	Pro	Ser	Pro	Glu	Ala	Pro	Xaa	Arg
1				5					10					15	
Asn	Arg	Arg	Arg	Ser	Ile	Trp	Gly	Phe	Arg	Arg	Leu	Ala	Pro	Arg	Asn
				20				25					30		
Phe	Leu	Asp	Leu	Ser	Leu	Ser	Ala	Val	Phe	Asp	Leu	Arg	Leu	Gln	
				35				40				45			

- (2) INFORMATION FOR SEQ ID NO:2687:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..37
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504261
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:
Met Ala Ser Ser Pro Val Ser Tyr Trp Cys Tyr Ser Cys Ser Arg Phe
1 5 10 15
Val Arg Val Ser Pro Ser Thr Xaa Val Cys Pro Glu Cys Asp Gly Gly
 20 25 30
Phe Leu Glu Gln Phe
 35

(2) INFORMATION FOR SEQ ID NO:2688:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..234
(D) OTHER INFORMATION: / Ceres Seq. ID 1504270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

actcgcgtcg sccccctcca ctgcaccagc gtcattggcgg tggcctcgac ctgcgcgctg 60
tccgccaagc ccgccacggc cccctcgccg ccgctcccg gatccgggct cctcgctctc 120
ggcggttcgcs cggccccgc cactgccgcy tggaggaggc tccgcgtgga ggcgatcagg 180
acgcagcggg agaagcagcg ggcggaggtg cccgtcgagg agtccgcccc cgcc

(2) INFORMATION FOR SEQ ID NO:2689:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..78
(D) OTHER INFORMATION: / Ceres Seq. ID 1504271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

Thr Arg Val Xaa Pro Leu His Cys Thr Ser Val Met Ala Val Ala Ser
1 5 10 15
Thr Ser Pro Leu Ser Ala Lys Pro Ala Thr Ala Pro Ser Pro Pro Ala
 20 25 30
Pro Gly Ser Gly Leu Leu Ala Leu Gly Val Arg Xaa Ala Pro Ala Thr
 35 40 45
Ala Ala Trp Arg Arg Leu Arg Val Glu Ala Ile Arg Thr Gln Arg Glu
 50 55 60
Lys Gln Arg Ala Glu Val Pro Val Glu Glu Ser Ala Pro Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1504272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Leu Ala Ser Xaa Pro Ser Thr Ala Pro Ala Ser Trp Arg Trp Pro Arg
1 5 10 15
Pro Arg Arg Cys Pro Pro Ser Pro Pro Arg Pro Pro Arg Arg Pro Leu
20 25 30
Pro Asp Pro Gly Ser Ser Leu Ser Ala Phe Xaa Arg Pro Pro Pro Leu
35 40 45
Pro Arg Gly Gly Gly Ser Ala Trp Arg Arg Ser Gly Arg Ser Gly Arg
50 55 60
Ser Ser Gly Arg Arg Cys Pro Ser Arg Ser Pro Pro Pro
65 70 75

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

Ser Arg Xaa Xaa Pro Pro Leu His Gln Arg His Gly Gly Gly Leu Asp
1 5 10 15
Leu Ala Ala Val Arg Gln Ala Arg His Gly Pro Leu Ala Ala Arg Ser
20 25 30
Arg Ile Arg Ala Pro Arg Ser Arg Arg Ser Xaa Gly Pro Arg His Cys
35 40 45
Arg Val Glu Glu Ala Pro Arg Gly Gly Asp Gln Asp Ala Ala Gly Glu
50 55 60
Ala Ala Gly Gly Gly Ala Arg Arg Gly Val Arg Pro Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1504274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

agtcggagca gggcaggggt tgcgtctcag ttcctggttg tggtgttgta agctcacagg	60
tttcttctct tcgcgtgass tagctagagt gggatcgaga ggaagaagga tgcgtgctg	120
cggaggcaac tgcgggtgcg gcasggantg caagtgcggc assggctgcg gagggtgcaa	180
gatgtacccg gacatggttg agcaggtgac caccaccacc accaccaga ctctcatcat	240
gggtgttgcg ccatccacgg gccaccgctg tgctcccttc ggcagccagg atgacagaag	300
taccatttct gccgcgtgag aggctcttca agcagcaaca ttacttccag aacttgacca	360
agcacaccta cctgaaaggc gctacgacgt gatcacctcc gtcgccatcc cccttgcact	420
cgctgcctc	

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1504275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:

```
Val Gly Ala Gly Gln Gly Leu Arg Leu Ser Ser Trp Leu Cys Cys Cys
1          5          10          15
Lys Leu Thr Gly Phe Phe Ser Ser Arg Xaa Xaa Ala Arg Val Gly Ser
20          25          30
Arg Gly Arg Arg Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa
35          40          45
Xaa Cys Lys Cys Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp
50          55          60
Met Val Glu Gln Val Thr Thr Thr Thr Thr Gln Thr Leu Ile Met
65          70          75          80
Gly Val Ala Pro Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln
85          90          95
Asp Asp Arg Ser Thr Ile Ser Ala Ala
100          105
```

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1504276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

```
Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa Xaa Cys Lys Cys
1          5          10          15
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Val Glu Gln
20          25          30
Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Val Ala Pro
35          40          45
Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln Asp Asp Arg Ser
50          55          60
Thr Ile Ser Ala Ala
65
```

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1504277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

```
agttgatccc atcggttcc ctttctctt ccccgatccc ctctctcccc cgatcccatc      60
caattccact tccacacccc ggccctcgcc gccgacgccg acgccgacgc cgccggccat      120
gtccaagtac ggcaccattc ccacctctc ctccgcgggc ggagggcccg tgcccctcgg      180
cggcgctccc cgctcgattt catctcccgc gccaaaggctc ggggcgcctc ggcstgggcg      240
acgc
```

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..81
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:

Val Asp Pro Ile Gly Phe Pro Phe Leu Phe Pro Asp Pro Leu Pro Pro
1 5 10 15
Pro Ile Pro Ser Asn Ser Thr Ser Thr Pro Arg Ala Ser Pro Pro Thr
20 25 30
Pro Thr Pro Thr Pro Pro Ala Met Ser Lys Tyr Gly Thr Ile Pro Thr
35 40 45
Ser Ser Ser Ala Gly Gly Gly Pro Val Pro Leu Gly Gly Ala Pro Arg
50 55 60
Ser Ile Ser Ser Pro Ala Pro Arg Leu Gly Ala Pro Arg Xaa Gly Arg
65 70 75 80
Arg

- (2) INFORMATION FOR SEQ ID NO:2697:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..80
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504279
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

Leu Ile Pro Ser Ala Ser Pro Ser Ser Ser Pro Ile Pro Phe Leu Pro
1 5 10 15
Arg Ser His Pro Ile Pro Leu Pro His Pro Gly Pro Arg Arg Arg Arg
20 25 30
Arg Arg Arg Arg Arg Arg Pro Cys Pro Ser Thr Ala Pro Phe Pro Pro
35 40 45
Pro Pro Pro Arg Ala Glu Gly Pro Cys Pro Ser Ala Ala Leu Pro Ala
50 55 60
Arg Phe His Leu Pro Arg Gln Gly Ser Gly Arg Leu Gly Xaa Gly Asp
65 70 75 80

- (2) INFORMATION FOR SEQ ID NO:2698:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..42
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504280
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

Met Ser Lys Tyr Gly Thr Ile Pro Thr Ser Ser Ser Ala Gly Gly Gly
1 5 10 15
Pro Val Pro Leu Gly Gly Ala Pro Arg Ser Ile Ser Ser Pro Ala Pro
20 25 30
Arg Leu Gly Ala Pro Arg Xaa Gly Arg Arg

35 40
(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

```
cctgatttcc tgaacacag atcatcatca ttcatggtca tggctatggc aaactcggca 60
acgatacctga ccgtcgttct ggctctcggg ctacggttcc tccgcgccgc agctccggcc 120
tccgcgcaga actgcggctg cccgccaggc tactgctgca gcaagttcgg ttactcgggc 180
accagcttcg actactgcaa tgccaacacg tgccagtccg gcccgtgcac g
```

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

```
Pro Asp Phe Leu Lys His Arg Ser Ser Phe Met Val Met Ala Met
1           5           10           15
Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu Ala Leu Gly Leu Ala
20           25           30
Phe Leu Arg Ala Ala Ala Pro Ala Ser Ala Gln Asn Cys Gly Cys Pro
35           40           45
Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys Gly Thr Ser Phe Asp
50           55           60
Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro Cys Thr
65           70           75
```

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

```
Met Val Met Ala Met Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu
1           5           10           15
Ala Leu Gly Leu Ala Phe Leu Arg Ala Ala Ala Pro Ala Ser Ala Gln
20           25           30
Asn Cys Gly Cys Pro Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys
35           40           45
Gly Thr Ser Phe Asp Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro
50           55           60
Cys Thr
65
```


(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

Met	Ala	Met	Ala	Asn	Ser	Ala	Thr	Ile	Leu	Thr	Val	Val	Leu	Ala	Leu
1				5					10					15	
Gly	Leu	Ala	Phe	Leu	Arg	Ala	Ala	Ala	Pro	Ala	Ser	Ala	Gln	Asn	Cys
			20					25					30		
Gly	Cys	Pro	Pro	Gly	Tyr	Cys	Cys	Ser	Lys	Phe	Gly	Tyr	Cys	Gly	Thr
			35				40					45			
Ser	Phe	Asp	Tyr	Cys	Asn	Ala	Asn	Thr	Cys	Gln	Ser	Gly	Pro	Cys	Thr
			50				55					60			

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

tacaaggcta	tttatgat	at tccagcaata	aaagaggatc	caacaaagt	gataccgatt	60
cttaggaaga	tctgttggt	cttgggtgcta	gcacctcatg	atcctatgca	atcaagcctt	120
ctcaatgcta	cactagagga	taaaaacctt	tcagaaatcc	caaatttcag	gttattactg	180
aagcagctgg	tcaccatgga	ggtgatacag	tggaacaagt	tgtgggaatt	cttcaaggag	240
gaatatgaga	aggagaagga	tcttcttggg	ggagctttgg	gtgccaaagc	ttcagaagat	300
ttgaggctga	ggattatcga	acataatatc	ttggttgtat	ccaagtacta	tgcaagggtt	360
accctcaaga	ggcttgccga	tcttctttgc	ctgactttgc	aggaggcaga	gaagcatctc	420
tcagacatgg	ttaactcgaa	atctctagt	gc			

(2) INFORMATION FOR SEQ ID NO:2704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

Tyr	Lys	Ala	Ile	Tyr	Asp	Ile	Pro	Ala	Ile	Lys	Glu	Asp	Pro	Thr	Lys
1				5					10					15	
Trp	Ile	Pro	Ile	Leu	Arg	Lys	Ile	Cys	Trp	Tyr	Leu	Val	Leu	Ala	Pro
			20					25					30		
His	Asp	Pro	Met	Gln	Ser	Ser	Leu	Leu	Asn	Ala	Thr	Leu	Glu	Asp	Lys
			35				40					45			
Asn	Leu	Ser	Glu	Ile	Pro	Asn	Phe	Arg	Leu	Leu	Leu	Lys	Gln	Leu	Val

50 55 60
Thr Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu
65 70 75 80
Glu Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys
85 90 95
Ala Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val
100 105 110
Val Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu
115 120 125
Leu Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val
130 135 140
Asn Ser Lys Ser Leu Val
145 150

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Met Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser
1 5 10 15
Glu Ile Pro Asn Phe Arg Leu Leu Leu Lys Gln Leu Val Thr Met Glu
20 25 30
Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu Tyr Glu
35 40 45
Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala Ser Glu
50 55 60
Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys
65 70 75 80
Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu Cys Leu
85 90 95
Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn Ser Lys
100 105 110
Ser Leu Val
115

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu
1 5 10 15
Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala
20 25 30
Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val
35 40 45
Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu
50 55 60

Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn
65 70 75 80
Ser Lys Ser Leu Val
85

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

ctccccggctc agactttctgc tgcagcgcct ccgycgccgc cgccgcatct aacgcaktcc	60
ctccgccgca gcccaggca agatggttct ccagaacgac attgatctgc kcaacccgcc	120
ggcagaactc gagaagctca agcacaagaa aaagagactc gtccagtcgc ccaactcctt	180
cttcatggat gttaagtgcc aggggtgctt cagcataacc actgtkttca gccactccca	240
gactgctgnt gkgtnngtca gaagctatgc agcggatagc ggtacattta tcgacagtkt	300
tc	

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Pro Gly Ser Asp Phe Cys Cys Ser Ala Ser Xaa Ala Ala Ala Ser	
1 5 10 15	
Asn Ala Xaa Pro Pro Gln Pro Glu Ala Arg Trp Phe Ser Arg Thr	
20 25 30	
Thr Leu Ile Cys Xaa Thr Arg Arg Gln Asn Ser Arg Ser Ser Ser Thr	
35 40 45	
Arg Lys Arg Asp Ser Ser Ser Arg Pro Thr Pro Ser Ser Trp Met Leu	
50 55 60	
Ser Ala Arg Gly Ala Ser Ala	
65 70	

(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

Met Val Leu Gln Asn Asp Ile Asp Leu Xaa Asn Pro Pro Ala Glu Leu	
1 5 10 15	
Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser	
20 25 30	
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Xaa	

35 40 45
Phe Ser His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala
50 55 60
Asp Thr Gly Thr Phe Ile Asp Ser
65 70

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Xaa Phe Ser
1 5 10 15
His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala Asp Thr
20 25 30
Gly Thr Phe Ile Asp Ser
35

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

accaaggaaa ttcacaaaga gatactagtc cctaccaaag catacttcct gaaacactct 60
tgcaatccac tgagtcctgt ttgttgagac ttgagacgca tagagctagc gtcgacaatg 120
tcgctcgtga ggcgcmssaa cgtgttcgac cccttctcga tggacctctg ggaccccttc 180
gacaccatgt tccgctccat cgtcccgtcg gcggcctcca ccaactccga gaccgccgtc 240
ttcgccage

(2) INFORMATION FOR SEQ ID NO:2712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

Gln Gly Asn Ser Gln Arg Asp Thr Ser Pro Tyr Gln Ser Ile Leu Pro
1 5 10 15
Glu Thr Leu Leu Gln Ser Thr Glu Ser Cys Leu Leu Arg Leu Glu Thr
20 25 30
His Arg Ala Ser Val Asp Asn Val Ala Arg Glu Ala Xaa Xaa Arg Val
35 40 45
Arg Pro Leu Leu Asp Gly Pro Leu Gly Pro Leu Arg His His Val Pro
50 55 60
Leu His Arg Pro Val Gly Gly Leu His Gln Leu Arg Asp Arg Arg Leu

80

(i) SEQUENCE CHARACTERISTICS:

- ```
(
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..44
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504313
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Leu | Val | Arg | Arg | Xaa | Asn | Val | Phe | Asp | Pro | Phe | Ser | Met | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Trp | Asp | Pro | Phe | Asp | Thr | Met | Phe | Arg | Ser | Ile | Val | Pro | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Thr | Asn | Ser | Glu | Thr | Ala | Val | Phe | Ala | Ser |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- ```
(i) (A) LENGTH: 464 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..464
      (D) OTHER INFORMATION: / Ceres Seq. ID 1504333
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:
```

cagaataaag	ataaaaaata	tggaactgga	aattaggcgt	aggaatcaa	caggatcagg	60
ctctaacaa	tatgttgaaa	ctgagactct	tgcaaagttt	gagttgatgg	atggtgctcc	120
tgtgagaggt	gaatctattc	cagtgaggct	gttcctgaca	ccctatgagt	tgaccccgac	180
ttaccgcaac	ataaacaaca	aattcagcgt	caagtattac	ctgaatctgg	tccttgtgga	240
cgaggaagat	cggaggtact	tcaagcagca	agagatcaca	atgtaccgtc	tccaagaatc	300
tccccctgcc	tcctagatcc	caacctgttg	catcatgttc	acttctcagg	ttttgtacaa	360
gtggacgctg	aggttagagc	aatgtcctgt	atataaacta	aaattccagaa	gagcgccaca	420
gctqggttact	qctatggcca	tgcacgctgc	actgtcgtgt	tcat		

(i) SEQUENCE CHARACTERISTICS:

- ```
(v) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504334
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Lys | Ile | Lys | Asn | Met | Glu | Leu | Glu | Ile | Arg | Arg | Arg | Glu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Gly | Ser | Gly | Ser | Asn | Thr | Tyr | Val | Glu | Thr | Glu | Thr | Leu | Ala | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Glu | Leu | Met | Asp | Gly | Ala | Pro | Val | Arg | Gly | Glu | Ser | Ile | Pro | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Phe | Leu | Thr | Pro | Tyr | Glu | Leu | Thr | Pro | Thr | Tyr | Arg | Asn | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Asn Asn Lys Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp  
65 70 75 80  
Glu Glu Asp Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg  
85 90 95  
Leu Gln Glu Ser Pro Pro Ala Ser  
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1504335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Met Glu Leu Glu Ile Arg Arg Arg Glu Ser Thr Gly Ser Gly Ser Asn  
1 5 10 15  
Thr Tyr Val Glu Thr Glu Thr Leu Ala Lys Phe Glu Leu Met Asp Gly  
20 25 30  
Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe Leu Thr Pro  
35 40 45  
Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys Phe Ser Val  
50 55 60  
Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp Arg Arg Tyr  
65 70 75 80  
Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu Ser Pro Pro  
85 90 95  
Ala Ser

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1504336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met Asp Gly Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe  
1 5 10 15  
Leu Thr Pro Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys  
20 25 30  
Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp  
35 40 45  
Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu  
50 55 60  
Ser Pro Pro Ala Ser  
65

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..466

(D) OTHER INFORMATION: / Ceres Seq. ID 1504370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ctactacgcc  | tgcctctcca | tcatgtcgct | ggtgatcctc | ctgcccttcg | ccatcgccat | 60  |
| ggagggggccc | aaggtgtggg | cggcgggctg | gcagacagca | gtcgccgaga | tcggtcccaa | 120 |
| cttcgtcttg  | tgggtggcgg | cgcagagcgt | gttctaccac | ctgtacaacc | aggtgtccta | 180 |
| catgtccctg  | gacgagatct | cgccgctcac | cttctccatc | ggcaacacca | tgaagcgcat | 240 |
| ctccgtcatc  | gtcgcgtcca | tcatcatctt | ccagacgccc | gtccagccca | tcaacgcgct | 300 |
| cggggccgcg  | atcgccatcc | tcggaacctt | catctactcc | caggccaagc | agtagccgcc | 360 |
| cttgscgcg   | cgtctggctc | tcaggcctca | gttcagttca | ccgccgaatc | agctcggcgc | 420 |
| tcgaagatat  | aacagattat | ataacttttt | gaggatatct | acctag     |            |     |

(2) INFORMATION FOR SEQ ID NO:2719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1504371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Arg | Leu | Pro | Leu | His | His | Val | Ala | Gly | Asp | Pro | Pro | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | His | Arg | His | Gly | Gly | Ala | Gln | Gly | Val | Gly | Gly | Gly | Leu | Ala | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Ser | Arg | Arg | Asp | Arg | Ser | Gln | Leu | Arg | Leu | Val | Gly | Gly | Gly | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Arg | Val | Leu | Pro | Pro | Val | Gln | Pro | Gly | Val | Leu | His | Val | Pro | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Asp | Leu | Ala | Ala | His | Leu | Leu | His | Arg | Gln | His | His | Glu | Ala | His |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Arg | His | Arg | Arg | Val | His | His | His | Leu | Pro | Asp | Ala | Arg | Pro | Ala |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Gln | Arg | Ala | Arg | Gly | Arg | His | Arg | His | Pro | Arg | Asn | Leu | His | Leu |
|     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Pro | Gly | Gln | Ala | Val | Ala | Ala | Leu | Xaa | Arg | Ala | Ser | Gly | Ser | Gln |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Ser | Val | Gln | Phe | Thr | Ala | Glu | Ser | Ala | Arg | Arg | Ser | Lys | Ile |     |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1504372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Ala | Cys | Leu | Ser | Ile | Met | Ser | Leu | Val | Ile | Leu | Leu | Pro | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Ala | Met | Glu | Gly | Pro | Lys | Val | Trp | Ala | Ala | Gly | Trp | Gln | Thr |
|     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Ala | Val | Ala | Glu | Ile | Gly | Pro | Asn | Phe | Val | Trp | Trp | Val | Ala | Ala | Gln |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser Leu Asp  
50 55 60  
Glu Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys Arg Ile  
65 70 75 80  
Ser Val Ile Val Ala Ser Ile Ile Ile Phe Gln Thr Pro Val Gln Pro  
85 90 95  
Ile Asn Ala Leu Gly Ala Ala Ile Ala Ile Leu Gly Thr Phe Ile Tyr  
100 105 110  
Ser Gln Ala Lys Gln  
115

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1504373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

Met Ser Leu Val Ile Leu Leu Pro Phe Ala Ile Ala Met Glu Gly Pro  
1 5 10 15  
Lys Val Trp Ala Ala Gly Trp Gln Thr Ala Val Ala Glu Ile Gly Pro  
20 25 30  
Asn Phe Val Trp Trp Val Ala Ala Gln Ser Val Phe Tyr His Leu Tyr  
35 40 45  
Asn Gln Val Ser Tyr Met Ser Leu Asp Glu Ile Ser Pro Leu Thr Phe  
50 55 60  
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ala Ser Ile  
65 70 75 80  
Ile Ile Phe Gln Thr Pro Val Gln Pro Ile Asn Ala Leu Gly Ala Ala  
85 90 95  
Ile Ala Ile Leu Gly Thr Phe Ile Tyr Ser Gln Ala Lys Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452

(D) OTHER INFORMATION: / Ceres Seq. ID 1504374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

ttagtgata tatgttatct ggggacaagg aaagtgctgc tatgaatgtg gcttcagttg 60  
tcggtatcca ggcagacaag gttcttgctg aagttaaacc acatgagaaa aagaagttca 120  
tatctgaact ccagaaagag cacaaggtag tcgccatggt tggtgacggc attaatgatg 180  
ccgcagcact agcttcagct gatgttggaa tcgcaatggg tggaggtgtt ggggcagcta 240  
gtgatgtatc ttcagttgta cttatgggca acaggttatc ccagcttatac gatgctttag 300  
agttgagtaa agagaccatg aagacgggtga agcaaaatct ttggtgggct ttcctgtata 360  
acattgttgg actaccatt gctgctggag cattgcttcc agctacgggg acgataactga 420  
caccatcaat agctggagct ctgatgggtt nt

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..149
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1504375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:

```
Ser Val Tyr Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val
1 5 10 15
Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys
20 25 30
Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys
35 40 45
Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala
50 55 60
Ser Ala Asp Val Gly Ile Ala Met Gly Gly Gly Val Gly Ala Ala Ser
65 70 75 80
Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile
85 90 95
Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn
100 105 110
Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala
115 120 125
Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala
130 135 140
Gly Ala Leu Met Gly
145
```

(2) INFORMATION FOR SEQ ID NO:2724:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..146
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1504376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

```
Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val Ala Ser Val
1 5 10 15
Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys Pro His Glu
20 25 30
Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys Val Val Ala
35 40 45
Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala Ser Ala Asp
50 55 60
Val Gly Ile Ala Met Gly Gly Gly Val Gly Ala Ala Ser Asp Val Ser
65 70 75 80
Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile Asp Ala Leu
85 90 95
Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn Leu Trp Trp
100 105 110
Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala Gly Ala Leu
115 120 125
Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala Gly Ala Leu
130 135 140
Met Gly
145
```

(2) INFORMATION FOR SEQ ID NO:2725:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504377  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:  
Met Asn Val Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala  
1 5 10 15  
Glu Val Lys Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys  
20 25 30  
Glu His Lys Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala  
35 40 45  
Ala Leu Ala Ser Ala Asp Val Gly Ile Ala Met Gly Gly Gly Val Gly  
50 55 60  
Ala Ala Ser Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser  
65 70 75 80  
Gln Leu Ile Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val  
85 90 95  
Lys Gln Asn Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro  
100 105 110  
Ile Ala Ala Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro  
115 120 125  
Ser Ile Ala Gly Ala Leu Met Gly  
130 135

(2) INFORMATION FOR SEQ ID NO:2726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..440  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| accacaccca cccacgaaa ccgtaagaag cgcagagtgt gagagagaga ggagcatcaa   | 60  |
| ggacgacgtg ggcaagatga tgcaggtgtt cgtgaagacg ctggcgggga agacgatcac  | 120 |
| gctggaggtg gagggcagcg acgacgccgt nagaacgtga aggccatgat ccagggcaag  | 180 |
| gaaggcatcc cgccggagga gcagcgccctc gtcttcgcgg gcaagcagct ggacgacgac | 240 |
| ggccgcaccc tggccgacta cggcgctccag aaggagtcca cgctgcacct ggagctgcgc | 300 |
| ctccgcggcg gcagcagggg cggctacccc atgggatccc gccagcctc cgcgagctcg   | 360 |
| cgcagaagta caacgagaac aagatggtct gccgcaagtg ctatgcgcgg cttccgccta  | 420 |
| gggcaaccaa ctgccgcaag                                              |     |

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..52  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:

Pro His Pro Pro His Glu Thr Val Arg Ser Ala Glu Cys Glu Arg Glu

1 5 10 15  
Arg Ser Ile Lys Asp Asp Val Gly Lys Met Met Gln Val Phe Val Lys  
20 25 30  
Thr Leu Ala Gly Lys Thr Ile Thr Leu Glu Val Glu Gly Ser Asp Asp  
35 40 45  
Ala Xaa Arg Thr  
50

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

Met Ile Gln Gly Lys Glu Gly Ile Pro Pro Glu Glu Gln Arg Leu Val  
1 5 10 15  
Phe Ala Gly Lys Gln Leu Asp Asp Asp Gly Arg Thr Leu Ala Asp Tyr  
20 25 30  
Gly Val Gln Lys Glu Ser Thr Leu His Leu Glu Leu Arg Leu Arg Gly  
35 40 45  
Gly Ser Arg Gly Gly Tyr Pro Met Gly Ser Arg Pro Ala Ser Ala Ser  
50 55 60  
Ser Arg Arg Ser Thr Thr Arg Thr Arg Trp Ser Ala Ala Ser Ala Met  
65 70 75 80  
Arg Gly Phe Arg Leu Gly Gln Pro Thr Ala Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

acatcgaggaa cgccgccgac gccgcagagg agacgcacag aggttagcac gccaagaagc 60  
gacctgagg gccaagtga agaagaagcg catnaggagg ctcaagagga akcgagaaa 120  
gatgaggcag agatccaagt aggcagatcg agatggattg tggacctgac tctcttcgtt 180  
atatgtacta cctccgttct tgaatatattt taaatatattg tcgttgctcgt cggt

(2) INFORMATION FOR SEQ ID NO:2730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

Thr Ser Gly Thr Pro Pro Thr Pro Gln Arg Arg Arg Ile Glu Val Ser  
1 5 10 15

Thr Arg Arg Ser Asp His Glu Gly Gln Val Glu Glu Glu Ala His Xaa  
20 25 30  
Glu Ala Gln Glu Glu Xaa Gln Lys Asp Glu Ala Glu Ile Gln Val Gly  
35 40 45  
Arg Ser Arg Trp Ile Val Asp Leu Thr Leu Phe Val Ile Cys Thr Thr  
50 55 60  
Ser Val Leu Glu Tyr Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:2731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

His Arg Glu Arg Arg Arg Arg Arg Gly Asp Ala Ser Arg Leu Ala  
1 5 10 15  
Arg Glu Glu Ala Thr Met Arg Ala Lys Trp Lys Lys Lys Arg Xaa Arg  
20 25 30  
Arg Leu Lys Arg Xaa Arg Arg Lys Met Arg Gln Arg Ser Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| cccagttgat  | gtgggttaagt | cgagaatgat  | gggtgactca | gcctacaaaa | gcactctcga | 60  |
| ttgttttgtg  | aagactctaa  | agaatgatgg  | ccctttggca | ttttacaaag | gcttcctgcc | 120 |
| aaactttgca  | agactgggat  | cttggaaatgt | gattatgttc | ttgacattgg | agcagggtca | 180 |
| aaagctgttt  | gtgaggaaag  | cgacaagctg  | aagatagagt | ttttgcagtc | aggtggcgta | 240 |
| caattgacgc  | acaggggttt  | tcttctatag  | acaaaagggg | agaaatgaca | cctccccctt | 300 |
| cgagaattgg  | ggaacaagga  | cagatctgac  | acctcaattg | cgagaaataa | aaataacagc | 360 |
| cgacagttgc  | atgatccctg  | aacgaataaa  | ttcagaacta | gaaacagatg | tcagtaaaca | 420 |
| acatgtgggtg | aatgttggaa  | cttgactgct  | ctagttcagt | gggcatctgt | tggt       |     |

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

Pro Val Asp Val Val Lys Ser Arg Met Met Gly Asp Ser Ala Tyr Lys  
1 5 10 15  
Ser Thr Leu Asp Cys Phe Val Lys Thr Leu Lys Asn Asp Gly Pro Leu

20 25 30  
Ala Phe Tyr Lys Gly Phe Leu Pro Asn Phe Ala Arg Leu Gly Ser Trp  
35 40 45  
Asn Val Ile Met Phe Leu Thr Leu Glu Gln Val Gln Lys Leu Phe Val  
50 55 60  
Arg Lys Ala Thr Ser  
65

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

Met Met Gly Asp Ser Ala Tyr Lys Ser Thr Leu Asp Cys Phe Val Lys  
1 5 10 15  
Thr Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr Lys Gly Phe Leu Pro  
20 25 30  
Asn Phe Ala Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu  
35 40 45  
Glu Gln Val Gln Lys Leu Phe Val Arg Lys Ala Thr Ser  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met Gly Asp Ser Ala Tyr Lys Ser Thr Leu Asp Cys Phe Val Lys Thr  
1 5 10 15  
Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr Lys Gly Phe Leu Pro Asn  
20 25 30  
Phe Ala Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu  
35 40 45  
Gln Val Gln Lys Leu Phe Val Arg Lys Ala Thr Ser  
50 55 60